

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 29, 2005, 04:49:33 ; Search time 3552 Seconds  
(without alignments)  
3819.668 Million cell updates/sec

Title: US-10-015-388a-54

Perfect score: 1432

Sequence: 1 MCFNKULLLAVLGWLFQIP.....LRAQGPFAARGERRGCSRA 280

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/cgn2.1/USPTO.spool\_P/US10015388/runat:28032005.130453.6142/app.query.fasta\_1.455  
-DB=GenEmbl -QWMT=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPCTL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500  
-DOCALLIGN=200 -THR SCORE=spt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10015388 @CGN 1.1.560 @runat:28032005.130453.6142 -NCPU=6 -ICPU=3  
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_hcg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_ats:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1432	100.0	3580	6	AX696985 Sequence
2	1432	100.0	3580	9	AY358467 Homo sapi
3	1432	100.0	4350	9	BC066640 Homo sapi
4	1432	100.0	4354	9	BC052568 Homo sapi

5	1432	100.0	4725	9	AF525398 Homo sapi
6	1424	99.4	3212	9	BC001092
7	1424	99.4	3212	9	BC008333 Homo sapi
8	1424	99.4	3212	9	BC008334 Homo sapi
9	934	65.2	129517	2	AC016400
10	934	65.2	148295	2	AC090510 Homo sapi
11	866	60.5	260033	2	AC099267
12	864	60.3	181602	10	AL935168
13	566.5	39.6	110000	2	AC106723_0
14	371.5	25.9	166294	2	BX537330
15	371.5	25.9	170138	5	BX569781
16	371.5	25.9	323764	2	BX569781
17	255	17.8	985	6	CQ729264
18	253.5	17.8	2151	5	BC081098
19	183.5	12.8	110000	2	AC106723_0
20	167.5	11.7	2192	3	AK174174
21	128	8.9	3904	6	CQ599307
22	128	8.9	3983	3	AY051770
23	128	8.9	4660	3	AF487678S2
24	128	8.9	7602	6	CQ599306
25	128	8.9	18737	6	CQ575162
26	128	8.9	30583	2	AC017314
27	128	8.9	171868	3	AC010118
28	128	8.9	257867	3	AC005557
29	128	8.9	303191	3	AE003472
30	127	8.9	4661	3	AF487678S2
31	116	8.1	223547	2	AC098514
32	114.5	8.0	177744	2	AC073954
33	113.5	7.9	92785	10	CNS07YOV
34	113.5	7.9	101777	9	AC105210
35	113.5	7.9	164959	9	AC087823
36	113.5	7.9	174906	9	AC067930
37	113.5	7.9	181075	10	CNS07YBP2
38	113.5	7.9	190784	10	AL645797
39	112	7.8	2760	10	MUSTWISTG
40	112	7.8	11894	1	AE012256
41	112	7.8	198423	2	AC148253
42	112	7.8	207636	2	AC019122
43	112	7.8	348942	1	BX572596
44	111.5	7.8	1104	6	AX663882
45	111.5	7.8	110000	1	AE000516_24
46	111.5	7.8	110000	1	AE016822_11
47	111.5	7.8	196140	2	AC084107
48	111.5	7.8	212370	10	AC122334
49	111.5	7.8	213308	2	AC079164
50	111.5	7.8	306050	1	BX248341
51	111.5	7.8	348247	1	BX842579
52	111	7.8	321250	1	SC093911
53	110.5	7.7	562	11	BV104927
54	110.5	7.7	110000	1	AE000516_26
55	110.5	7.7	232605	1	AE017222
56	110.5	7.7	233835	2	AC132778
57	110.5	7.7	306550	1	BX248342
58	110	7.7	1362	1	AY029247
59	110	7.7	4693	8	AB073881
60	110	7.7	114085	9	AC093734
61	110	7.7	307551	1	AP003015
62	109.5	7.6	34503	2	AC151612
63	109.5	7.6	139962	14	AY386264
64	109	7.6	1362	1	AY029240
65	109	7.6	1362	1	AY029244
66	109	7.6	1362	1	AY029249
67	109	7.6	1712	6	I34703
68	109	7.6	2351	1	PSEEXOS
69	109	7.6	300425	1	AP005038
70	108.5	7.6	1457	6	AX331540
71	108.5	7.6	1457	9	HSBHLH
72	108.5	7.6	39474	3	AC016024
73	108	7.5	76513	8	AE016820_14
74	108	7.5	179447	2	AC060806
75	108	7.5	180846	2	AC145151
76	108	7.5	187235	2	AC113428
77	108	7.5	223984	2	AC097915





224	100	7.0	155525	8	AC130597	AC130597 Oryza sat	297	98	6.8	3262	8	AK072348	AK072348 Oryza sat
225	100	7.0	226013	2	AC073680	AC073680 Mus muscu	298	98	6.8	4722	9	HSA576290	HSA576290 Homo sapi
226	100	7.0	298700	1	AP005951	AP005951 Bradyrhiz	299	98	6.8	6390	1	D85027	D85027 Thermus sp.
227	100	7.0	300425	1	AP005022	AP005022 Streptomy	300	98	6.8	10663	1	AE002084	AE002084 Deinococc
228	99.5	6.9	1362	1	AY029252	AY029252 Pseudomon	301	98	6.8	10871	1	AE004643	AE004643 Pseudomon
229	99.5	6.9	1777	8	AK066539	AK066539 Oryza sat	302	98	6.8	14542	1	AF056246	AF056246 Xanthomon
230	98.5	6.9	1800	6	AR560758	AR560758 Sequence	303	98	6.8	45603	1	AY196994	AY196994 Streptomy
231	99.5	6.9	2232	9	BC015152	BC015152 Homo sapi	304	98	6.8	110000	1	AE000516_06	AE000516_06 Continuation (3 of
232	99.5	6.9	2246	9	BC038111	BC038111 Homo sapi	305	98	6.8	110000	1	AE000516_05	AE000516_05 Continuation (6 of
233	99.5	6.9	2870	9	HSTW1STGN	X91662 H. sapiens t	306	98	6.8	110000	2	AP006498_5	AP006498_5 Continuation (6 of
234	99.5	6.9	3994	1	AF016221	AF016221 Xanthomon	307	98	6.8	118339	8	AP003962	AP003962 Oryza sat
235	99.5	6.9	8595	1	ABNTRSG	Z37984 Azospirillum	308	98	6.8	123721	2	OSJN01008	OSJN01008 Oryza sat
236	98.5	6.9	12411	1	AE004659	AE004659 Pseudomon	309	98	6.8	143341	5	EX088595	EX088595 Zebraphis
237	99.5	6.9	16702	9	HSTW1STGE	Y10871 H. sapiens t	310	98	6.8	147821	9	AP0104241	AP0104241 Homo sapi
238	99.5	6.9	115003	9	AC073111	AC073111 Homo sapi	311	98	6.8	148947	8	AP004397	AP004397 Oryza sat
239	99.5	6.9	116603	2	AL157901	AL157901 Homo sapi	312	98	6.8	151498	9	AC027139	AC027139 Homo sapi
240	99.5	6.9	135810	9	AC023392	AC023392 Homo sapi	313	98	6.8	171279	2	AC022183	AC022183 Homo sapi
241	99.5	6.9	174593	10	AL807828	AL807828 Mouse DNA	314	98	6.8	173379	9	AP002360	AP002360 Homo sapi
242	98.5	6.9	175120	9	AC004687	AC004687 Homo sapi	315	98	6.8	175762	5	AL772332	AL772332 Zebraphis
243	99.5	6.9	313846	1	AE017234	AE017234 Mycobacte	316	98	6.8	176756	2	AC148734	AC148734 Callithri
244	99	6.9	1362	1	AY029242	AY029242 Pseudomon	317	98	6.8	177852	2	CR385028	CR385028 Danio rer
245	99	6.9	2154	10	BC026486	BC026486 Mus muscu	318	98	6.8	179816	2	AC074188	AC074188 Homo sapi
246	99	6.9	8634	3	AY528743	AY528743 Trypanoso	319	98	6.8	181331	2	CR376771	CR376771 Danio rer
247	99	6.9	138390	14	AY261359	AY261359 Bovine he	320	98	6.8	197192	2	AC148637	AC148637 Callithri
248	99	6.9	153013	2	AC122150	AC122150 Danio rer	321	98	6.8	221953	2	EX928743	EX928743 Danio rer
249	99	6.9	210220	2	AC127868	AC127868 Rattus no	322	98	6.8	244683	2	CR392363	CR392363 Danio rer
250	99	6.9	211330	10	AL646088	AL646088 Mouse DNA	323	98	6.8	276289	1	AE017306	AE017306 Thermus t
251	99	6.9	244478	2	AC130167	AC130167 Rattus no	324	98	6.8	276800	1	SC0939115	SC0939115 Streptomy
252	99	6.9	301950	1	AP006570	AP006570 Gloeobact	325	98	6.8	281450	1	AP005032	AP005032 Streptomy
253	99	6.9	305520	1	AE016780	AE016780 Pseudomon	326	98	6.8	300450	1	AP005960	AP005960 Bradyrhiz
254	99	6.9	349116	1	AP003003	AP003003 Mesorhizo	327	98	6.8	320050	1	EX248336	EX248336 Mycobacte
255	98.5	6.9	1362	1	AY029243	AY029243 Pseudomon	328	98	6.8	333550	2	AC113256	AC113256 Rattus no
256	98.5	6.9	1565	9	AF265210	AF265210 Homo sapi	329	98	6.8	343320	2	AC113256	AC113256 Rattus no
257	98.5	6.9	2362	9	BC046359	BC046359 Homo sapi	330	98	6.8	348624	1	EX640441	EX640441 Bordetell
258	98.5	6.9	2572	9	BC046359	BC046359 Homo sapi	331	98	6.8	348624	1	EX640441	EX640441 Bordetell
259	98.5	6.9	10429	1	AE004875	AE004875 Pseudomon	332	98	6.8	348624	1	EX640441	EX640441 Bordetell
260	98.5	6.9	12272	1	AE005898	AE005898 Caulobact	333	97.5	6.8	6927	1	AF319543	AF319543 Streptomy
261	98.5	6.9	11593	1	AE011883	AE011883 Xanthomon	334	97.5	6.8	11224	6	BD217186	BD217186 DNA encod
262	98.5	6.9	12022	1	AE012146	AE012146 Xanthomon	335	97.5	6.8	11224	6	BD217186	BD217186 DNA encod
263	98.5	6.9	12271	1	AE011862	AE011862 Xanthomon	336	97.5	6.8	12460	1	AE004903	AE004903 Pseudomon
264	98.5	6.9	13257	1	AE014648	AE014648 Bifidobac	337	97.5	6.8	14815	1	AF331073	AF331073 Amycolato
265	98.5	6.9	20328	2	AC014603	AC014603 Drosophil	338	97.5	6.8	37948	1	AF079138	AF079138 Streptomy
266	98.5	6.9	23786	9	HSA45C1	Z98272 Human DNA s	339	97.5	6.8	37948	6	BD217173	BD217173 DNA encod
267	98.5	6.9	35512	3	AC092774	AC092774 Leishmani	340	97.5	6.8	38506	6	BD232534	BD232534 Recombina
268	98.5	6.9	39170	9	AC005202	AC005202 Homo sapi	341	97.5	6.8	38506	6	AR271680	AR271680 Sequence
269	98.5	6.9	90104	6	C0588086	C0588086 Sequence	342	97.5	6.8	38506	6	AR271680	AR271680 Sequence
270	98.5	6.9	92750	2	AC121230	AC121230 Leishmani	343	97.5	6.8	128136	1	AF440524	AF440524 Pseudomon
271	98.5	6.9	124629	8	OSJN00062	AL606618 Oryza sat	344	97.5	6.8	128136	1	AF440524	AF440524 Pseudomon
272	98.5	6.9	128809	2	AC105931	AL663067 Mouse DNA	345	97.5	6.8	147764	2	AC138461	AC138461 Homo sapi
273	98.5	6.9	129043	9	CNS01D7D	AL162591 Human DNA	346	97.5	6.8	154673	2	EX927192	EX927192 Danio rer
274	98.5	6.9	133069	2	AC026836	AL132712 Human chr	347	97.5	6.8	173913	2	AC139181	AC139181 Pan trogl
275	98.5	6.9	138203	8	AP005528	AC026836 Homo sapi	348	97.5	6.8	174777	9	AC136616	AC136616 Homo sapi
276	98.5	6.9	158241	3	AC115483	AP005528 Oryza sat	349	97.5	6.8	174930	9	AC145889	AC145889 Pan trogl
277	98.5	6.9	190948	8	AP005529	AC115483 Drosophil	350	97.5	6.8	160907	8	AC120990	AC120990 Oryza sat
278	98.5	6.9	201167	10	AL663067	AP005529 Oryza sat	351	97.5	6.8	162041	2	AC137797	AC137797 Homo sapi
279	98.5	6.9	201167	9	AL162591	AL663067 Mouse DNA	352	97.5	6.8	170914	2	CR450729	CR450729 Danio rer
280	98.5	6.9	206685	2	AC147592	AL162591 Human DNA	353	97.5	6.8	173913	2	AC139181	AC139181 Pan trogl
281	98.5	6.9	260418	9	AE006463	AC147592 Bos tauru	354	97.5	6.8	174777	9	AC136616	AC136616 Homo sapi
282	98.5	6.9	264401	3	AE003640	AE006463 Homo sapi	355	97.5	6.8	175691	9	AC136440	AC136440 Homo sapi
283	98.5	6.9	299050	1	SC0939104	AE003640 Drosophil	356	97.5	6.8	175691	9	AC136440	AC136440 Homo sapi
284	98.5	6.9	299800	1	AP005028	AL339104 Streptomy	357	97.5	6.8	177565	8	AC092388	AC092388 Oryza sat
285	98.5	6.9	303885	1	DR0SADH01	AP005028 Streptomy	358	97.5	6.8	178037	9	AC095043	AC095043 Homo sapi
286	98.5	6.9	308050	3	DR0SADH01	AE003407 Drosophil	359	97.5	6.8	179013	9	AC022370	AC022370 Homo sapi
287	98.5	6.9	348866	1	EX640426	EX640426 Mouse DNA	360	97.5	6.8	181432	9	EX649480	EX649480 Human DNA
288	98.5	6.9	349880	6	AX492782	EX640426 Bordetell	361	97.5	6.8	187731	10	AC140307	AC140307 Mus muscu
289	98.5	6.9	349880	6	AX553949	AX492782 Sequence	362	97.5	6.8	187891	2	AC140903	AC140903 Homo sapi
290	98	6.8	1493	6	CQ776406	AX553949 Sequence	363	97.5	6.8	194508	2	AC145316	AC145316 Homo sapi
291	98	6.8	1493	6	AX052732	CQ776406 Sequence	364	97.5	6.8	203413	2	CR394546	CR394546 Danio rer
292	98	6.8	1493	6	AX557300	AX052732 Sequence	365	97.5	6.8	204649	8	AC120986	AC120986 Oryza sat
293	98	6.8	1493	6	HUMA2MGRAP	AX557300 Sequence	366	97.5	6.8	214025	9	AC007882	AC007882 Homo sapi
294	98	6.8	1917	9	BC034287	M63959 Human alpha	367	97.5	6.8	214110	9	AC007908	AC007908 Homo sapi
295	98	6.8	2192	10	MMY15742	BC034287 Homo sapi	368	97.5	6.8	215050	1	AL646084	AL646084 Ralstonia
296	98	6.8	2934	6	AX654505	Y15742 Mus musculu	369	97.5	6.8	218758	10	AC131712	AC131712 Mus muscu
						AX654505 Sequence							AC133536

370	97.5	6.8	246941	2	AC145215	AC145215 Homo sapi	443	96.5	6.7	110000	1	AE017283_19	Continuation (20 o
371	97.5	6.8	254633	2	CR762389	CR762389 Danio rer	444	96.5	6.7	110000	1	BS571965_05	Continuation (6 of
C 372	97.5	6.8	256584	2	AC133754	AC133754 Rattus no	C 445	96.5	6.7	110000	1	BS571966_27	Continuation (28 o
373	97.5	6.8	271708	2	AC094667	AC094667 Rattus no	C 446	96.5	6.7	112467	9	HS050513	Z98052 Human DNA s
374	97.5	6.8	298550	2	AC094667	AC094667 Rattus no	C 447	96.5	6.7	136367	9	AC098874	AC098874 Homo sapi
C 375	97.5	6.8	298550	1	AP005029	AP005029 Streptomy	C 448	96.5	6.7	154218	9	AC020663	AC020663 Homo sapi
376	97.5	6.8	300425	1	AP005037	AP005037 Streptomy	C 449	96.5	6.7	155749	2	AC135345	AC135345 Homo sapi
C 377	97.5	6.8	300425	8	AE017090	AE017090 Oryza sat	C 450	96.5	6.7	160842	2	AC124090	AC124090 Homo sapi
C 378	97.5	6.8	300774	1	AE016912	AE016912 Chromobac	C 451	96.5	6.7	177574	9	AC124086	AC124086 Homo sapi
C 379	97.5	6.8	309050	1	SC0939117	AE0939117 Streptomy	C 452	96.5	6.7	177613	9	AC124089	AC124089 Homo sapi
380	97	6.8	1499	6	BD134425	BD134425 Human nuc	C 453	96.5	6.7	184695	2	AC145147	AC145147 Homo sapi
381	97	6.8	1499	6	AX524958	AX524958 Sequence	C 454	96.5	6.7	188766	9	AC135329	AC135329 Homo sapi
382	97	6.8	1519	6	HS0480130	HS0480130 Sequence	C 455	96.5	6.7	190289	14	MC060315	U60315 Molluscum c
C 383	97	6.8	2898	1	AE095676	AE095676 Xanthomon	C 456	96.5	6.7	194490	9	AC140899	AC140899 Homo sapi
C 384	97	6.8	3120	9	HS058917	HS058917 Homo sapien	C 457	96.5	6.7	195397	2	AC135718	AC135718 Homo sapi
C 385	97	6.8	3223	6	AR034066	AR034066 Sequence	C 458	96.5	6.7	205191	2	AC138807	AC138807 Homo sapi
C 386	97	6.8	3223	6	AR097656	AR097656 Sequence	C 459	96.5	6.7	205191	2	AC142537	AC142537 Homo sapi
C 387	97	6.8	3223	6	AR097733	AR097733 Sequence	C 460	96.5	6.7	234228	2	AC145314	AC145314 Homo sapi
C 388	97	6.8	3223	6	AR102359	AR102359 Sequence	C 461	96.5	6.7	234228	2	AC15852	AC15852 Rattus no
C 389	97	6.8	3223	6	ARI04870	ARI04870 Sequence	C 462	96.5	6.7	304282	1	AE016910	AE016910 Chromobac
C 390	97	6.8	3223	6	ARI131081	ARI131081 Sequence	C 463	96.5	6.7	349260	1	BS572595	BS572595 Rhodospheu
C 391	97	6.8	3223	6	ARI37603	ARI37603 Sequence	C 464	96.5	6.7	349260	1	BS569690	BS569690 Synetochoc
C 392	97	6.8	3223	6	AR453137	AR453137 Sequence	C 465	96.5	6.7	349652	1	BS569690	BS569690 Synetochoc
C 393	97	6.8	3223	6	BD023246	BD023246 Method fo	C 466	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 394	97	6.8	3223	6	BC011624	BC011624 Homo sapi	C 467	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 395	97	6.8	3223	9	BC011624	BC011624 Homo sapi	C 468	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 396	97	6.8	7291	12	ASPSVPFAZI	Y07573 psvpaz1 pl	C 469	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 397	97	6.8	7294	12	ASPSVPFAZI	Y07573 psvpaz1 pl	C 470	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 398	97	6.8	7294	12	ASPSVPFAZI	Y07573 psvpaz1 pl	C 471	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 399	97	6.8	7438	6	AX816382	AX816382 Sequence	C 472	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 400	97	6.8	7573	6	AX114870	AX114870 Sequence	C 473	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 401	97	6.8	7573	6	AX114870	AX114870 Sequence	C 474	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 402	97	6.8	10000	1	AE012335	AE012335 Xanthomon	C 475	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 403	97	6.8	10811	1	AE012335	AE012335 Xanthomon	C 476	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 404	97	6.8	11196	1	AE012055	AE012055 Xanthomon	C 477	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 405	97	6.8	11461	1	AE007275	AE007275 Sinorhizo	C 478	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 406	97	6.8	15719	4	BT416457	BT416457 Bos tauru	C 479	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 407	97	6.8	37106	1	AY228335	AY228335 Xanthomon	C 480	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 408	97	6.8	37186	1	MSGV244	MSGV244 Mycobacte	C 481	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 409	97	6.8	63882	7	AY349011	AY349011 Burkholde	C 482	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 410	97	6.8	110000	1	AE000516_02	Continuation (3 of	C 483	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 411	97	6.8	110000	1	AE000516_31	Continuation (32 o	C 484	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 412	97	6.8	110000	1	BS571965_37	Continuation (28 o	C 485	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 413	97	6.8	110000	1	CP000010_27	Continuation (29 o	C 486	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 414	97	6.8	110000	8	AE016816_5	Continuation (6 of	C 487	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 415	97	6.8	117612	10	AL591366	AL591366 Mouse DNA	C 488	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 416	97	6.8	138580	2	CR388100	CR388100 Danio rer	C 489	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 417	97	6.8	148301	2	CR384049	CR384049 Danio rer	C 490	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 418	97	6.8	185925	5	AL954176	AL954176 Zebrafish	C 491	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 419	97	6.8	193159	9	AC006946	AC006946 Homo sapi	C 492	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 420	97	6.8	194641	10	AC132462	AC132462 Mus muscu	C 493	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 421	97	6.8	213184	2	CR749750	CR749750 Danio rer	C 494	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 422	97	6.8	228327	5	AL844514	AL844514 Zebrafish	C 495	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 423	97	6.8	229800	1	AP005028	AP005028 Streptomy	C 496	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 424	97	6.8	301443	1	AE017239	AE017239 Mycobacte	C 497	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 425	97	6.8	313800	1	SC0939114	SC0939114 Streptomy	C 498	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 426	97	6.8	318050	1	EX248344	EX248344 Mycobacte	C 499	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 427	97	6.8	31957	1	EX842572	EX842572 Mycobacte	C 500	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 428	97	6.8	343050	1	EX248334	EX248334 Mycobacte	C 501	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 429	97	6.8	34805	1	EX640434	EX640434 Bordetell	C 502	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 430	97	6.8	346287	1	EX640434	EX640434 Bordetell	C 503	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 431	97	6.8	347894	1	EX640431	EX640431 Mycobacte	C 504	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 432	97	6.8	348676	1	EX842581	EX842581 Mycobacte	C 505	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 433	96.5	6.7	969	6	AE060905	AE060905 Sequence	C 506	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 434	96.5	6.7	1362	1	AY029248	AY029248 Pseudomon	C 507	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 435	96.5	6.7	3278	6	AX714327	AX714327 Sequence	C 508	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 436	96.5	6.7	3278	14	MOCDNRAP	MOCDNRAP Molluscum c	C 509	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 437	96.5	6.7	6709	9	AE004710	AE004710 Pseudomon	C 510	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 438	96.5	6.7	11873	9	D78345	D78345 Human DNA f	C 511	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 439	96.5	6.7	21013	9	D78345	D78345 Human DNA f	C 512	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 440	96.5	6.7	52797	1	AE068845	AE068845 Mycobacte	C 513	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 441	96.5	6.7	64920	1	AE008925	AE008925 Xanthomon	C 514	96	6.7	349652	1	BS569690	BS569690 Synetochoc
C 442	96.5	6.7	101043	9	AE010539	AE010539 Homo sapi	C 515	96	6.7	349652	1	BS569690	BS569690 Synetochoc



C 662	94.5	6.6 190665	5	EX470086	735	94	6.6 222726	9	AC135069	AC135069 Homo sapi
C 663	94.5	6.6 191356	9	AC005041	C 736	94	6.6 230525	5	BX784028	BX784028 Zebrafish
C 664	94.5	6.6 202844	2	AC110211	C 737	94	6.6 231545	2	BX914198	BX914198 Danio rer
C 665	94.5	6.6 207281	2	CR847891	C 738	94	6.6 240094	2	AC118491	AC118491 Rattus no
C 666	94.5	6.6 234541	2	AC094891	C 739	94	6.6 243836	2	AC116094	AC116094 Rattus no
C 667	94.5	6.6 236223	2	AC121220	C 740	94	6.6 244957	2	BX950211	BX950211 Danio rer
C 668	94.5	6.6 241836	10	AC019302	C 741	94	6.6 260198	2	AC099138	AC099138 Rattus no
C 669	94.5	6.6 252513	2	AC098926	C 742	94	6.6 266132	2	AC099138	AC099138 Rattus no
C 670	94.5	6.6 256759	2	AC126002	C 743	94	6.6 268374	2	AC118769	AC118769 Streptomy
C 671	94.5	6.6 289102	1	SC0939119	C 744	94	6.6 299800	1	AP005040	AP005040 Streptomy
C 672	94.5	6.6 299050	1	AC128976	C 745	94	6.6 300349	1	AE017319	AE017319 Desulfov
C 673	94.5	6.6 300350	2	AC096574	C 746	94	6.6 300880	1	AE016917	AE016917 Chromobac
C 674	94.5	6.6 300491	2	AC094205	C 747	94	6.6 300880	1	AE016917	AE016917 Chromobac
C 675	94.5	6.6 300600	1	AP005369	C 748	94	6.6 306650	2	AC026340	AC026340 Homo sapi
C 676	94.5	6.6 300900	1	AP005939	C 749	94	6.6 309805	2	AC026340	AC026340 Homo sapi
C 677	94.5	6.6 302178	1	AE016918	C 750	94	6.6 310967	1	AE016869	AE016869 Pseudomon
C 678	94.5	6.6 303550	1	SC0939131	C 751	94	6.6 313846	1	AE017234	AE017234 Mycobacte
C 679	94.5	6.6 325483	1	AP005050	C 752	94	6.6 345012	1	BX572607	BX572607 Rhodopseu
C 680	94.5	6.6 326050	1	EX321864	C 753	94	6.6 345012	1	BX572607	BX572607 Rhodopseu
C 681	94	6.6 612	9	SO848164	C 754	94	6.5 2313	6	CQ735404	CQ735404 Sequence
C 682	94	6.6 1901	10	RNO113845	C 755	94	6.5 2319	9	HSM805518	HSM805518 Homo sapi
C 683	94	6.6 2130	1	AY299348	C 756	94	6.5 2396	8	AK070971	AK070971 Oryza sat
C 684	94	6.6 2158	9	AK096934	C 757	94	6.5 3542	6	AR338742	AR338742 Sequence
C 685	94	6.6 2444	8	ENU74303	C 758	94	6.5 4632	6	AK090482	AK090482 Homo sapi
C 686	94	6.6 2763	6	AX653205	C 759	94	6.5 4808	3	BT009943	BT009943 Drosophil
C 687	94	6.6 4700	10	BC068231	C 760	94	6.5 5468	6	CQ588087	CQ588087 Sequence
C 688	94	6.6 9316	1	AF077869	C 761	94	6.5 5630	3	DMU60591	DMU60591 Drosophila
C 689	94	6.6 10602	1	AE004874	C 762	94	6.5 5630	3	AR130851	AR130851 Sequence
C 690	94	6.6 11733	1	AE012393	C 763	94	6.5 5630	6	AR178592	AR178592 Sequence
C 691	94	6.6 12842	1	AE005742	C 764	94	6.5 5635	6	AR211708	AR211708 Sequence
C 692	94	6.6 15497	1	AF134348	C 765	94	6.5 5688	1	AF145039	AF145039 Streptomy
C 693	94	6.6 18366	1	AF299295	C 766	94	6.5 7000	8	SPBC115	SPBC115 Amycolatops
C 694	94	6.6 18767	3	LMFL5649	C 767	94	6.5 10772	1	AE011659	AE011659 Xanthomon
C 695	94	6.6 45998	9	HSU81031	C 768	94	6.5 11352	1	AE005855	AE005855 Caulobact
C 696	94	6.6 58343	1	AB080954	C 769	94	6.5 15724	1	AE004522	AE004522 Pseudomon
C 697	94	6.6 73511	2	HS65A6	C 770	94	6.5 25336	1	MSG3367	MSG3367 Mycobacte
C 698	94	6.6 91395	2	AC150974	C 771	94	6.5 47981	1	AF263245	AF263245 Micromono
C 699	94	6.6 110000	1	AE016822	C 772	94	6.5 47981	6	AX112026	AX112026 Sequence
C 700	94	6.6 110000	2	LMFLCHR31_17	C 773	94	6.5 49838	9	HS387822	HS387822 Human DNA
C 701	94	6.6 110000	2	LMFLCHR31_18	C 774	94	6.5 66788	6	CQ363727	CQ363727 Sequence
C 702	94	6.6 110000	2	LMFLCHR31_09	C 775	94	6.5 77314	9	AC024884	AC024884 Homo sapi
C 703	94	6.6 119199	2	AP003812	C 776	94	6.5 103837	1	AE000516	AE000516 Saccharo
C 704	94	6.6 123160	9	AL353719	C 777	94	6.5 108584	2	AC096833	AC096833 Continuation (8 of
C 705	94	6.6 123828	9	AP000353	C 778	94	6.5 109349	2	AC096833	AC096833 Continuation (11 of
C 706	94	6.6 138780	8	AP004344	C 779	94	6.5 110000	1	AP006618	AP006618 Burkholde
C 707	94	6.6 158810	8	AP006286	C 780	94	6.5 110000	1	BX571965	BX571965 Rattus no
C 708	94	6.6 159174	5	BX005385	C 781	94	6.5 110000	8	CP000010	CP000010 Continuation (4 of
C 709	94	6.6 160848	2	AC009647	C 782	94	6.5 110603	9	HSJ421D16	HSJ421D16 Human DNA
C 710	94	6.6 160892	2	CR381637	C 783	94	6.5 118183	8	AC090433	AC090433 Chlamydom
C 711	94	6.6 161803	9	AC021028	C 784	94	6.5 133765	9	HS675E13	HS675E13 Homo sapi
C 712	94	6.6 163194	3	LMFP214	C 785	94	6.5 156820	9	AC074323	AC074323 Chlamydom
C 713	94	6.6 163698	10	AC115876	C 786	94	6.5 168794	8	AC087726	AC087726 Chlamydom
C 714	94	6.6 170891	2	AC102118	C 787	94	6.5 174372	2	AC119136	AC119136 Rattus no
C 715	94	6.6 170893	2	AC122297	C 788	94	6.5 174852	2	AC1010195	AC1010195 Homo sapi
C 716	94	6.6 171266	2	BX323586	C 789	94	6.5 184222	9	HSJ421D16	HSJ421D16 Human DNA
C 717	94	6.6 178754	2	AC120264	C 790	94	6.5 184222	9	HSJ421D16	HSJ421D16 Human DNA
C 718	94	6.6 181157	10	AC121789	C 791	94	6.5 184474	9	AL137026	AL137026 Human DNA
C 719	94	6.6 182760	2	AC120395	C 792	94	6.5 214125	10	AC083948	AC083948 Mus muscu
C 720	94	6.6 185897	2	AC145188	C 793	94	6.5 244800	1	BX842584	BX842584 Mycobacte
C 721	94	6.6 187005	10	AC124470	C 794	94	6.5 265302	2	AC097895	AC097895 Rattus no
C 722	94	6.6 193277	10	AC104324	C 795	94	6.5 278492	1	BX248347	BX248347 Mycobacte
C 723	94	6.6 193394	2	CR388077	C 796	94	6.5 293050	1	SC0939116	SC0939116 Streptomy
C 724	94	6.6 194763	2	AC150852	C 797	94	6.5 298550	1	AP005029	AP005029 Streptomy
C 725	94	6.6 195129	10	AL627069	C 798	94	6.5 299650	1	AE017240	AE017240 Mycobacte
C 726	94	6.6 202103	2	CR848044	C 799	94	6.5 299986	1	AE017240	AE017240 Mycobacte
C 727	94	6.6 205642	9	AC016586	C 800	94	6.5 300800	1	AP005036	AP005036 Pseudomon
C 728	94	6.6 207454	2	AL129934	C 801	94	6.5 301708	1	AE016792	AE016792 Streptomy
C 729	94	6.6 210971	5	AL954188	C 802	94	6.5 302998	1	AE016921	AE016921 Chromobac
C 730	94	6.6 211544	9	AC025165	C 803	94	6.5 303050	1	BX321860	BX321860 Nitrosomo
C 731	94	6.6 213591	2	AC141759	C 804	94	6.5 324050	1	BX248335	BX248335 Mycobacte
C 732	94	6.6 214485	2	AC123416	C 805	94	6.5 347894	1	BX640431	BX640431 Bordetell
C 733	94	6.6 216844	2	AC130788	C 806	94	6.5 348997	1	BX572600	BX572600 Rhodopseu
C 734	94	6.6 217026	2	CR396592	C 807	94	6.5 349640	1	BX572600	BX572600 Rhodopseu

C 808	93	6.5	1024	3	CFCRP10	X13489 Crithidia f	C 881	93	6.5	265382	2	AC114439	AC114439 Rattus no
C 809	93	6.5	1419	9	BC016028	BC016028 Homo sapi	C 882	93	6.5	268510	2	AC095840	AC095840 Rattus no
C 810	93	6.5	1443	4	AF157019	AF157019 Bos tauru	C 883	93	6.5	298900	1	AP005937	AP005937 Bradyrhiz
C 811	93	6.5	1683	1	AX337497	AX337497 Myxococcu	C 884	93	6.5	299991	1	AE016776	AE016776 Pseudomon
C 812	93	6.5	1748	6	AX058217	AX058217 Sequence	C 885	93	6.5	300425	1	AP005038	AP005038 Pseudomon
C 813	93	6.5	2217	6	CQ720538	CQ720538 Sequence	C 886	93	6.5	301457	1	AE016924	AE016924 Chronobac
C 814	93	6.5	3554	6	CQ843120	CQ843120 Sequence	C 887	93	6.5	303855	1	AE017230	AE017230 Mycobacte
C 815	93	6.5	3554	9	AK126087	AK126087 Homo sapi	C 888	93	6.5	310029	1	AE016868	AE016868 Pseudomon
C 816	93	6.5	3573	6	CQ724709	CQ724709 Sequence	C 889	93	6.5	347950	1	AP003013	AP003013 Mesorhizo
C 817	93	6.5	3627	9	HS4576305	HS4576305 Homo sapi	C 890	93	6.5	348171	1	BE640412	BE640412 Bordetell
C 818	93	6.5	4027	1	AE021363	AE021363 Xanthomon	C 891	93	6.5	348525	1	BE640428	BE640428 Bordetell
C 819	93	6.5	4184	9	HS4576307	HS4576307 Homo sapi	C 892	92.5	6.5	978	10	MMU18658	U18658 Mus muscu
C 820	93	6.5	4275	1	XCU28802	U28802 Xanthomonas	C 893	92.5	6.5	1208	4	AF526394	AF526394 Sus scrofa
C 821	93	6.5	8851	1	AY124589	AY124589 Agriomyces	C 894	92.5	6.5	1310	10	AF099020	AF099020 Mus muscu
C 822	93	6.5	9316	1	AF077869	AF077869 Streptomy	C 895	92.5	6.5	2625	8	AK069218	AK069218 Oryza sat
C 823	93	6.5	10381	1	AE012495	AE012495 Xanthomon	C 896	92.5	6.5	2948	10	BC034126	BC034126 Mus muscu
C 824	93	6.5	11320	1	AE012110	AE012110 Xanthomon	C 897	92.5	6.5	3030	6	AR220782	AR220782 Sequence
C 825	93	6.5	11427	1	AE004931	AE004931 Pseudomon	C 898	92.5	6.5	3040	8	AK110154	AK110154 Oryza sat
C 826	93	6.5	12933	1	AE005985	AE005985 Caulobact	C 899	92.5	6.5	3169	8	AK110093	AK110093 Oryza sat
C 827	93	6.5	13068	6	CQ790429	CQ790429 Sequence	C 900	92.5	6.5	3420	9	HS0804095	AL832784 Homo sapi
C 828	93	6.5	13668	1	AE004907	AE004907 Pseudomon	C 901	92.5	6.5	3492	9	BC042651	BC042651 Homo sapi
C 829	93	6.5	14939	1	AE005092	AE005092 Halobacte	C 902	92.5	6.5	3498	9	BC004270	BC004270 Homo sapi
C 830	93	6.5	15081	6	CQ790448	CQ790448 Sequence	C 903	92.5	6.5	3498	9	BC007203	BC007203 Homo sapi
C 831	93	6.5	17553	6	CQ790449	CQ790449 Sequence	C 904	92.5	6.5	3751	9	AK000363	AK000363 Homo sapi
C 832	93	6.5	32776	3	LMFL8342	AL122012 Leishmani	C 905	92.5	6.5	4000	1	XCAVIR	X68781 X.campestri
C 833	93	6.5	35197	9	AC005782	AC005782 Homo sapi	C 906	92.5	6.5	4394	1	HPU80806	U80806 Hydrogenoph
C 834	93	6.5	52754	6	AX695689	AX695689 Sequence	C 907	92.5	6.5	4408	6	CQ850342	CQ850342 Sequence
C 835	93	6.5	88421	6	AX417445	AX417445 Sequence	C 908	92.5	6.5	4408	9	AK127465	AK127465 Homo sapi
C 836	93	6.5	105828	1	AP005965	AP005965 Bradyrhiz	C 909	92.5	6.5	4504	9	AK074115	AK074115 Homo sapi
C 837	93	6.5	108424	10	AL669827	AL669827 Mouse DNA	C 910	92.5	6.5	4663	10	BC053081	BC053081 Mus muscu
C 838	93	6.5	110000	1	AE016822_06	Continuation (7 of	C 911	92.5	6.5	5364	1	SGKSACPG	X77865 S.grievus g
C 839	93	6.5	110000	1	AE017282_17	Continuation (18 o	C 912	92.5	6.5	5749	8	AF490339	AF490339 Phytophth
C 840	93	6.5	110000	1	AP006618_53	Continuation (54 o	C 913	92.5	6.5	5749	8	AF490339	AF490339 Phytophth
C 841	93	6.5	110000	1	AP006618_54	Continuation (55 o	C 914	92.5	6.5	5996	1	BPEBVG	M25401 B.pertussis
C 842	93	6.5	110000	1	BE571966_16	Continuation (17 o	C 915	92.5	6.5	6353	1	AY457916	AY457916 Marine al
C 843	93	6.5	110000	2	LMFLCR36_17	Continuation (18 o	C 916	92.5	6.5	10044	1	AE012020	AE012020 Xanthomon
C 844	93	6.5	115866	9	AL627422	AL627422 Human DNA	C 917	92.5	6.5	10511	1	AE012093	AE012093 Xanthomon
C 845	93	6.5	124112	2	AC137573	AC137573 Homo sapi	C 918	92.5	6.5	12837	1	AY057934	AY057934 Xanthomon
C 846	93	6.5	137560	6	CQ830057	CQ830057 Sequence	C 919	92.5	6.5	13104	1	AE004656	AE004656 Pseudomon
C 847	93	6.5	137560	6	AX754989	AX754989 Sequence	C 920	92.5	6.5	13621	1	AE004794	AE004794 Pseudomon
C 848	93	6.5	138701	8	AP003243	AP003243 Oryza sat	C 921	92.5	6.5	14857	1	AE009543	AE009543 Brucella
C 849	93	6.5	141469	2	AC148179	AC148179 Zea mays	C 922	92.5	6.5	19601	1	AB070944	AB070944 Streptomy
C 850	93	6.5	141636	5	BX005235	BX005235 Zebrafish	C 923	92.5	6.5	35100	6	I96182	I96182 Sequence 19
C 851	93	6.5	149050	1	ML0672114	AL672114 Mesorhizo	C 924	92.5	6.5	42874	9	HSU63963	U63963 Human CSP-1
C 852	93	6.5	150201	8	CNS080C7	AL928777 Oryza sat	C 925	92.5	6.5	45375	5	AF328738	AF328738 Agelaius
C 853	93	6.5	152040	2	CNS080C7	AC139547 Homo sapi	C 926	92.5	6.5	68254	2	AC117408_3	Continuation (4 of
C 854	93	6.5	153791	2	AC119629	AC119629 Rattus no	C 927	92.5	6.5	84664	10	EX005298	EX005298 Mouse DNA
C 855	93	6.5	154076	2	AC023273	AC023273 Homo sapi	C 928	92.5	6.5	85163	1	AY048670	AY048670 Streptomy
C 856	93	6.5	158033	2	AC135991	AC135991 Homo sapi	C 929	92.5	6.5	86431	6	AR406002_7	Continuation (8 of
C 857	93	6.5	162208	8	AP0073321	AP0073321 Homo sapi	C 930	92.5	6.5	110000	1	EX571966_25	Continuation (26 o
C 858	93	6.5	163702	8	AP004849	AP004849 Oryza sat	C 931	92.5	6.5	110000	2	AC087331_3	Continuation (4 of
C 859	93	6.5	163776	2	AC135994	AC135994 Homo sapi	C 932	92.5	6.5	110000	2	LMFLCHR34_16	Continuation (17 o
C 860	93	6.5	164711	2	AC139564	AC139564 Homo sapi	C 933	92.5	6.5	110000	2	AR406002_6	Continuation (7 of
C 861	93	6.5	165715	2	CR759743	CR759743 Danio rer	C 934	92.5	6.5	131918	8	AP003570	AP003570 Oryza sat
C 862	93	6.5	166484	2	AC026830	AC026830 Homo sapi	C 935	92.5	6.5	132825	2	CR457442	CR457442 Danio rer
C 863	93	6.5	1766871	2	AC150824	AC150824 Callithiri	C 936	92.5	6.5	137907	2	AC151640	AC151640 Dasypus n
C 864	93	6.5	180797	2	AC149172	AC149172 Papio anu	C 937	92.5	6.5	143883	9	CNS01DSL	AL121819 Human chr
C 865	93	6.5	183937	2	AC037435	AC037435 Mus muscu	C 938	92.5	6.5	146663	8	AP004558	AP004558 Oryza sat
C 866	93	6.5	184148	2	AC148725	AC148725 Pongo pyg	C 939	92.5	6.5	149500	2	AC138636	AC138636 Leishmani
C 867	93	6.5	184252	2	AC139565	AC139565 Homo sapi	C 940	92.5	6.5	151038	8	AP005441	AP005441 Oryza sat
C 868	93	6.5	184981	9	AC008659	AC008659 Homo sapi	C 941	92.5	6.5	155024	8	AP004665	AP004665 Oryza sat
C 869	93	6.5	188448	9	AC139426	AC139426 Homo sapi	C 942	92.5	6.5	155432	8	AP003247	AP003247 Oryza sat
C 870	93	6.5	188596	9	AC120045	AC120045 Homo sapi	C 943	92.5	6.5	162496	2	AC044846	AC044846 Mus muscu
C 871	93	6.5	190050	1	AL646080	AL646080 Ralstonia	C 944	92.5	6.5	168874	10	AC132135	AC132135 Mus muscu
C 872	93	6.5	200724	9	AL139382	AL139382 Human DNA	C 945	92.5	6.5	170365	9	AL390920	AL390920 Human DNA
C 873	93	6.5	205737	2	AC021445	AC021445 Mus muscu	C 946	92.5	6.5	170459	2	AC150302	AC150302 Papio anu
C 874	93	6.5	208136	2	AC151042	AC151042 Callithiri	C 947	92.5	6.5	172099	2	AC023837	AC023837 Homo sapi
C 875	93	6.5	215050	1	AL646057	AL646057 Ralstonia	C 948	92.5	6.5	172214	2	AC011210	AC011210 Homo sapi
C 876	93	6.5	215131	10	AC119951	AC119951 Mus muscu	C 949	92.5	6.5	172676	9	AC117439	AC117439 Homo sapi
C 877	93	6.5	221805	10	AC116474	AC116474 Rattus no	C 950	92.5	6.5	174383	2	EX323991	EX323991 Danio rer
C 878	93	6.5	225238	2	AC097825	AC097825 Rattus no	C 951	92.5	6.5	176011	10	AL645862	AL645862 Mouse DNA
C 879	93	6.5	226735	2	AC121120	AC121120 Mus muscu	C 952	92.5	6.5	176258	10	AC147624	AC147624 Mus muscu
C 880	93	6.5	249360	2	AC127920	AC127920 Rattus no	C 953	92.5	6.5	177726	9	AC148671	AC148671 Macaca mu

954	92.5	6.5	178023	10	AC130718	AC130718 Mus muscu	1027	92	6.4	163376	8	OSJN00254	AL731612 Oryza sat
955	92.5	6.5	184346	10	AC122283	Mus muscu	1028	92	6.4	165718	2	AC127508	AL731612 Oryza sat
956	92.5	6.5	186431	6	AX596303	Sequence	1029	92	6.4	166007	2	HSBA245A6	AL121749 Human DNA
c 957	92.5	6.5	190014	9	AC113268	Papio anu	1030	92	6.4	166176	2	EX927372	EX927372 Danio rer
958	92.5	6.5	195485	9	AL591846	Human DNA	c1031	92	6.4	167380	9	AP006242	AP006242 Homo sapi
959	92.5	6.5	197632	2	CR792419	Danio rer	1032	92	6.4	162931	2	AC111190	AC111190 Homo sapi
960	92.5	6.5	210301	9	AF307337	Homo sapi	1033	92	6.4	174164	9	AC116166	AC116166 Homo sapi
961	92.5	6.5	211219	2	CR790363	Danio rer	c1034	92	6.4	181241	9	AC080128	AC080128 Homo sapi
962	92.5	6.5	213050	1	AL646067	Ralstonia	c1035	92	6.4	181593	2	CR848006	CR848006 Danio rer
c 963	92.5	6.5	213881	2	AC150564	Bos tauru	1036	92	6.4	187688	9	AP003066	AP003066 Homo sapi
c 964	92.5	6.5	229220	10	AC0591519	Mus muscu	1037	92	6.4	192128	2	AC013382	AC013382 Homo sapi
965	92.5	6.5	233144	2	AC110317	Rattus no	c1038	92	6.4	195119	5	EX649594	EX649594 Zebrafish
966	92.5	6.5	233755	2	CR812465	Danio rer	1039	92	6.4	195808	2	AL591182	AL591182 Homo sapi
967	92.5	6.5	258174	2	AC079429	Mus muscu	c1040	92	6.4	196451	9	AC112784	AC112784 Homo sapi
968	92.5	6.5	270094	2	AC106083	Rattus no	1041	92	6.4	196507	2	AC135177	AC135177 Homo sapi
969	92.5	6.5	287203	2	AC133986	Rattus no	c1042	92	6.4	197999	2	AC134688	AC134688 Homo sapi
c 970	92.5	6.5	299425	1	AP005049	Streptomy	1043	92	6.4	200966	2	EX927115	EX927115 Danio rer
c 971	92.5	6.5	300717	1	AE017229	Mycobacte	1044	92	6.4	202012	5	EX088583	EX088583 Zebrafish
972	92.5	6.5	345012	1	EX572607	Rhodosphe	c1045	92	6.4	202981	2	EX465228	EX465228 Danio rer
973	92.5	6.5	349354	1	EX640416	Bordetell	c1046	92	6.4	207822	2	AC109321	AC109321 Homo sapi
c 974	92	6.4	606	9	PT8488168	Pan trogl	c1047	92	6.4	223097	2	AC129874	AC129874 Rattus no
c 975	92	6.4	1236	6	E02708	RNA sequenc	c1048	92	6.4	223575	10	AC130819	AC130819 Mus muscu
c 976	92	6.4	1881	6	AR541804	Sequence	c1049	92	6.4	228783	2	AC094377	AC094377 Rattus no
977	92	6.4	2224	6	AX747800	Sequence	c1050	92	6.4	234714	2	EX957235	EX957235 Danio rer
978	92	6.4	2224	9	AX079426	Homo sapi	1051	92	6.4	251610	2	AC094526	AC094526 Rattus no
979	92	6.4	2388	1	AY497529	Xanthomon	c1052	92	6.4	253431	2	AC094604	AC094604 Rattus no
980	92	6.4	2408	8	AY049725	Tranetes	1053	92	6.4	255128	2	AC102905	AC102905 Mus muscu
981	92	6.4	2589	3	BMU16274	Bombyx mori	1054	92	6.4	267861	2	CG628327	CG628327 Danio rer
982	92	6.4	2723	3	BFL580840	Xanthomon	c1055	92	6.4	277991	2	EX950222	EX950222 Danio rer
c 983	92	6.4	3029	6	AX834352	Sequence	c1056	92	6.4	278040	5	AL954847	AL954847 Zebrafish
c 984	92	6.4	3029	9	AX096755	Homo sapi	c1057	92	6.4	280810	2	AC046188	AC046188 Homo sapi
985	92	6.4	3054	5	DRE428850	Danio rer	1058	92	6.4	297050	1	AP006569	AP006569 Gloeobact
986	92	6.4	3617	10	AS018791	Rattus no	c1059	92	6.4	300550	1	AP005021	AP005021 Streptomy
c 987	92	6.4	3764	1	AY148878	Methylosi	c1060	92	6.4	301482	1	AE016916	AE016916 Chromobac
c 988	92	6.4	4771	1	AF021263	Streptomy	1061	92	6.4	302898	1	AE017238	AE017238 Mycobacte
c 989	92	6.4	9344	14	AE049100	Hepatit	c1062	92	6.4	348068	1	EX572604	EX572604 Rhodosphe
990	92	6.4	10222	1	AE004685	Sequence	c1063	92	6.4	348525	1	EX640428	EX640428 Bordetell
991	92	6.4	10460	1	AE011791	Xanthomon	1064	92	6.4	349442	1	EX640447	EX640447 Bordetell
992	92	6.4	10466	1	AE011977	Xanthomon	c1065	91.5	6.4	961	10	BC038863	BC038863 Mus muscu
993	92	6.4	11152	1	AE012525	Xanthomon	c1066	91.5	6.4	1141	10	MUSTI11D	M58564 Mouse TTS11
c 994	92	6.4	11213	1	AE004950	Pseudomon	c1067	91.5	6.4	1208	6	AX110160	AX110160 Sequence
c 995	92	6.4	11378	1	AE001967	Deinococc	c1068	91.5	6.4	1211	6	AX103760	AX103760 Sequence
c 996	92	6.4	13017	1	AE005861	Caulobact	c1069	91.5	6.4	1600	9	AF523834	AF523834 Homo sapi
c 997	92	6.4	13349	1	AY599747	Pseudomon	c1070	91.5	6.4	1600	9	HS3370184	AL591562 Novel hum
998	92	6.4	15085	9	AE002038	Deinococc	1071	91.5	6.4	1816	9	BC050403	BC050403 Homo sapi
999	92	6.4	22723	9	AF107890	Homo sapi	1072	91.5	6.4	2041	9	AK090885	AK090885 Homo sapi
c1000	92	6.4	28028	2	AC104504	Trypanoso	c1073	91.5	6.4	2064	9	AF258570	AF258570 Homo sapi
c1001	92	6.4	35116	9	AC004151	Homo sapi	1074	91.5	6.4	2084	1	AY423558	AY423558 Streptomy
c1002	92	6.4	35736	2	AC151604	Emiliania	c1075	91.5	6.4	2193	9	ORAIGECA	M15399 Orangutan I
1003	92	6.4	37513	2	AC137639	Homo sapi	c1076	91.5	6.4	2507	1	MXAFRZ	J04157 M.xanthus f
1004	92	6.4	37604	9	AP006588	Homo sapi	c1077	91.5	6.4	2792	6	AX746933	AX746933 Sequence
1005	92	6.4	37867	1	AF086791	Zymomonas	c1078	91.5	6.4	2792	9	AK091359	AK091359 Homo sapi
c1006	92	6.4	40595	9	AC133540	Homo sapi	c1079	91.5	6.4	3044	6	AX833814	AX833814 Sequence
1007	92	6.4	4042	2	AC101394	Mus muscu	c1080	91.5	6.4	3044	9	AK095851	AK095851 Homo sapi
c1008	92	6.4	48908	8	AC007197	Arabidops	c1081	91.5	6.4	3541	1	AF102271	AF102271 Streptomy
c1009	92	6.4	95108	2	AC127818	Rattus no	c1082	91.5	6.4	3559	3	BRL223578	AF223578 Branchios
c1010	92	6.4	110000	1	AP006618_13	Continuation (14 o	c1083	91.5	6.4	4808	3	BT009988	BT009988 Drosophil
c1011	92	6.4	110000	2	LMFLCHR1B_09	Continuation (10 o	c1084	91.5	6.4	8321	6	AX803733	AX803733 Sequence
c1012	92	6.4	122803	5	EX005291	Zebrafish	1085	91.5	6.4	8431	4	BTHYR	X02815 Bovine mRNA
1013	92	6.4	124104	9	AC061979	Homo sapi	c1086	91.5	6.4	8599	14	BHVUS12	Z381199 Bovine herp
1014	92	6.4	125780	8	OSJN00277	Oryza sat	1087	91.5	6.4	10408	1	AE010409	AE010409 Methanopy
c1015	92	6.4	130596	2	AC018962	Homo sapi	1088	91.5	6.4	10635	1	AE008475	AE008475 Streptoco
c1016	92	6.4	131691	9	AC096765	Homo sapi	1089	91.5	6.4	10936	1	AE014397	AE014397 Brucella
1017	92	6.4	137300	9	AC090764	Homo sapi	c1090	91.5	6.4	11735	1	AE004896	AE004896 Pseudomon
c1018	92	6.4	138979	2	AC141667	Apis mell	c1091	91.5	6.4	12027	1	AE005728	AE005728 Caulobact
c1019	92	6.4	142525	9	AC105752	Homo sapi	1092	91.5	6.4	12092	1	AE012096	AE012096 Xanthomon
c1020	92	6.4	144000	9	AC123764	Homo sapi	1093	91.5	6.4	12652	1	AE005786	AE005786 Caulobact
1021	92	6.4	147184	2	AC135778	Homo sapi	1094	91.5	6.4	15080	8	D82879	D82879 Chlorella v
c1022	92	6.4	149637	10	AC133089	Mus muscu	1095	91.5	6.4	15516	1	AE012060	AE012060 Xanthomon
c1023	92	6.4	151009	2	AC135784	Homo sapi	1096	91.5	6.4	18796	6	CQ363729	CQ363729 Sequence
1024	92	6.4	152559	2	AC135787	Homo sapi	1097	91.5	6.4	24798	1	PST297529	AE0297529 Pseudomon
c1025	92	6.4	157216	2	AC008244	Homo sapi	1098	91.5	6.4	49220	7	AX120035	AX120035 Bacteriop
1026	92	6.4	158730	2	AC093313	Trypanoso	1099	91.5	6.4	49269	8	AX135499	AX135499 Oryza sat



c1100	91.5	6.4	80554	2	AP004143	AP004143 Oryza sat	c1173	91	6.4	2997	6	AX552616	AX552616 Sequence
c1101	91.5	6.4	82682	9	AB104726	AB104726 Homo sapi	1174	91	6.4	3021	6	CQ725525	CQ725525 Sequence
c1102	91.5	6.4	86260	9	HS337018	AL008726 Human DNA	1175	91	6.4	3156	5	AF009012	AF009012 Gallus ga
c1103	91.5	6.4	86829	9	AC011382	AC011382 Homo sapi	c1176	91	6.4	3158	6	AX552614	AX552614 Sequence
c1104	91.5	6.4	92564	9	AY007685	AY007685 Homo sapi	c1177	91	6.4	3241	6	AX833813	AX833813 Sequence
c1105	91.5	6.4	102571	9	BS000241	BS000241 Pan trogl	c1178	91	6.4	3241	9	AK095848	AK095848 Homo sapi
c1106	91.5	6.4	104419	8	AP003995	AP003995 Oryza sat	c1179	91	6.4	3389	3	BT001806	BT001806 Drosophila
c1107	91.5	6.4	107823	2	AC138132	AC138132 Pan trogl	c1180	91	6.4	4138	9	AY193890	AY193890 Homo sapi
c1108	91.5	6.4	110000	1	AE017180_37	Continuation (38 o	c1181	91	6.4	4257	12	CVU07648	U07648 Cloning vec
c1109	91.5	6.4	110000	1	AE017282_12	Continuation (13 o	1182	91	6.4	4358	10	BC060187	BC060187 Mus muscu
c1110	91.5	6.4	110000	1	AP006618_02	Continuation (3 of	1183	91	6.4	4367	10	AK129439	AK129439 Mus muscu
c1111	91.5	6.4	110000	1	AP006618_17	Continuation (18 o	1184	91	6.4	4433	9	AK024506	AK024506 Homo sapi
c1112	91.5	6.4	110000	2	AC127191_2	Continuation (13 of	1185	91	6.4	4734	9	AB007857	AB007857 Homo sapi
c1113	91.5	6.4	124882	9	AC090064	AC090064 Homo sapi	1186	91	6.4	4849	1	MX083800	MX083800 Myxococcus
c1114	91.5	6.4	127003	8	CNS08C9C	AL732537 Oryza sat	1187	91	6.4	4881	9	BC039204	BC039204 Homo sapi
c1115	91.5	6.4	132544	1	AF521085	AF521085 Streptomy	1188	91	6.4	4882	10	BC046464	BC046464 Mus muscu
c1116	91.5	6.4	132768	9	AC011376	AC011376 Homo sapi	1189	91	6.4	5003	5	BBU18939	BBU18939 Batrachoco
c1117	91.5	6.4	139755	2	AC151511	AC151511 Dasyptus n	1190	91	6.4	5061	1	RLE431175	RL431175 Rhizobium
c1118	91.5	6.4	142363	10	AL845548	AL845548 Mouse DNA	c1191	91	6.4	5508	1	WXA133131	WXA133131 Myxococcu
c1119	91.5	6.4	145337	8	AP005301	AP005301 Oryza sat	1192	91	6.4	8366	1	AF072709	AF072709 Streptomy
c1120	91.5	6.4	152910	8	AP005537	AP005537 Oryza sat	c1193	91	6.4	8900	8	AB112468	AB112468 Chlamydom
c1121	91.5	6.4	152974	8	AC135497	AC135497 Oryza sat	c1194	91	6.4	9667	3	AY442174	AY442174 Trypanoso
c1122	91.5	6.4	153670	2	AL355295	AL355295 Homo sapi	c1195	91	6.4	10249	1	AF088856	AF088856 Vogesella
c1123	91.5	6.4	159810	9	AL356433	AL356433 Human DNA	1196	91	6.4	10542	1	AE004852	AE004852 Pseudomon
c1124	91.5	6.4	161156	9	AL355039	AL355039 Homo sapi	1197	91	6.4	12433	1	AE004828	AE004828 Pseudomon
c1125	91.5	6.4	161531	8	AP004880	AP004880 Oryza sat	c1198	91	6.4	12775	1	AB000735	AB000735 Nocardiolo
c1126	91.5	6.4	161795	2	AC126542	AC126542 Homo sapi	1199	91	6.4	21953	6	CQ792619	CQ792619 Sequence
c1127	91.5	6.4	162451	9	AL353597	AL353597 Human DNA	c1200	91	6.4	24081	6	AX598605	AX598605 Sequence
c1128	91.5	6.4	167131	8	CNS08C8L	AL731881 Oryza sat	c1201	91	6.4	40962	9	AP005888	AP005888 Homo sapi
c1129	91.5	6.4	167961	2	AP002422	AP002422 Homo sapi	1202	91	6.4	45661	9	AP005888	AP005888 Homo sapi
c1130	91.5	6.4	172654	2	AC067737	AC067737 Homo sapi	c1203	91	6.4	52101	6	AX598593	AX598593 Sequence
c1131	91.5	6.4	173979	2	AC149625	AC149625 Papilo anu	1204	91	6.4	82868	1	AJ620477	AJ620477 Nocardioce
c1132	91.5	6.4	176148	9	AC010798	AC010798 Homo sapi	1205	91	6.4	82868	6	CQ792587	CQ792587 Sequence
c1133	91.5	6.4	177285	2	AC130354	AC130354 Homo sapi	c1206	91	6.4	82868	6	CQ792604	CQ792604 Sequence
c1134	91.5	6.4	178825	2	AP001203	AP001203 Homo sapi	1207	91	6.4	90502	9	AC108676	AC108676 Homo sapi
c1135	91.5	6.4	182917	2	AC025291	AC025291 Homo sapi	c1208	91	6.4	110000	1	AE018822_19	Continuation (20 o
c1136	91.5	6.4	182735	9	AC129919	AC129919 Homo sapi	c1209	91	6.4	110000	1	AP006618_06	Continuation (7 of
c1137	91.5	6.4	182781	2	AC087814	AC087814 Homo sapi	1210	91	6.4	110000	1	AP006618_36	Continuation (37 o
c1138	91.5	6.4	184469	2	AL365447	AL365447 Homo sapi	c1211	91	6.4	110000	1	BX571965_01	Continuation (2 of
c1139	91.5	6.4	184641	9	AL327455	AL327455 Homo sapi	1212	91	6.4	110000	2	AC095759_2	Continuation (3 of
c1140	91.5	6.4	188956	9	AL591493	AL591493 Human DNA	c1213	91	6.4	110000	2	AP006500_03	Continuation (4 of
c1141	91.5	6.4	188956	9	AL591493	AL591493 Human DNA	c1214	91	6.4	111332	1	AY273869	AY273869 Pseudomon
c1142	91.5	6.4	198177	2	AC141421	AC141421 Pan trogl	1215	91	6.4	116983	8	OSJN00051	OSJN00051 Oryza sat
c1143	91.5	6.4	200089	10	AL683888	AL683888 Mouse DNA	1216	91	6.4	123254	2	AC145054	AC145054 Felis cat
c1144	91.5	6.4	210538	10	AC132455	AC132455 Mus muscu	1217	91	6.4	129505	9	AL590385	AL590385 Human DNA
c1145	91.5	6.4	213612	2	AC148589	AC148589 Pan trogl	c1218	91	6.4	144689	8	AP004307	AP004307 Oryza sat
c1146	91.5	6.4	239893	2	AC107521	AC107521 Rattus no	1219	91	6.4	146313	8	OSJN00261	OSJN00261 Oryza sat
c1147	91.5	6.4	241087	14	AF480884	AF480884 Chimpanze	1220	91	6.4	152418	9	AC100803	AC100803 Homo sapi
c1148	91.5	6.4	274676	1	AE017305	AE017305 Thermsus t	1221	91	6.4	155757	2	AC118548	AC118548 Homo sapi
c1149	91.5	6.4	284300	2	AC111967	AC111967 Rattus no	1222	91	6.4	157419	2	AC025389	AC025389 Homo sapi
c1150	91.5	6.4	299925	1	AP005045	AP005045 Streptomy	1223	91	6.4	159130	2	AC026847	AC026847 Homo sapi
c1151	91.5	6.4	300100	1	SC0939123	AL939123 Streptomy	c1224	91	6.4	159264	2	AC092419	AC092419 Homo sapi
c1152	91.5	6.4	302550	1	AP006581	AP006581 Glosofact	c1225	91	6.4	159664	2	AL592441	AL592441 Homo sapi
c1153	91.5	6.4	303550	1	SC0939118	AL939118 Streptomy	c1226	91	6.4	160541	2	AC007944	AC007944 Homo sapi
c1154	91.5	6.4	310029	1	AE016861	AE016861 Pseudomon	c1227	91	6.4	160984	9	AC092453	AC092453 Homo sapi
c1155	91.5	6.4	314100	1	SC0939106	AL939106 Streptomy	c1228	91	6.4	162867	9	AC135966	AC135966 Homo sapi
c1156	91.5	6.4	334108	1	AE016857	AE016857 Pseudomon	1229	91	6.4	166005	8	AC120506	AC120506 Oryza sat
c1157	91.5	6.4	346547	1	AP003012	AP003012 Mesorhizo	c1230	91	6.4	166234	9	AC018629	AC018629 Homo sapi
c1158	91.5	6.4	348014	1	EX640430	EX640430 Bordetell	c1231	91	6.4	169347	9	AC007327	AC007327 Homo sapi
c1159	91.5	6.4	349726	1	EX640421	EX640421 Bordetell	1232	91	6.4	171177	9	AC092040	AC092040 Homo sapi
c1160	91	6.4	969	11	BV179107	BV179107 sqm10389	1233	91	6.4	172552	5	BX005365	BX005365 Zebraphish
c1161	91	6.4	1236	6	EO2578	EO2578 DNA encodin	c1234	91	6.4	177466	1	AE001826	AE001826 Deinococc
c1162	91	6.4	1275	9	AE191416	AE191416 Homo sapi	c1235	91	6.4	179354	2	CR354588	CR354588 Danio rer
c1163	91	6.4	1590	6	AR173222	AR173222 Sequence	c1236	91	6.4	180096	2	CR391999	CR391999 Danio rer
c1164	91	6.4	1908	6	AR164599	AR164599 Sequence	c1237	91	6.4	180223	9	AC062017	AC062017 Homo sapi
c1165	91	6.4	2094	9	CR456580	CR456580 Homo sapi	1238	91	6.4	181627	2	AL359264	AL359264 Homo sapi
c1166	91	6.4	2311	6	CQ730056	CQ730056 Sequence	c1239	91	6.4	184019	9	AC099544	AC099544 Homo sapi
c1167	91	6.4	2325	9	HS47730	AJ000730 Homo sapi	1240	91	6.4	184543	5	BX571681	BX571681 Zebraphish
c1168	91	6.4	2367	6	AX747772	AX747772 Sequence	c1241	91	6.4	185997	5	BX470139	BX470139 Zebraphish
c1169	91	6.4	2367	9	AK092858	AK092858 Homo sapi	c1242	91	6.4	187201	2	AC113860	AC113860 Rattus no
c1170	91	6.4	2367	5	AY687628	AY687628 Gallus ga	c1243	91	6.4	187578	9	AC096952	AC096952 Homo sapi
c1171	91	6.4	2540	6	EO6801	EO6801 gDNA encodi	1244	91	6.4	188574	2	AC131063	AC131063 Homo sapi
c1172	91	6.4	2698	9	AK091527	AK091527 Homo sapi	1245	91	6.4	196648	2	AC009673	AC009673 Homo sapi



c1246	91	6.4	198261	9	AC016825	AC016825 Homo sapi	1319	90.5	6.3	60385	9	AC009511	Homo sapi
c1247	91	6.4	198602	10	AL450395	Mouse DNA	1320	90.5	6.3	66241	2	AC019757	Drosophila
c1248	91	6.4	202050	1	AL646065	Ralstonia	c1321	90.5	6.3	77457	1	AF210249	Streptomy
c1249	91	6.4	202301	1	AE017286	Desulfovi	1322	90.5	6.3	77740	1	AF540993	Pseudomon
c1250	91	6.4	207383	2	CR381676	CR381676	c1323	90.5	6.3	78210	1	AB070949	Streptomy
c1251	91	6.4	210074	9	AC010837	Homo sapi	1324	90.5	6.3	97000	9	AP003966	Homo sapi
c1252	91	6.4	210508	9	AC135612	Pan trogl	c1325	90.5	6.3	100354	2	AC150130	Gallus ga
c1253	91	6.4	212199	9	AL445199	Human DNA	c1326	90.5	6.3	105027	1	AJ617740	Pseudomon
c1254	91	6.4	217594	1	AP002086	Agrobacte	c1327	90.5	6.3	110000	1	AE016822_06	Continuation (7 of
c1255	91	6.4	220050	1	AL646074	Ralstonia	c1328	90.5	6.3	110000	1	AE006618_22	Continuation (23 o
c1256	91	6.4	232760	2	AC141423	Pan trogl	c1329	90.5	6.3	110000	1	AP006618_48	Continuation (49 o
c1257	91	6.4	232893	2	AC096182	Rattus no	1330	90.5	6.3	110000	1	CP000011_03	Continuation (8 of
c1258	91	6.4	236522	2	CR376793	Danio rer	c1331	90.5	6.3	110000	2	LMFLCHR18_07	Continuation (6 of
c1259	91	6.4	237725	2	EX293996	EX293996	1332	90.5	6.3	110000	8	AE016817_05	Continuation (6 of
c1260	91	6.4	238108	2	BX248332	BX248332	c1333	90.5	6.3	120808	10	AL662862	Mouse DNA
c1261	91	6.4	240977	10	AL513352	Mouse DNA	c1334	90.5	6.3	122437	9	AC022498	AC022498 Homo sapi
c1262	91	6.4	249871	2	AC118143	Rattus no	c1335	90.5	6.3	130528	8	AP003202	AP003202 Oryza sat
c1263	91	6.4	254464	2	AC117040	Rattus no	c1336	90.5	6.3	133023	10	AL645982	AL645982 Mouse DNA
c1264	91	6.4	270991	2	AC136210	Gallus ga	c1337	90.5	6.3	143300	8	AP003630	AP003630 Oryza sat
c1265	91	6.4	273413	2	AC079314	Homo sapi	1338	90.5	6.3	150272	2	AP005923	AP005923 Oryza sat
c1266	91	6.4	295150	1	SC093916	Streptomy	1339	90.5	6.3	154098	9	AC134043	AC134043 Homo sapi
c1267	91	6.4	299600	1	AP005941	Bradyrhiz	1340	90.5	6.3	156561	8	AP006723	AP006723 Oryza sat
c1268	91	6.4	300327	1	AE017228	Mycobacte	c1341	90.5	6.3	160142	9	AC093684	AC093684 Homo sapi
c1269	91	6.4	300425	1	AP005041	Streptomy	c1342	90.5	6.3	164051	6	C0875911	C0875911 Sequence
c1270	91	6.4	300700	1	AP006573	Gloeobact	c1343	90.5	6.3	167344	3	AC093438	AC093438 Drosophill
c1271	91	6.4	301995	1	AE016779	Pseudomon	1344	90.5	6.3	168008	9	AC008544	AC008544 Homo sapi
c1272	91	6.4	302178	1	AE016918	Chromobac	c1345	90.5	6.3	170023	9	AC024951	AC024951 Homo sapi
c1273	91	6.4	309267	1	AE017235	Mycobacte	c1346	90.5	6.3	174314	3	AC011066	AC011066 Drosophill
c1274	91	6.4	325353	2	AC120909	Rattus no	1347	90.5	6.3	176027	2	AL732575	AL732575 Mus muscu
c1275	91	6.4	325482	2	BX004858	Danio rer	c1348	90.5	6.3	176051	9	AC023490	AC023490 Homo sapi
c1276	91	6.4	343243	1	BX640414	BX640414	1349	90.5	6.3	176146	2	AC023124	AC023124 Homo sapi
c1277	91	6.4	348014	1	BX640430	Bordetell	1350	90.5	6.3	180136	10	AL732557	AL732557 Mouse DNA
c1278	90.5	6.3	861	9	HS4339387	AY339387 Homo sapi	c1351	90.5	6.3	181103	3	AC011065	AC011065 Drosophill
c1279	90.5	6.3	1017	13	AY487480	AY487480 Unculture	c1352	90.5	6.3	181253	9	AC099065	AC099065 Homo sapi
c1280	90.5	6.3	1370	8	AK069887	AK069887 Oryza sat	c1353	90.5	6.3	183155	2	AL591169	AL591169 Homo sapi
c1281	90.5	6.3	1722	9	BC047320	BC047320 Homo sapi	1354	90.5	6.3	185080	9	AL954258	AL954258 Pan trogl
c1282	90.5	6.3	1904	9	HS0801326	AL133055 Homo sapi	c1355	90.5	6.3	186063	9	AC104417	AC104417 Homo sapi
c1283	90.5	6.3	1962	6	CQ733707	CQ733707 Sequence	1356	90.5	6.3	186553	2	AC150177	AC150177 Gallus ga
c1284	90.5	6.3	2105	6	BD132812	BD132812 Plant and	c1357	90.5	6.3	190211	2	AC150083	AC150083 Gallus ga
c1285	90.5	6.3	2105	6	AX031231	AX031231 Sequence	1358	90.5	6.3	192863	2	AC147313	AC147313 Pan trogl
c1286	90.5	6.3	2170	9	EC041015	EC041015 Homo sapi	1359	90.5	6.3	193689	2	AC066603	AC066603 Homo sapi
c1287	90.5	6.3	2183	14	AF214005	AF214005 Banana st	c1360	90.5	6.3	205794	9	AC010864	AC010864 Homo sapi
c1288	90.5	6.3	2364	9	AK000271	AK000271 Homo sapi	1361	90.5	6.3	211414	2	AC150057	AC150057 Gallus ga
c1289	90.5	6.3	2835	6	AX136351	AX136351 Sequence	c1362	90.5	6.3	214387	2	AC137537	AC137537 Canis fam
c1290	90.5	6.3	2835	6	BD123628	BD123628 Secretary	c1363	90.5	6.3	218067	2	AC150058	AC150058 Gallus ga
c1291	90.5	6.3	2835	9	AK075543	AK075543 Homo sapi	c1364	90.5	6.3	219205	10	AL611985	AL611985 Mouse DNA
c1292	90.5	6.3	3210	9	EC050477	EC050477 Homo sapi	1365	90.5	6.3	222605	1	AP002555	AP002555 Escherich
c1293	90.5	6.3	3340	10	BC079869	BC079869 Mus muscu	1366	90.5	6.3	239347	2	AC099240	AC099240 Rattus no
c1294	90.5	6.3	3823	1	AB021364	AB021364 Xanthom	1367	90.5	6.3	248717	2	BX470107	BX470107 Danio rer
c1295	90.5	6.3	4324	1	SOL300305	SOL300305 Streptomy	c1368	90.5	6.3	265341	3	AE003634	AE003634 Drosophill
c1296	90.5	6.3	6036	6	CQ586932	CQ586932 Sequence	c1369	90.5	6.3	265524	3	AE003541	AE003541 Drosophill
c1297	90.5	6.3	6126	14	PV1318065	AJ318065 Pseudorab	1370	90.5	6.3	287510	2	CR753823	CR753823 Danio rer
c1298	90.5	6.3	7441	6	CQ597803	CQ597803 Sequence	c1371	90.5	6.3	296500	1	SC0939128	SC0939128 Streptomy
c1299	90.5	6.3	8223	6	CQ586931	CQ586931 Sequence	1372	90.5	6.3	298550	1	AP005047	AP005047 Streptomy
c1300	90.5	6.3	9277	6	CQ729952	CQ729952 Sequence	c1373	90.5	6.3	299450	1	AP006580	AP006580 Gloeobact
c1301	90.5	6.3	9287	9	HUMCOL781	L02870 Human alpha	1374	90.5	6.3	299925	1	AP005039	AP005039 Streptomy
c1302	90.5	6.3	10029	1	AE012787	AE012787 Chlorobiu	1375	90.5	6.3	300052	1	AE017232	AE017232 Mycobacte
c1303	90.5	6.3	11565	1	AE011677	AE011677 Xanthom	1376	90.5	6.3	300425	1	AP005022	AP005022 Streptomy
c1304	90.5	6.3	11589	1	AE002079	AE002079 Deinococc	1377	90.5	6.3	301675	1	AP005027	AP005027 Streptomy
c1305	90.5	6.3	12296	1	AE001950	AE001950 Deinococc	c1378	90.5	6.3	311000	1	SC0939122	SC0939122 Streptomy
c1306	90.5	6.3	13431	1	AE005044	AE005044 Halobact	c1379	90.5	6.3	311963	1	AE016872	AE016872 Pseudomon
c1307	90.5	6.3	20256	6	CQ875919	CQ875919 Sequence	c1380	90.5	6.3	339650	1	SC0939108	SC0939108 Streptomy
c1308	90.5	6.3	29132	1	STH575648	STH575648 Streptomy	c1381	90.5	6.3	346274	1	BX640443	BX640443 Bordetell
c1309	90.5	6.3	32896	1	AY52397285	AY523976 Azospiril	c1382	90	6.3	612	9	CJ488165	CJ488165 Callithri
c1310	90.5	6.3	32821	2	AC020288	AC020288 Drosophill	c1383	90	6.3	624	9	CCA488163	CCA488163 Cebus cap
c1311	90.5	6.3	34875	6	CQ861683	CQ861683 Sequence	1384	90	6.3	1173	1	AY259141	AY259141 Streptomy
c1312	90.5	6.3	34875	9	AC005329	AC005329 Homo sapi	1385	90	6.3	1195	6	AX321627	AX321627 Sequence
c1313	90.5	6.3	35581	9	AC005331	AC005331 Homo sapi	c1386	90	6.3	1402	6	AX463508	AX463508 Sequence
c1314	90.5	6.3	35868	1	AC011617	AC011617 Leishmani	1387	90	6.3	2003	6	CQ718085	CQ718085 Sequence
c1315	90.5	6.3	38516	1	AF540992	AF540992 Pseudomon	1388	90	6.3	2456	8	AK072099	AK072099 Oryza sat
c1316	90.5	6.3	48423	6	BD184770	BD184770 Nucleic a	c1389	90	6.3	2550	6	CQ730790	CQ730790 Sequence
c1317	90.5	6.3	48908	1	AF204241	AF204241 Sequence	c1390	90	6.3	2878	9	AF228710	AF228710 Homo sapi
c1318	90.5	6.3	49723	2	AP004374	AP004374 Oryza sat	c1391	90	6.3	3306	9	BC022938	BC022938 Homo sapi

1382	1382	90	6.3	3333	1	AY492259	AY492259 Corynebacterium	1382	1382	90	6.3	193050	1	AL646062	AL646062 Ralstonia
1393	1393	90	6.3	3426	1	AY495678	AY495678 Xanthomonas	1393	1393	90	6.3	193059	2	AL646062	AL646062 Ralstonia
1394	1394	90	6.3	4434	6	CQ735134	CQ735134 Sequence	1394	1394	90	6.3	194244	2	AX322553	AX322553 Homo sapi
1395	1395	90	6.3	5005	9	AB011099	AB011099 Homo sapi	1395	1395	90	6.3	195652	9	AC093572	AC093572 Pan trogl
1396	1396	90	6.3	7234	1	AY101609	AY101609 Myxococcus	1396	1396	90	6.3	200249	2	AC145063	AC145063 Pan trogl
1397	1397	90	6.3	7282	9	HSNMDAR1A	HSNMDAR1A	1397	1397	90	6.3	200836	2	AC011965	AC011965 Homo sapi
1398	1398	90	6.3	8312	1	AB178023	AB178023 Ralstonia	1398	1398	90	6.3	201088	9	AL589733	AL589733 Human DNA
1399	1399	90	6.3	9752	1	AJ746243	AJ746243 Stenotrophomonas	1399	1399	90	6.3	205050	1	AL646082	AL646082 Ralstonia
1400	1400	90	6.3	10135	1	AE006017	AE006017 Caulobacter	1400	1400	90	6.3	205930	10	AC113533	AC113533 Mus muscu
1401	1401	90	6.3	11064	1	AE004853	AE004853 Pseudomonas	1401	1401	90	6.3	207050	1	AL646063	AL646063 Ralstonia
1402	1402	90	6.3	11512	1	AE011729	AE011729 Xanthomonas	1402	1402	90	6.3	209859	5	EX005398	EX005398 Zebrafish
1403	1403	90	6.3	11691	1	AE004947	AE004947 Pseudomonas	1403	1403	90	6.3	217335	1	AE016946	AE016946 Bacteroid
1404	1404	90	6.3	1702	1	AE004529	AE004529 Pseudomonas	1404	1404	90	6.3	225614	2	EX936454	EX936454 Danio rer
1405	1405	90	6.3	13299	1	AE006000	AE006000 Caulobacter	1405	1405	90	6.3	228633	5	EX649600	EX649600 Zebrafish
1406	1406	90	6.3	12444	1	AE004777	AE004777 Pseudomonas	1406	1406	90	6.3	230945	10	AC122898	AC122898 Mus muscu
1407	1407	90	6.3	12608	1	AE000073	AE000073 Rhizobium	1407	1407	90	6.3	250313	2	CR788310	CR788310 Danio rer
1408	1408	90	6.3	14149	1	AE005986	AE005986 Caulobacter	1408	1408	90	6.3	254977	2	AC117353	AC117353 Rattus no
1409	1409	90	6.3	14750	1	AE005796	AE005796 Caulobacter	1409	1409	90	6.3	258871	2	AC095418	AC095418 Rattus no
1410	1410	90	6.3	17112	1	AE004997	AE004997 Halobacter	1410	1410	90	6.3	258581	2	CR394526	CR394526 Danio rer
1411	1411	90	6.3	45289	3	CRG33924	CRG33924	1411	1411	90	6.3	258320	2	AC146196	AC146196 Pan trogl
1412	1412	90	6.3	50000	6	AX535264	AX535264 Sequence	1412	1412	90	6.3	287050	3	EX538350	EX538350 Cryptospor
1413	1413	90	6.3	50000	6	AX535266	AX535266 Sequence	1413	1413	90	6.3	289350	1	AP006572	AP006572 Gloeobact
1414	1414	90	6.3	59816	1	AP333038	AP333038 Streptomyces	1414	1414	90	6.3	293700	1	AP005944	AP005944 Bradyrhiz
1415	1415	90	6.3	70106	9	AC024293	AC024293 Homo sapi	1415	1415	90	6.3	302298	1	AE016788	AE016788 Pseudomon
1416	1416	90	6.3	73800	1	AF286216	AF286216 Pseudomonas	1416	1416	90	6.3	303225	1	AE017236	AE017236 Mycobacte
1417	1417	90	6.3	73920	10	AC091397	AC091397 Rattus no	1417	1417	90	6.3	305584	1	AE016920	AE016920 Chromobac
1418	1418	90	6.3	75898	14	AY190604	AY190604 Halovirus	1418	1418	90	6.3	311963	1	AE016872	AE016872 Pseudomon
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1420	1420	90	6.3	93119	9	AL451006	AL451006 Human DNA	1420	1420	90	6.3	320040	6	A79350	A79350 Sequence 1
1421	1421	90	6.3	93582	9	AC090881	AC090881 Homo sapi	1421	1421	90	6.3	320040	6	A33002	A33002 Sequence 1
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1425	1425	90	6.3	110000	1	AP006640_10	Continuation (11 o	1425	1425	90	6.3	349306	1	EX842575	EX842575 Mycobacte
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## ALIGNMENTS

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LOCUS	AX696985	Sequence 53 from Patent WO0078961.				
DEFINITION	AX696985					
ACCESSION	AX696985					
VERSION	AX696985.1	GI:29497985				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1					
AUTHORS	Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L., Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A., Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I., Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.					
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same					
JOURNAL	Patent: WO 0078961-A 53 28-DEC-2000; Genentech Inc. (US)					
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Pred. No.:	2,84e-97	Length:	3580			
Score:	1432.00	Matches:	280			
Percent Similarity:	100.00%	Conservative:	0			
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Query Match:	100.00%	Indels:	0			

DB: 6 Gaps: 0

US-10-015-388A-54 (1-280) x AX696985 (1-3580)

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Qy 41 ThrValAlaProGluHisGlyLeuAspAsnAlaProValValAspGlnGlnLeuLeuTyr 60  
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Qy 61 ThrCysCysProTyrIleGlyGluLeuArgLysLeuLeuAlaSerTrpValSerGlySer 80  
 Db 387 ACCTGCTGCCCTACATCGAGAGCTCCGGAACCTGCTCGCTTCTGTGGTGTCTAGGCAGT 446

Qy 81 SerGlyArgSerGlyGlyPheMetArgLysIleThrProThrThrThrSerLeuGly 100  
 Db 447 AGTGACGAGGTGGGGCTTCTATGAGGAAATCACCCACACCTACCCAGCCCTGGGA 506

Qy 101 AlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAlaGlnAlaPheHis 120  
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Qy 121 AsnGlnProProSerLeuArgThrValGluPheValAlaGluArgIleGlySerAsn 140  
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Qy 141 CysValLysHisIleValAlaThrLeuValAlaAspLeuValArgGlnAlaGluSerLeu 160  
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Qy 181 IleLeuCysSerGlnLeuCysProHisGlyAlaGlnAlaLeuAlaLeuGlyArgGluPhe 200  
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Qy 221 ValLeuSerSerAlaGluAsnIleAlaValGlyLeuAlaThrGluLysAlaCysAlaTrp 240  
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 ACCESSION AY358467  
 VERSION AY358467.1 GI:37182057  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 3580)  
 AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,

Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
 Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,  
 Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,  
 Stinson,J., Vagstad,A., Vanden,R., Watanabe,C., Wleand,D., Woods,K.,  
 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
 Goddard,A., Wood,W.I. and Godowski,P.  
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
 A Bioinformatics Assessment  
 Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL  
 PUBMED 12975309  
 REFERENCE 2 (bases 1 to 3580)  
 AUTHORS Clark,H.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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## ORIGIN

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US-10-015-388A-54 (1-280) x AY358467 (1-3580)

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Qy 81 SerGlyArgSerGlyGlyPheMetArgLysIleThrProThrThrThrSerLeuGly 100  
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Qy 101 AlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAlaGlnAlaPheHis 120



Wed Mar 30 09:32:46 2005

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Pred. No.:		1432.00	Matches: 280
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US-10-015-388A-54 (1-280) x BC066640 (1-4350)			
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RESULT 4			
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LOCUS			
DEFINITION Homo sapiens congenital dyserythropoietic anemia, type I, mRNA			

(cDNA clone IMAGE:6645406), partial cds.	
ACCESSION	BC052568
VERSION	BC052568.1
KEYWORDS	GI:30851636
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 4354) Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,P.S., Wagner,L., Shennen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schect,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raja,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullah,S.J., Bosak,S.A., McSwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahy,J., Helton,E., Kettelman,M., Madan,A., C., Shevchenko,Y., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Green,E.D., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Schmutz,J., Myers,R.M., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Skalska,U., Smalius,D.E., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 4354) Strausberg,R.
AUTHORS	Direct Submission
TITLE	Submitted (16-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
JOURNAL	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
REMARK	Contact: MGC help desk
COMMENT	Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a> Contact: <a href="mailto:nisc_mgc@nigr.nih.gov">nisc_mgc@nigr.nih.gov</a> Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgenev,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRAL Plate: 47 Row: 0 Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction.
source	Location/Qualifiers 1. 4354 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6645406" /tissue_type="Ovary, teratocarcinoma" /clone_lib="NIH_MGC_109"

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/Note="Vector: pOTB7"
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/db_xref="locusID:146059"
/db_xref="MIM:607465"
<1.3689
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/codon_start=3
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/db_xref="locusID:146059"
/db_xref="MIM:607465"
/translation="GMAAVLSELLREESVAAVVRWIAARSTQGSSEDNAGEAALSSLR
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SRPSLSDPPNLSNLEEFPPVSGVPPGPTGTPSRINPTPVEERSLSPKTCFTS
PPISCVSSQSDALTSFGLGPPGCSLQEREMLRKRSKQLQSQPTPTCTPEL
GSPRSRTGSLTDEPADPARVSSRQLRBLVALVSVCAENLVLNLFLEFVFLQFLT
ARMVYAKDSPELSPAVLDSLEPLFOSIHDVCFVAVQVLECHFOVLSNLDKGTLL
LAENRLLCFSPALQGLRRAAEGSVAKVFLVMPSTOAVSFQBPETDNANFSSDRAP
HTFKQRYFVEVLREWDHEEPDWEKGLGSRIRAMQQLSAAACHSHFVRLPQK
QLLQMCQSPGAGTGLGEAPDVLMLGADKLRLRQERLMAPOSSGGPCPPPTFP
GCQGFDFIILSASFQFNHLMDSLSKIQLNGLALPOHEPNDEDESVDWQGER
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RGLQARRAVLTPVLEFSPADHVPLLEYVDFITLLRLHSLVLSQSESEGMCF
LNKLLALLVGLWLFQIPVPEDLFELEGPVAVEDVTVAPEHGLDNAPVVDQLLYT
CCPYIGELKLLASWSSSSSGSGSPMKIPTPTTYSLGAQPSQTSQGLQALQAQFF
HNQPSLRTPFVFAERIGSCVRHIIKATLVADLVRAESLLQBLQVTOGEEGDDPAQ
LLETLCQSPHQAALGRFCQKSPGAVRALLPEETPAALVSSAENIATVGLATE
KACAWLSANIITALLIRREKAAVSRITRAQGPPEPARRGRCRACEHAPLPSHLIS
EIKDVLASVGRPDDEGVSEHLEQLQGLQTLRCQFLCPAECHLAKSCVELAS
LIVADQIPILGPPAQRRLRGOARELLHMLSLMKEDFGVPLQLLHSPNVLGLAD
TRPREWDLILLRLELVZKGLMGRMEIEACLGSLHQAWPGDFAEELATLSNLFLAEP
HLPEPQLRACELVQPNRGTVLAQS"
ORIGIN
Alignment Scores:
Pred. No.: 3 56e-97 Length: 4354
Score: 1432.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-015-388A-54 (1-280) x BC052568 (1-4354)
Qy 1 MetCysPheLeuAsnLysLeuLeuLeuLeuAlaValLeuGlyTrpLeuPheGlnIlePro 20
Db 2214 ATGTGTTTCTGAACAAGCTGCTGCTACTTGTCTGCTGGGCTGCTTTTCCAGATTCCC 2273
Qy 21 ThrValProGluAspLeuPheLeuGluGluGlyProSerTyrAlaPheGluValAsp 40
Db 2274 ACAGTCCCTGAGGACTGTGTTCTTCTGGAAGAGGCTCCCTCATATGCTTTGAGGTGGAC 2333
Qy 41 ThrValAlaProGluHisGlyLeuAspAsnAlaProValValAspGlnGlnLeuLeuTyr 60
Db 2334 ACAGTAGCCCCAGACATGGCTTGGACATATGCGCTGTGGGACGACGACGCTGCTCTAC 2393
Qy 61 ThrCysCysProTyrIleGlyLeuLeuArgLysLeuLeuAlaSerTrpValSerGlySer 80
Db 2394 ACCTGCTGCCCTACATCGGAGAGCTCGGAAACTGCTCGCTTGTGGGTGTGAGGCAGT 2453
Qy 81 SerGlyArgSerGlyGlyPheMetArgLysIleThrProThrThrThrThrSerLeuGly 100
Db 2454 AGTGACGAGGTGGGGGCTTCATGAGGAAATACCCCCACACTACACACGACGCTGGGA 2513
Qy 101 AlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAlaGlnAlaPhePheHis 120
Db 2514 GCCCAGCCTTCCAGACACGACGAGGGGCTGACGGGCACAGCTGCGCCAGGCCTTTTTCAC 2573
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Qy 121 AenGlnProProSerLeuArgArgThrValGluPheValAlaGluArgIleGlySerAen 140
Db 2574 AACACGCGCGCTCTCTTGGCGCGACCGCTAGAGTTCTGTGGCAGAAAGAAATGGATCAAC 2633
Qy 141 CysValLysHisIleLysAlaThrLeuValAlaAlaSerLeuValAtqGlnAlaGluSerLeu 160
Db 2634 TGTGTCAAAACATATCAAGGCTACACTGTGTGGCAGATCTGTGGTGGCGCAGGAGTGCATT 2693
Qy 161 LeuGlnGluGlnLeuValThrGlnGlyGluGluGlyGlyAspProAlaGlnLeuLeuGlu 180
Db 2694 CTCCAAGAGCAGCTGGTGACACAGGAGAGGAGGAGAGGAGAGGAGGAGGAGGAGGAGGAG 2753
Qy 181 IleLeuCysSerGlnLeuCysProHisGlyAlaGlnAlaLeuAlaLeuGlyArgGluPhe 200
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Qy 201 CysGlnArgLysSerProGlyValAlaValArgAlaLeuLeuProGluGluThrProAlaAla 220
Db 2814 TGTCAAGAGAGAGCCCTGGGGCTGTGGGGCTGTGGGGCTGTGGGGCTGTGGGGCTGTGGGG 2873
Qy 221 ValLeuSerSerAlaGluAsnIleAlaValGlyLeuAlaThrGluLysAlaCysAlaTrp 240
Db 2874 GTTCTGAGCAGTCGACAGAAACATTGCTGTGGGGCTGTGGGGCTGTGGGGCTGTGGGG 2933
Qy 241 LeuSerAlaAenIleThrAlaLeuIleArgArgGluValLysAlaAlaValSerArgThr 260
Db 2934 CTGTGAGCAACATCACAGCAGCTGATCAGGAGGAGGAGTGAAGAGCAGCAGTGTGTCGACA 2993
Qy 261 LeuArgAlaGlnGlyProGluProAlaAlaArgGlyGluArgGlyCysSerArgAla 280
Db 2994 CTTGAGCCCGAGGCTGCTGAACCTGCTGCCCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3053
RESULT 5
AF525398 4725 bp mRNA linear PRI 01-JAN-2003
LOCUS Homo sapiens codanin I mRNA, partial cds.
DEFINITION AF525398
ACCESSION AF525398.1 GI:27451597
VERSION AF525398.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4725)
AUTHORS Dgany, O., Avidan, N., Delaunay, J., Krasnov, T., Shalmon, L.,
Shalev, H., Bidelitz-Markus, T., Kapelushnik, J., Catlan, D.,
Pariente, A., Tulliez, M., Cretien, A., Schischmanoff, P.O.,
Iolascon, A., Fibach, E., Koren, A., Roessler, J., Le Merrier, M.,
Yaniv, I., Zaizov, R., Ben-Asher, E., Olender, T., Lancet, D.,
Beckmann, J.S. and Tamary, H.
Congenital dyserythropoietic anemia type I is caused by mutations
in codanin-1
Am. J. Hum. Genet. 71 (6), 1467-1474 (2002)
JOURNAL 22340442
MEDLINE 12434312
PUBMED 2 (bases 1 to 4725)
REFERENCE Ben-Asher, E.
AUTHORS Direct Submission
TITLE Submitted (27-JUN-2002) Molecular Genetics, The Weizmann Institute
JOURNAL of Science and the Schneider Medical Center, Hertzfel Street,
Rehovot 76100, Israel
FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="15"
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<1.3798
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/protein_id="AAO14994.1"
CDS
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**Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting**

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/HLN at: <http://image.llnl.gov>  
 Series: IRAL Plate: 7 Row: b Column: 15  
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

## FEATURES

Source

**. Location/Qualifiers**

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1. 3212
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3506144"
/tissue_type="Kidney, re
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note="vector: pOTB7"
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gen

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<1. .3212
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/note="synonyms: CDD"
/db_xref="LocusID:1"
/db_xref="MIM:60746"
<1. .2256
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**CDS**

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/db_xref="MIM:1607465"
/translation="FBKGLSGRIARL
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SSFOFNHLMDSLSKLTQELNGLQ
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FQIPTVEDPDLFEGSESPAYEPD
TSSGSSGSGSGFMRKLTPTTTSL
VAERIGSNVCKHITAVDLVAPPE
AQAALGSGVEFQKSPGCAVWALPE
IRREVKAANVSTLRQAQPEPARGEE
DPDSESPHEUQLHMLGSLQWEDCR
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RELVEKGLMGASMETEACLGSLHQQA
ONPNRGTVLQWAE"

```

## ORIGIN

**Alignment Score:**

Pred. No.:	9, 926-97	Length:	3212
Argument Scores:		Matches:	279
Score:	1424.00	Conservative:	0
Percent Similarity:	99.64%	Mismatches:	1
Best Local Similarity:	99.64%	Indels:	0
Query Match:	99.44%	Gaps:	0
DB:	9		

US-10-015-388A-54 (1-280) x BC001092 (1-3212)

[illegible]

Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,  
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 23 Row: d Column: 14  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis.

## FEATURES

## source

Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3506145"  
/tissue\_type="Kidney, renal cell adenocarcinoma"  
/clone\_lib="NIH MGC\_14"  
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/note="Vector: pOTB7"  
<1. 2256  
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WLVEFLFADHVPLEYRDI FTLLRLHSLSLVLSQSEGMCFNLKLLLVGLWL  
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RELVEKGLMRMEIEACLSGLHQAQWPGDFAEELATLSNLFLAEPLPEPOLRACELY  
QPNRGTVLAQS"

## CDS

121 AsnGlnProSerLeuArgArgThrValGluPheValAlaGluArgGlyGlySerAsn 140  
1141 AACGAGCGGCTCTTCGCGCGGACGTAGAGTTCGTGGCAGAAAGAAATTTGGATCAAC 1200  
141 CysVallyshisHslelysaAlaThrLeuValAlaAspLeuValArgGlnAlaGluSerIeu 160  
1201 TGTGCAAAATATCAAGGCTACACTGGTGGCAGATCTGGTGGCCAGGAGGATCACTT 1260  
161 LeuGlnGluGlnLeuValThrGlnGlyGluGlyGlyGlyGlyGlyGlyGlyGlyGlyGlu 180  
1261 CTCAAGAGCAGCAGCTGGTGGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320  
181 IleLeuCysSerGlnLeuCysProHisGlyAlaGlnAlaLeuAlaLeuGlyArgGluPhe 200  
1321 ATCTTGTGTTCCAGCTGTGCCCTCACGGGCGCCAGGCATTTGGCCTTGGGCGGAGTTC 1380  
201 CysGlnArgIysSerProGlyAlaValArgAlaLeuLeuProGluGluThrProAlaAla 220  
1381 TGTCAAAGGAAGAGCCCTGGGGCTGTGTGGCGCTGTGTCCAGAGGAGACCCCGGAGCC 1440  
221 ValLeuSerSerAlaGluAsnIleAlaValGlyLeuAlaThrGluLysAlaCysAlaTrp 240  
1441 GTTCTGAGCAGTGCAGAGAACATTTGCTGTGGGGCTTGCACAGAGAAAGCTGTGTCTGG 1500  
241 LeuSerAlaAsnIleThrAlaLeuIleArgArgGluValLysAlaAlaValSerArgThr 260  
1501 CTGTGAGCCACATCAGCAGCATCTGATCAGGAGGAGGAGTGAAGCAGCAGTGTGATCGCAC 1560  
261 LeuArgAlaGlnGlyProGluProAlaAlaArgGlyGluArgGlyGlyGlyGlyGlyGly 280  
1561 CTTCGAGCCAGGGTCTCTGAACCTGTCTCCCGGGGAGCGGAGGGGCTGTCTCCCGGCGCC 1620

## RESULT 8

## BC008334

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REMARK

## COMMENT

## FEATURES

## FEATURES

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## ORIGIN

## Alignment Scores:

## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

## US-10-015-388a-54 (1-280) x BC008333 (1-3212)

## QY

## 1 MetCysPheLeuAsnLysLeuLeuLeuAlaValLeuGlyTrpLeuPheGlnIlePro 20

## DB

## 781 ATGTGTTCTTGACAAAGCTGTGCTACTTGTCTGCTGGGCTGGCTTTCCAGATTCC 840

## QY

## 21 ThrValProGluAspLeuPheLeuGluGluGlyProSerTyralaPheGluValAsp 40

## DB

## 841 ACAGTCCCTGAGGACTTGTCTTCTGGAAGAGGTCCTCATATGCTTTCAGGTGGAC 900

## QY

## 41 ThrValAlaProGluHisGlyLeuAspAsnAlaProValValAspGlnGlnLeuTytr 60

## DB

## 901 ACAGTAGCCCGCAGAGATGCTTGGCAATATGCGCTGTGTGGACAGCAGCTGTCTTAC 960

## QY

## 61 ThrCysCysProTyrlleGlyGluLeuArgLysLeuLeuAlaSerTrpValSerGlySer 80

## DB

## 961 ACCTGCTGCCCTTACATCGAGAGCTCCGGAAACTGCTGCTGCTGGGTGTGAGCAT 1020

## QY

## 81 SerGlyArgSerGlyGlyPheMetArgLysIleThrProThrThrThrThrSerLeuGly 100

## DB

## 1021 AGTGGAGGAGTGGGGCTTCATGAGGAAATCAACCCACCACTACCACTGAGCTGGGA 1080

## QY

## 101 AlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAlaGlnAlaPheHis 120

## DB

## 1081 GCCCAGGCTTCCAGACCCAGCGGGGCTGCAGGCACAGCTCGCCCGGCGCTTTTCCAC 1140

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 23 Row: d Column: 13.  
Location/Qualifiers

## FEATURES

## FEATURES

## FEATURES

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## FEATURES

## FEATURES

## FEATURES





```
Qy 199 ----- 199
Db 25478 TCTTCTTTTCATGCTCTTTTCTTCTCCCTGGCCCAATCTCTATAAGCCCTGCACCT 25537
Qy 199 ----- 199
Db 25538 GGCTGTAGGCTTCTGTGGCAAAAGCAAACTAGTGTGGGAGCGTGTGTGATGCTG 25597
Qy 199 ----- 199
Db 25598 TGGGCTGCAGCTGGGCTGTCTTTCTTCTGGCACCTGGGCTGGGCTGGGCGGAGGCAAC 25657
Qy 199 ----- 199
Db 25658 GGTGCTCTCTTCAAGGTACAGCTCCAGGCTCAGGGCTTGGTGTCACTCGGGGCATTTA 25717
Qy 200 -----ph 200
Db 25718 CTTCTGCAGCCAGGCTGAAATACCCAGAGATCACTGACCCCATCTGTCCCTTTTAGGTT 25777
Qy 200 eCysGlnArgLysSerProGluAlaValArgAlaLeuLeuProGluGluThrProAlaAl 220
Db 25778 CTGTCAAAAGGAGAGCCCTTGGGCTGTGGGCTGTGGGCTGTCTTCAGAGGAGACCCCGGCAGC 25837
Qy 220 a----- 220
Db 25838 -CGTACGTGTGAGGGAGGCTGTCACTAGCAGGCCAGGCAGTTGTGGGAGGTGCACGGA 25896
Qy 220 ----- 220
Db 25897 GTAGTCTGAGGCTGCGGAGGGTGTGTGGGGCGGGTCTGAGTCTGCTGCGCATCCT 25956
Qy 221 -----ValLeuSe 223
Db 25957 TTGTTGACCCAGCCCTCCCTAGCCCTGACTCTGTAGTCTGTCTTTCGAGGTTCTGAG 26016
Qy 223 rSerAlaGluAenLeuAlaValGluLeuAlaThrGluLysAlaCysAlaThrLeuSerAl 243
Db 26017 CAGTGCAGAGAACATTTGTGTGGGCTGTCAACAGAGAAAGCCTGTGTCTGTGTGCTCAGC 26076
Qy 243 aAsnIle----- 245
Db 26077 CAACAT-CACAGGTAAGTCTCTGGATGGGGAGTGCTGTAATCAAGTGTGTTTAAAGATGG 26135
Qy 245 ----- 245
Db 26136 ACTGCAGAGAGTCAGAGGCATCTTGTGGCGATGGGACTGAGACCCAGTAGGAACAGC 26195
Qy 245 ----- 245
Db 26196 AAAAGGCATGGTTAGCATGTGTGAACCTGTGCAGGGCCCTCCCGTGAATTCCTTCCCAT 26255
Qy 246 -----ThrAlaLeuIleArgGluValLysAlaAlaValSerArgThrIle 261
Db 26256 CTCCTCTGCCCCCAGCAGCTGATCAGGAGGAGGTGAAGCAGCAGTGTGCTGCACACT 26315
Qy 261 uArgAlaGlnGlyProGluProAlaAlaArgGluArgGlyCysSerArgAla 280
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RESULT 10
AC090510/c AC090510 148295 bp DNA linear PRI 19-JAN-2002
LOCUS AC090510 Homo sapiens chromosome 15 clone CTD-2036P10 map 15q21.1, complete
DEFINITION AC090510 sequence.
ACCESSION AC090510
VERSION AC090510.4 GI:18249987
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

REFERENCE  
AUTHORS

1 (bases 1 to 148295)

Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,  
Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,  
Pate,D. and Hood,L.

Sequencing of human chromosome 15 D15S146-D15S117 region

TITLE  
JOURNAL

Unpublished

REFERENCE  
AUTHORS

2 (bases 1 to 148295)

Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,  
Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Madan,A.,  
Nesbitt,R., Traicoff,R. and Hood,L.

TITLE  
JOURNAL

Direct Submission

Submitted (27-FEB-2001) Multimegabase Sequencing Center, Institute  
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA  
98105, USA

REFERENCE  
AUTHORS

3 (bases 1 to 148295)

Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,  
Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,  
Pate,D. and Hood,L.

TITLE  
JOURNAL

Direct Submission

Submitted (19-JAN-2002) Multimegabase Sequencing Center, Institute  
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA  
98105, USA

## COMMENT

On Jan 19, 2002 this sequence version replaced gi:17436948.

----- Genome Center

Center: Multimegabase Sequencing Center

Center code: UMWSC

Web site: http://chroma.mbt.washington.edu/msg\_www

Contact: leaowen@systembiology.org

----- Summary Statistics

Sequencing vector: pUC18; L08752

Chemistry: Dye-terminator Big Dye; 90% of reads

Chemistry: Dye-primer Big Dye; 10% of reads

Assembly program: Phrap; version 0.990399

Note: data from AC018362 [Drafting center UMWSC] ans AC068727

[Drafting center UMWSC] were added for finishing.

## FEATURES

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the extent possible."

1. 6205

/note="overlap with RP11-265N6 AC018362."

100366. 148295

/note="overlap with RP11-90M11 AC068727."

## ORIGIN

Alignment Scores:

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Score: 934.00 Matches: 275

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Best Local Similarity: 32.74% Mismatches: 5

Query Match: 65.22% Indels: 565

DB: Gaps: 8

US-10-015-388A-54 (1-280) x AC090510 (1-148295)

Qy 17 ----- 17

Db 91140 CAGAGTGGGTCAGATTTGGAGAGAGTTCTACAGCTGAAGATGGGAGTGGCGAATG 91081

Qy 17 ----- 17

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Qy 17 ----- 17

Db 91140 CAGAGTGGGTCAGATTTGGAGAGAGTTCTACAGCTGAAGATGGGAGTGGCGAATG 91081

Qy 17 ----- 17

Db 91140 CAGAGTGGGTCAGATTTGGAGAGAGTTCTACAGCTGAAGATGGGAGTGGCGAATG 91081

Qy 17 ----- 17

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Qy 17 ----- 17

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Qy 17 ----- 17

Db 91140 CAGAGTGGGTCAGATTTGGAGAGAGTTCTACAGCTGAAGATGGGAGTGGCGAATG 91081

Qy 17 ----- 17

Db 91140 CAGAGTGGGTCAGATTTGGAGAGAGTTCTACAGCTGAAGATGGGAGTGGCGAATG 91081

Qy 17 ----- 17

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Qy 17 ----- 17

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Db 91080 TCTGAGTCGGAATGAGGCAAGGCTGGAAGACGAGAGGTTTCAGAAAGSCCTGGGGATTCC 91021  
QY 17 ----- 17  
Db 91020 CATCATCTCAGAGGTGGCTGCTTTTGAAGCTGGCGCTACACCTGGGACCGTGCAGGAGG 90961  
QY 18 -----Glnile 19  
Db 90960 TGGGTGGGTGGGTGGGGTCTCTGAAGTTGACCTGAAATTTGTGACTGTCTTGCCAGATT 90901  
QY 20 ProThrValProGluAspLeuPheLeuGluGlyProSerTyrAlaPheLeuVal 39  
Db 90900 CCCACAGTCCCTGAGGACTGTGCTTTCTGGAAGAGGGTCCCTCATATGCTTTGAGGTG 90841  
QY 40 AspThrValAlaProGluHisGlyLeu----- 48  
Db 90840 GACACAGTAGCCCCAGAGCATGGCTT-GGTGAGTCTGGGTTCGCGAGAGCCATGGGA 90782  
QY 48 ----- 48  
Db 90781 AACTCAGGAATAAGAAAGTGGGCTGCTGGGAGGCCAGCCAGGGGCGAGATGTAAACC 90722  
QY 48 ----- 48  
Db 90721 TTGTAAAGCCCTGCCAACTGCTCTTCTGGGTGCGCTGGGGAGGGCGAGTCTGCTG 90662  
QY 49 -----AspAlaValProValValAspGlnGlnLeuLeuTyrThr 61  
Db 90661 ACACCAACCTTTTCTCCAGGACAATGCGCTGTGTGGTGGACAGCAGCTGCTCTACACC 90602  
QY 62 CysCysProTyrIle----- 66  
Db 90601 TGCTGCCCTTACATCGGTGAGCACCGGTCTTCCCTGGACGGTCTTGGTGTCTGCTCCTCCA 90542  
QY 66 ----- 66  
Db 90541 TGAGTACCCAAAGGACCCCTTGGCCAGCTCCCTTGGATATTGCTCCGTTTCATAGTC 90482  
QY 66 ----- 66  
Db 90481 ATTCTGGGTATCTGAGCCTTTGACTCCAAAGTAAAGTCCATGATACTTTAGGAGGGG 90422  
QY 67 -----GlyGluLeuArgLysLeu 73  
Db 90421 AGAGGGTCTCGAACTGAGAACTTGGACTTCACTGATACAGAGAGCTCCGGAATCTGCT 90362  
QY 73 uAlaSerTrpValSerGlySerGlyArgSerGlyGlyPheMetArgLysIleThrPr 93  
Db 90361 CGCTTCGTGGGTGTCAGGCAGTAGTGGACGGAGTGGGGCTTTCATGAGGAAATCACCCC 90302  
QY 93 oThrThrThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeu----- 110  
Db 90301 CACCACTACACAGCCTGGAGCCAGCCTTCCAGACCAGCCAGGGGCTGCAGGTAAG 90242  
QY 110 ----- 110  
Db 90241 GGCAGGCGGAGACAGCCGTGGGGAATAATGAGGGGGGTGGGGCGGGGACAGGAGGC 90182  
QY 111 -----GlnAlaGlnLeuAlaGlnAlaPhePh 119  
Db 90181 TGGAGGAAGCCTTGCTGCTCTCCCTCCTCCCGCCAGGCACAGCTCGCCCGAGCCCTTTT 90122  
QY 119 eHisAnGlnProProSerLeuArgThrValGluPheValAlaGluArgIleGlySe 139  
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QY 147 ----- 147

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Db 89882 GCCTCTTTCCGATTAACCTCCCAACCATCCCAACCTTGTGTCTCCCTGCTGCAGGGGTAC 89823  
QY 148 -----Th 148  
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QY 168 nGlyGluGlyGlyAspProAlaGlnLeuLeuGluIleLeuCysSerGlnLeuCysPr 188  
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Db 89702 TCACGGGGCCAGGCAITGGCCCTGGGGCGGAGTAAGCAGCGCTGTCCATTGTATCCA 89643  
QY 199 ----- 199  
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QY 199 ----- 199  
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QY 199 ----- 199  
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QY 199 ----- 199  
Db 89402 GGTGCTCTTCCAAGGTACAGCCTCCAGGTTCAGGGGCTTGTGTGCTCTCGGGGCAATTA 89343  
QY 200 -----ph 200  
Db 89342 CTTCTGACGCCAGGCTGAAATACCCAGAGATCACTGACCCCATCTGTCTCTTCTTCTTCTT 89283  
QY 200 eCysGlnArgLysSerProGlyAlaValArgAlaLeuLeuProGluGluThrProAlaAl 220  
Db 89282 CTGTCAAAGGAAGAGCCCTGGGGCTGTGGGGCTGTGCGGGGCTGCTTCCAGAGGAGACCCCGGCAGC 89223  
QY 220 a----- 220  
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QY 220 ----- 220  
Db 89163 GTAGTCTGAGGCTGCGGAGGGTGTGTGGGGCGGGGTGCTGTGCTCGACTCTGGCATCCT 89104  
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Db 89103 TTGTTCACCCAGCCCTCCCTAGCCCTGACTCTGTAGTTCTGTTCGAGGTTCTGAG 89044  
QY 223 rSerAlaGluAsnIleAlaValGlyLeuAlaThrGluLysAlaCysAlaIlePLeuSerAl 243  
Db 89043 CAGTCACAGAACATTTGTGTGGGGCTTGCACAGAGAAAGCTGTGCTTGGCTGTGCTCAGC 88984  
QY 243 aAsnIle----- 245  
Db 88983 CAACAT-CACAGGTAAGTCTCTGATGGGGAGTGGCTGAATCAAGTGTTTAAAAAGTGG 88925  
QY 245 ----- 245  
Db 88924 ACTGGCAGAGCTCAGAGCATCTTTGTGGGCGATGGGACTGAGCCAGTAGGAACACAGC 88865



QY 245 ----- 245

Db 88864 AAAAGCATGGTTAGCATGTGAACCTGTGTCAGGCGCCCTCCGCGATTCTTTCCCAT 88805

QY 246 -----ThralaLeulleArgArgCluVallysAlaAlaValSerArgThrie 261

Db 88804 CTCCTCTGCCCCCAGCAGCACTGTCAGGAGGAGGTGAAGCAGCAGTGAGTCGCACACT 88745

QY 261 uArgAlaGlnGlyProGluPuAlaAlaArgGlyGluArgGlyCysSerArgAla 280

Db 88744 TCGAGCCAGGCTCTGTAACCTGTGTCGCGGGGAGCGAGGGCTCTCTCCGCGCC 88687

RESULT 11

AC099267

LOCUS Rattus norvegicus clone CH230-223L3, \*\*\* SEQUENCING IN PROGRESS

DEFINITION \*\*\* 11 unordered pieces.

ACCESSION AC099267.5 GI:30578709

VERSION HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 260033)

AUTHORS Muzny D, Marie, Metzker M, Lee, Abramson S, Adams C, Alder J, Allen C, Allen H, Albrooks S, Amin A, Anguiano D, Anyalebechi V, Aoyagi A, Ayodeji M, Baca S, Baden H, Baldwin D, Bandaranaike D, Barber M, Barnstead M, Benahmed F, Biwaite K, Blair J, Blankenburg K, Blyth P, Brown M, Bryant N, Buhay C, Burch P, Burrell K, Calderon E, Cardenas V, Carter K, Cavazos I, Ceasar H, Center A, Chacko J, Chavez D, Chen G, Chen R, Chen Y, Chen Z, Chu J, Cleveland C, Cockrell R, Cox C, Coyle M, Cree A, D'Souza L, Davila M, Davis C, Davy-Carroll L, De Anda C, Dederich D, Delgado O, Dengson S, Deramo C, Ding Y, Dinh H, Divya K, Draper H, Dugan-Rocha S, Dunn A, Durbin K, Duval B, Eaves K, Egan A, Escotto M, Eugene C, Evans C, Falls T, Fan G, Fernandez S, Finley M, Flagg N, Forbes L, Foster M, Foster P, Fraser C, Gabisi A, Ganta R, Garcia A, Garner T, Garza M, Gebregioris E, Geer K, Gill R, Grady M, Guerra R, Guevara W, Gunaratne P, Haaland W, Hamill C, Hamilton C, Hamilton K, Harvey Y, Havlak P, Hawes A, Henderson N, Hernandez J, Hernandez R, Hines S, Hladun S, Hodgson A, Hognes M, Hollins B, Howells S, Hulyk S, Hume J, Idlebird D, Jackson A, Jackson L, Jacob L, Jiang H, Johnson B, Johnson R, Jolivet A, Karpathy S, Kelly S, Kelly S, Khan Z, King L, Kovar C, Kowis C, Kraft C, Lebow H, Levan J, Lewis L, Li Z, Liu J, Liu J, Liu W, Liu Y, London P, Longacre S, Lopez J, Lorensuewa L, Loulsegged H, Lorado R, Lu X, Ma J, Maheshwari M, Mahindaratne M, Mahmoud M, Malloy K, Mangum A, Mangum B, Mapua P, Martin K, Martin R, Martinez E, Mawhinney S, McLeod M, McNeill T, Meenen E, Milosavljevic A, Miner G, Minja E, Montemayor J, Moore S, Morgan M, Morris K, Morris S, Munidasa M, Murphy M, Nair L, Nankervis C, Neal D, Newton N, Nguyen N, Norris S, Parks K, Nwakoelameh O, Okwunou G, Olarnpunsagoon A, Pal S, Parkes K, Paternak S, Paul H, Perez A, Perez L, Pfankoch C, Plopper F, Poindexter A, Popovic D, Primus E, Pu L, Pu L, Puazo M, Quiroz J, Rachin E, Reeves K, Regier M, Reigh R, Reilly B, Reilly M, Ren Y, Reuter M, Richards S, Riggs F, Rives C, Rodkey T, Rojas A, Rose M, Rose R, Ruiz S, Sanders W, Savery G, Scherer S, Scott G, Shatman S, Shen H, Shetty J, Shvartsbeyn A, Sisson I, Sitter C, Smajd D, Sneed A, Sodergren E, Song X, Sorelle R, Sosa J, Steimle M, Strong R, Sutton A, Svatek A, Taber P, Taylor C, Taylor T, Thomas N, Thomas S, Tingey A, Trejos Z, Usmani K, Valas R, Vera V, Villanasa D, Waldron L, Walker B, Wang J, Wang Q, Wang S, Warren J, Warren R, Wei X, White F, Williams G, Willson R, Wleczyk R, Wooden H, Worley K, Wright D, Wright R, Wu J, Yakub S, Yen J, Yoon L, Yoon V,

Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

Unpublished

2 (bases 1 to 260033)

Direct Submission

Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 260033)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:2321447.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center of Medicine

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GJNH

Center clone name: CH230-223L3

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 234700 bases at least Q40

Consensus quality: 239776 bases at least Q30

Consensus quality: 242937 bases at least Q20

Estimated insert size: 248755; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: Estimated insert size may differ from sequence length (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

\* 1 226385: contig of 226385 bp in length

\* 226386 226485: gap of unknown length

\* 226486 232811: contig of 6326 bp in length

\* 232812 232911: gap of unknown length

\* 232912 244866: contig of 11955 bp in length

\* 244867 244966: gap of unknown length

\* 244967 248097: contig of 3131 bp in length

\* 248098 248197: gap of unknown length

\* 248198 249262: contig of 1065 bp in length

\* 249263 250363: gap of unknown length

\* 250364 250548: contig of 1186 bp in length

\* 250549 252326: contig of 1678 bp in length

\* 252327 252426: gap of unknown length

\* 252427 253828: contig of 1402 bp in length

\* 253829 253928: gap of unknown length

\* 253929 255915: contig of 1987 bp in length







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QY 36 AlaPheGluValAspThrValAlaProGluHisGlyLeu----- 48
Db 13520 GCCTTTGAGGTGACTACAACTGCTTTCAGAGCATGGTTTGGTGAGTGTCCACACAGATAAA 13461
QY 48 ----- 48
Db 13460 TGAGCTGAATAGATAAGGACCCAGACAGACCAGACTAGGGAAGACTTAAAGACGGTCCAT 13401
QY 48 ----- 48
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QY 49 -----AspIleAlaProValValAspGlnGlnLeuLeuTyr 60
Db 13340 CAGCATTTGGTCTGTCTTCTCCCCAGGACAGTGTACCTGTTGTGGACAGCAGCTGTATAT 13281
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QY 66 ----- 66
Db 13220 ATGGCTTGGCTGTGTCATGATACCCAAAGGACCTCACTCCTCAGCATACTGTTCTGTCT 13161
QY 66 ----- 66
Db 13160 TTAGGCTCTGTGTTACTTCATTCGTCTTTGCCCCAAAGGCCATGATGTTTGGGGAGG 13101
QY 67 -----GlyGluLeuArgLysLe 72
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QY 72 uLeuAlaSerTrpValSerGlySerArgSerGlyGlyPheMetArgLysIleTh 92
Db 13040 GCTTGTCTCTGGTTTCAGGAAGCAGTGGGGGAGTGAGGCTTTGTGAGGAAATCAC 12981
QY 92 rProThrThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeu----- 110
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QY 110 ----- 110
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QY 146 ----- 146
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Db 12440 TGGTGGCAGCGGGGACAGAGAGGGGAGATCCAGCACAGCTTTTGGAAATCCTTGTGTCTC 12381
QY 185 InLeuCysProHisGlyValaGlnAlaLeuAlaLeuGlyArgGlu----- 199
Db 12380 AACTCTGCCCCCATGGGGCCCCCAAGCATTGACCCAGGGGGGAGTAAGAACTGTTAAATCT 12321
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QY 199 ----- 199
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QY 200 -----PheC 201
Db 11900 TTTGTGAGTCACTACACTATCCGACATTCGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 11841
QY 201 YsGlnArgLysSerProGlyAlaValArgAlaLeuLeuProGluGluThrProAlaAla- 220
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QY 220 ----- 220
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QY 220 ----- 220
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QY 221 -----ValLeuS 223
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QY 223 erSerAlaGluAsnIleAlaValGlyLeuAlaThrGluLysAlaCysAlaThrLeuSerA 243
Db 11600 GCAGTGCAGAAACATTCGTGTGGGGCTTGGCAGAGAAAGCCCTGCTCTTGTGTGTGAG 11541
QY 243 laAsnIleThr----- 246
Db 11540 CCAACATCACAGGTGAGTCTAGGAAGGAGTGTGACCAAGCTTTTAAAGGTGGACA 11481
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QY 246 ----- 246
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Qy      224 rAlaGluAenIleAlaValGlyVleuAlaThrGluLySAlaCysAlaTrpLeuSerAlaAs 244
Db      59276 TGCAGAGAACATTGCTGTGGGGCTTGCACAGAGAAAGCCTGTGCTGTGCTGTGAGCCAA 59335
Qy      244 nile----- 245
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Qy      245 ----- 245
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Qy      245 ----- 245
Db      59455 AGGCATGGTTAGCATGTGTGAACCTGTGCAGGCGCCCTCCCGTGATTCCTTTCCCATTCCTC 59514
Qy      246 -----ThrAlaLeuLeuArgArgGluValLySAlaAlaValSerArgThrLeuAr 262
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RESULT 14
BX537330/c
LOCUS      166294 bp      DNA      linear      HTG 06-OCT-2004
DEFINITION      Danio rerio clone DKEYP-104A11, WORKING DRAFT SEQUENCE.
ACCESSION      BX537330
VERSION      BX537330.8  GI:53850156
KEYWORDS      HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Danio rerio (zebrafish)
ORGANISM      Danio rerio
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
              Cypriniformes; Cyprinidae; Danio.
              1 (bases 1 to 166294)
              Leongamornlert, D.
              Direct Submission
              Submitted (05-OCT-2004) Wellcome Trust Sanger Institute, Hinxton,
              Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
              zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
              On Oct 6, 2004 this sequence version replaced gi:52213873.
              ----- Genome Center
              Center: Wellcome Trust Sanger Institute
              Center code: SC
              Web site: http://www.sanger.ac.uk
              Contact: zfish-help@sanger.ac.uk
              ----- Project Information
              ----- Summary Statistics
              Assembly program: XGAP4; version 4.5
              Consensus quality: 166177 bases at least Q40
              Consensus quality: 166251 bases at least Q30
              Consensus quality: 166280 bases at least Q20
              Insert size: 166294; sum-of-contigs
              Insert size: 156143; 4.0% error; agarose-fp
              Quality coverage: 7.07x in Q20 bases; sum-of-contigs Quality
              coverage: 7.57x in Q20 bases; agarose-fp

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\* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs \* are represented as runs of N. The order of the pieces \* is believed to be correct as given, however the sizes \* of the gaps between them are based on estimates that have

\* provided by the submittor.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 \* 1 166294: contig of 166294 bp in length.

#### FEATURES

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 clone\_end:SP6  
 vector\_side:left"

#### misc\_feature

#### ORIGIN

Alignment Scores:  
 Pred. No.: 3.27e-16 Length: 166294  
 Score: 371.50 Matches: 122  
 Percent Similarity: 32.48% Conservative: 31  
 Best Local Similarity: 25.90% Mismatches: 43  
 Query Match: 25.94% Indels: 277  
 DB: 2 Gaps: 7

US-10-015-388A-54 (1-280) x BX537330 (1-166294)

Qy 49 AsphenAlaProValValAspGlnGlnLeuLeuThrCysCysProTyrile----- 66  
 Db 10286 GACACATCCCATTAGTGGACCAACAGCTTCTACACTTGCTGCCATATTT-GGGTAA 10228  
 Qy 66 ----- 66  
 Db 10227 GAGCAAGCTCCTCTGGRAAATGTGCTTCAGAAATTATGATTCGACAAAGAAATACAGTA 10168  
 Qy 67 -----GlyGluLeuArg 70  
 Db 10167 CATTTCTAATGATGGTGATGATTATCTTTTACATCATTTCTTTTGAAGGGAGTTCT 10108  
 Qy 71 LysLeuLeuAlaSerTrpValSerGlySerGlyArgSerGlyGlyPheMetArgLys 90  
 Db 10107 AAACCTTCTGCTGCTTTGTGCTGTAGACATCTCAAGAGTGGAGGCTTGATTGCGCAG 10048  
 Qy 91 IleThrProThrThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeu 110  
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 Db 9868 CACAACCAACCCCTTCTCTGAGGCGGTACTGTAGAGTTTGTGTGAGAGGTCGCGCTCC 9809  
 Qy 140 AsnCysValLySHisIleLys----- 146  
 Db 9808 AACTGCGTCAAAACACATTAAAGTCAGTCTCCAAGATTTTGTGACCCCTTTTCTTTCTAGTC 9749  
 Qy 146 ----- 146  
 Db 9748 CATGCAATTAATTTTACATTTGTTTTTATCATTTTCCCTAATTCATGTTGTCGCGAGA 9689  
 Qy 147 AlaThrLeuValAlaAspLeuValArgGlnAlaGluSerLeuLeuGlnGlnGluVal 166  
 Db 9688 GCAACACTTGTGTTGGAGCTTGTGAGGGGTGTGAGAAACTCTCAGGGATAGTTG--- 9632  
 Qy 167 ThrGlnGlyGluGluGlyGlyAspProAlaGlnLeuLeuGluLeuLeuLeuLeuLeu 186

```

Db 9631 -----GATGAGGGCGTAAACACTGCCAGCTAAACGACTATCTGTCTCAGCTG 9578
QY 187 CysProHisGlyAlaGlnAlaLeu-----AlaLeu-GlyArg----- 198
Db 9577 TGTGATCGGGCATGCAAGCTCTGGAGAGAGCAACAGGCTCAATGGCTTGTCTTTTCTT 9518
QY 198 ----- 198
Db 9517 TTAAGTATTGGCAACACTTTATTTTGGAGGTCGGTTGAGTATTAGTAGACTGTCTGCT 9458
QY 198 ----- 198
Db 9457 TAATATCTGTTGATATCTGTTAATATCTGCTCTTCAACAGACTTCAACTGACTATAAG 9398
QY 198 ----- 198
Db 9397 AAACTTTGCAAGTACATGTCATTTTACCAACCCCTAACCTCAACCCCTAACCTA 9338
QY 198 ----- 198
Db 9337 ACAGCTTAATTAATCTAATGAGAATTAGTTGGCATGTAGTGCATGTAACTTAAATT 9278
QY 198 ----- 198
Db 9277 TAGCAACGGACCACCAATAAAGTCTGACCAAGTTTTTTGTTAAAGTAAACATGTT 9218
QY 199 ----- 199
Db 9217 TTTCAACACTCTTTTGTATCTAGATGCTTTTGTCTCATCATGTCATGATAGTCTGCAG 9158
QY 202 narglySerProGlyAlaValArgAlaLeuLeuProGluGluThrProAlaAla----- 220
Db 9157 TGAGATGCTCCAGGAGCTGTCGAGTCTTCTTCTCTGGAGACTCTCTCTCTGTCGAG 9098
QY 220 ----- 220
Db 9097 TAAACAGCTGTTAGTTCGTTAGTTCAGTCCATTAATACTCGCTTATTTATTTAATT 9038
QY 220 ----- 220
Db 9037 TAAAAAACAAGCTATGAGTATGATTAATAATTGCTTTGAGATGCTGTTAAATGTGCTG 8978
QY 221 -----ValLeuSerAlaGluAsnileAlaValGlyLeuAlaThrGluLysAlaC 238
Db 8977 TGGTTAGTCTTGACCAAGCTATGAGCATCACCCTGTTGGCTACAGAAAGGCTT 8918
QY 238 ysAlaTrpLeuSerAlaAsnileThrAla 247
Db 8917 GCAGCTGGCTGTCTTCCACATCACAAGT 8889

RESULT 15
BX569781/c 170138 bp DNA linear VRT 07-JUL-2004
LOCUS Zebrafish DNA sequence from clone DKEY-72L18 in linkage group 17,
DEFINITION complete sequence.
ACCESSION BX569781
VERSION 7
KEYWORDS HTG.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 170138)
Direct Submission
Submitted (07-JUL-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 8, 2004 this sequence version replaced gi:46802300.
----- Genome Center
Center: Wellcome Trust Sanger Institute

```

Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: [zfish-help@sanger.ac.uk](mailto:zfish-help@sanger.ac.uk)

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Emi, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see

[http://www.sanger.ac.uk/Projects/D\\_rerio/fishmask.shtml](http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml) DKEY-72L18 is from a Zebrafish BAC library

VECTOR: pIndigoBAC-5.

FEATURES  
 Location/Qualifiers  
 1..170138  
 /organism="Danio rerio"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="DKEY-72L18"  
 /clone\_lib="DanioKey"

# ORIGIN

## Alignment Scores:

Pred. No.:	336e-16	Length:	170138
Score:	371.50	Matches:	122
Percent Similarity:	32.48%	Conservative:	31
Best Local Similarity:	25.90%	Mismatches:	43
Query Match:	25.94%	Indels:	277
DB:	5	Gaps:	7

US-10-015-388A-54 (1-280) x BX569781 (1-170138)

QY 49 AspAsnAlaProValValAspGlnGlnLeuLeuThrCysCysProTyrlle----- 66

Db 112256 GACACATCCCATTTAGTAGGACCAACAGCTTCTTACACTTGTCTGCTCCATATTT-GGGTAA 112198

QY 66 ----- 66

Db 112197 GAGCAAGCTCCTCTGGAAAAATGTCTTCAGAAATTATGATTGTCACAAAGAAATACAGTA 112138

QY 67 -----GlyGluLeuArg 70

Db 112137 CATTTCTAATTGATGCTGATGATTATTTTATCATCATCTTTTGAAGGGGAGTTTCGT 112078

QY 71 LysLeuLeuAlaSerTrpValSerGlySerGlyArgSerGlyGlyPheMetArgLys 90

Db 112077 AAACATCTCTGCTGCTTTTGTGCTGTGTAGCATCTCAAGATGGAGGCTTGATTCGCAAG 112018

QY 91 IleThrProThrThrThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeu 110

Db 112017 ATCACCCCAACGCTCTCTGAGAACCAAGGGTCTCTCGACTATACAGCTTCACAGCAGAACTT 111958



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111 GlnAlaGln----- 113
111957 CAGGT-AAACTGCCAGCAAATGCTCTCCATCTGTAGTATAATCGATAGTATGTTTTTAAT 111899
114 -----LeuAlaGlnAlaPhe 119
111898 GAGAGTTCATTAAATGTTTTTGGATGTTTTTAACAAGGTGACCTGGACGAGCCCTTTTTT 111839
120 HisAsnGlnProProSerLeuArgThrValGluPheValAlaGluArgIleGlySer 139
111838 CACAACCAACCCCTTCTCTCAGGCGTACTGTAGAGTTTGTGCTGAGAGGGTCGGCTCC 111779
140 AsnCysValLysHisIleLys----- 146
111778 AACTGCGTCAAACACATTAAAGTCAGTCTCCAAGATTTTGTAGCCCTTTTTTCTTCTTAGTC 111719
146 ----- 146
111718 CATGCAAAATTACTTTACATTTGTTTTTTTATCATTTTCATTTCCCTAACTGTGTGGCAGA 111659
147 AlaThrLeuValAlaAspLeuValArgGlnAlaGluSerLeuLeuGlnGlnLeuVal 166
111658 GCAACACTGTGTGGAGCTTGTGAGGGGTGGTGAAGAACTCTCAGGGATAGCTTG--- 111602
167 ThrGlnGlyGluGlyGlyAspProAlaGlnLeuLeuGluIleLeuCysSerGlnLeu 186
111601 -----GGTATGGAGGGCGTAAACACACTGCCAAGCTAAACGACTGTATCTGTGCTCAGCTG 111548
187 CysProHisGlyAlaGlnAlaLeu-----AlaLeu-GlyArg----- 198
111547 TGTGATGGCGGCATGCAAGCTCTGGAGAGAGCAACACAGGTCAATGGCTTGTCTTTTCTT 111488
198 ----- 198
111487 TTAAGTATTTGGCAACACTTTATTTTGACGGTCCGTTTGAGTATTAGTAGACTGCTGCT 111428
198 ----- 198
111427 TAATATCTGTTGATATCTGTTAATATCTGCTCTCTCAACAGACTTTCAACTGACTATAAG 111368
198 ----- 198
111367 AAACCTTGGCAAGTACATGTCATTTTACACCAACCCTAACCTAACCCCTAACCTA 111308
198 ----- 198
111307 ACAGTCTAATTATTAATCTAATGAGAAATTAGTTGGCATGTAGTGCATTTGTAACTTAAAT 111248
198 ----- 198
111247 TAGCAACGGACCATCAAAATAAAGTCTGACCAAGTTTTTTGTTTAAAGTAAACATGTT 111188
199 -----GlupheCysG1 202
111187 TTCATAACATCTTTTGATCTAGATGCTTTTTGCTCATCATGTATGATAGGTTCTGCAG 111128
202 nArgLysSerProGlyAlaValArgAlaLeuProGluGluThrProAlaAlaA----- 220
111127 TGAGATGCTCCAGGAGCTGTCGAGATTCTTCTCTCTGAGACCTCTCTCTCTGTCGAG 111068
220 ----- 220
111067 TAAACACAGTCGTAGTTGTTAGTTAGTTCAGTCCATTAAATCTCGCTTATTTTATTGTTAAT 111008
220 ----- 220
111007 TAAAAAACAAGCTATAGGATGATAAATAATTTGCTTTGAGATGTTGTTAAAAATGTGTG 110948
221 -----ValLeuSerSerAlaGluAsnIleAlaValAlaGlyLeuAlaThrGluLysAlaC 238
110947 TGGTTTAGTCTTGACCACTAAGCATACACCACTCGTGTGGCTACAGAAAGGCTT 110888
238 ySalatrpLeuSerAlaAsnIlethrAla 247

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Run on: March 29, 2005, 08:32:35 ; Search time 487 Seconds  
(without alignments)  
3403.547 Million cell updates/sec

Title: US-10-015-388A-54

Perfect score: 1432

Sequence: 1 MCFINKLILLAVLWLFQIP.....LRAQPRPAARGRRGCSRA 280

Scoring table: BLOSUM62

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description
RESULT 1					
ID	AA058112	standard; cDNA; 3580 BP.			
DE	Human PRO1295 nucleotide sequence	SEQ ID NO:28.			
PN	WO200053750-A1.				
PD	14-SEP-2000.				
PA	(GETH ) GENENTECH INC.				
Best Local Similarity:	100.00%				Mismatches: 0
Query Match:	100.00%				Indels: 0
RESULT 2					
ID	AAA37037	standard; cDNA; 3580 BP.			
DE	Human PRO1295 (UNQ664) cDNA sequence	SEQ ID NO:53.			
PN	WO200012708-A2.				
PD	09-MAR-2000.				
PA	(GETH ) GENENTECH INC.				
Best Local Similarity:	100.00%				Mismatches: 0
Query Match:	100.00%				Indels: 0
RESULT 3					
ID	AAF54239	standard; DNA; 3580 BP.			
DE	DNA encoding protein of the invention	#16.			
PN	WO200078961-A1.				
PD	28-DEC-2000.				
PA	(GETH ) GENENTECH INC.				
Best Local Similarity:	100.00%				Mismatches: 0
Query Match:	100.00%				Indels: 0
RESULT 4					
ID	AC068276	standard; cDNA; 3580 BP.			
DE	Novel human secreted and transmembrane protein	PRO1295 cDNA.			
PN	US2003073130-A1.				
PD	17-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Best Local Similarity:	100.00%				Mismatches: 0
Query Match:	100.00%				Indels: 0
RESULT 5					
ID	ACH04378	standard; cDNA; 3580 BP.			
DE	Human cDNA encoding secreted/transmembrane protein	PRO1295.			
PN	US2003044841-A1.				
PD	06-MAR-2003.				
PA	(GETH ) GENENTECH INC.				
Best Local Similarity:	100.00%				Mismatches: 0
Query Match:	100.00%				Indels: 0

RESULT 6

ID AC067922 standard; cDNA; 3580 BP.

DE Novel human secreted and transmembrane protein PRO1295 cDNA.

PN US2003073129-A1.

PD 17-APR-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 7

ID ADC17922 standard; cDNA; 3580 BP.

DE Human PRO polynucleotide #16.

PN US2003064925-A1.

PD 03-APR-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 8

ID ADD70568 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003099625-A1.

PD 29-MAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 9

ID ADD39645 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003083462-A1.

PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 10

ID ADD70091 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003054406-A1.

PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 11

ID ADD38212 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003096955-A1.

PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 12

ID ADD39168 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003096954-A1.

PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 13

ID ADD38691 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003092061-A1.

PD 15-MAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 14

ID ADD40122 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003082627-A1.

PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 15

ID ADD40122 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003082627-A1.

PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

Wed Mar 30 09:32:46 2005

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ID ADE50343 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 16
ID ADE19955 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 17
ID ADE49866 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 18
ID ADE21424 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 19
ID ADF29849 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 20
ID ADF55742 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 21
ID ADH99246 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 22
ID ADE96426 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 23
ID ADF25737 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 24
ID ADF24636 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 25
ID ADF29372 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 26
ID ADE96903 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 27
ID ADH02941 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 28
ID ADH03895 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 29
ID ADH03418 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 30
ID ADH04372 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 31
ID ADH61373 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 32
ID ADL94572 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 33
ID ADO05609 standard; DNA; 4725 BP.
DE Human erythrocyte differentiation factor, Codanin-1 encoding DNA.
```

PN WO2004035535-A2.  
 PD 29-APR-2004.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Indels: 0  
 Query Match: 100.00%  
 RESULT 34  
 ID AB211689 standard; cDNA; 1833 BP.  
 DE Human polynucleotide SEQ ID NO 571.  
 PN WO200270539-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Indels: 0  
 Query Match: 88.34%  
 RESULT 35  
 ID ADM44207 standard; cDNA; 2240 BP.  
 DE Novel human arginine-rich protein cDNA #571.  
 PN US2004053250-A1.  
 PD 18-MAR-2004.  
 PA (TANG/) TANG Y T.  
 PA (XUEA/) XUE A.  
 PA (DRMA/) DRMANAC R T.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Indels: 0  
 Query Match: 88.34%  
 RESULT 36  
 ID AHH99000 standard; cDNA; 403 BP.  
 DE Human EST-derived coding sequence SEQ ID NO: 857.  
 PN WO200154477-A2.  
 PD 02-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 98.45% Mismatches: 2  
 Indels: 0  
 Query Match: 46.58%  
 RESULT 37  
 ID ABL19883 standard; DNA; 3904 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11122.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Best Local Similarity: 22.94% Mismatches: 87  
 Indels: 58  
 Query Match: 8.94%  
 RESULT 38  
 ID ABL19882 standard; DNA; 7602 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11119.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Best Local Similarity: 22.94% Mismatches: 87  
 Indels: 58  
 Query Match: 8.94%  
 RESULT 39  
 ID ABL03786 standard; cDNA; 18737 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 5840.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Best Local Similarity: 22.94% Mismatches: 87  
 Indels: 58  
 Query Match: 8.94%  
 RESULT 40  
 ID ADQ87067 standard; cDNA; 2340 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #3943.  
 PN WO2004060370-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Best Local Similarity: 24.04% Mismatches: 119  
 Indels: 81  
 Query Match: 7.86%  
 RESULT 41  
 ID ABK42709 standard; DNA; 17761 BP.  
 DE Genomic sequence #608 encoding novel human connective tissue polypeptide.  
 PN WO200155343-A1.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 27.66% Mismatches: 97  
 Indels: 97

Query Match: 7.82% Indels: 88  
 RESULT 42  
 ID AAK79415 standard; DNA; 17761 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34227.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 27.66% Mismatches: 97  
 Indels: 88  
 Query Match: 7.82%  
 RESULT 43  
 ID ADS60865 standard; DNA; 17761 BP.  
 DE Connective tissue related genomic DNA #608.  
 PN US2003054375-A1.  
 PD 20-MAR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 27.66% Mismatches: 97  
 Indels: 88  
 Query Match: 7.82%  
 RESULT 44  
 ID ACA38667 standard; DNA; 1104 BP.  
 DE Prokaryotic essential gene #20324.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 25.42% Mismatches: 89  
 Indels: 60  
 Query Match: 7.79%  
 RESULT 45  
 ID AB271082 standard; DNA; 1104 BP.  
 DE Mycobacterium tuberculosis protein encoding DNA SEQ ID NO:42.  
 PN WO2003000721-A2.  
 PD 03-JAN-2003.  
 PA (MITR-) MICROBIOLOGICAL RES AUTHORITY.  
 Best Local Similarity: 25.42% Mismatches: 89  
 Indels: 60  
 Query Match: 7.79%  
 RESULT 46  
 ID ACA40617 standard; DNA; 1107 BP.  
 DE Prokaryotic essential gene #22274.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 25.42% Mismatches: 89  
 Indels: 60  
 Query Match: 7.79%  
 RESULT 47  
 Best Local Similarity: 25.42% Mismatches: 89  
 Indels: 60  
 Query Match: 7.79%  
 RESULT 48  
 Best Local Similarity: 25.42% Mismatches: 89  
 Indels: 60  
 Query Match: 7.79%  
 RESULT 49  
 Best Local Similarity: 27.36% Mismatches: 98  
 Indels: 34  
 Query Match: 7.72%  
 RESULT 50  
 Best Local Similarity: 27.36% Mismatches: 98  
 Indels: 34  
 Query Match: 7.72%  
 RESULT 51  
 ID AAT671835 standard; DNA; 1712 BP.  
 DE Pseudomonas aeruginosa exoenzyme S gene.  
 PN US5599665-A.  
 PD 04-FEB-1997.  
 PA (MCWR-) MCW RES FOUND INC.  
 Best Local Similarity: 23.36% Mismatches: 128  
 Indels: 123  
 Query Match: 7.61%  
 RESULT 52  
 ID ABL63712 standard; DNA; 1457 BP.  
 DE Breast cancer related gene sequence SEQ ID NO:2049.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Best Local Similarity: 26.43% Mismatches: 104  
 Indels: 77  
 Query Match: 7.58%  
 RESULT 53  
 ID ADF65592 standard; DNA; 1457 BP.  
 DE Human mRNA for B-HLH binding protein DNA.  
 PN WO2003072827-A1.

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PD 04-SEP-2003.	PA (FIVE-) FIVE PRIME THERAPEUTICS INC.	124
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.	Best Local Similarity: 22.01%	Mismatches: 123
Best Local Similarity: 26.43%	Indels:	
Query Match: 7.58%		
RESULT 54		
ID AAS94864 standard; DNA; 1678 BP.		
DE Human DNA sequence #119 expressed during foam cell differentiation.		
PD WO200177389-A2.		
PD 18-OCT-2001.		
PA (INCY-) INCYTE GENOMICS INC.		
Best Local Similarity: 28.42%	Mismatches: 90	
Query Match: 7.51%	Indels: 86	
RESULT 55		
ID ADP65052 standard; DNA; 1396 BP.		
DE Human twist homologue (acrocephalosyndactyl 3) DNA sequence.		
PD WO2003072827-A1.		
PD 04-SEP-2003.		
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.		
Best Local Similarity: 28.32%	Mismatches: 95	
Query Match: 7.37%	Indels: 78	
RESULT 56		
ID ADQ22344 standard; DNA; 1664 BP.		
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5164.		
PD WO2004048938-A2.		
PD 10-JUN-2004.		
PA (PROT-) PROTEIN DESIGN LABS INC.		
Best Local Similarity: 28.32%	Mismatches: 95	
Query Match: 7.37%	Indels: 78	
RESULT 57		
ID AAS67977 standard; cDNA; 1980 BP.		
DE DNA encoding novel human diagnostic protein #3781.		
PD WO200175067-A2.		
PD 11-OCT-2001.		
PA (HYSE-) HYSEQ INC.		
Best Local Similarity: 26.99%	Mismatches: 108	
Query Match: 7.37%	Indels: 96	
RESULT 58		
ID ABD02086 standard; DNA; 1350 BP.		
DE Pseudomonas aeruginosa polynucleotide #690.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 25.23%	Mismatches: 98	
Query Match: 7.30%	Indels: 127	
RESULT 59		
ID ABD02116 standard; DNA; 3054 BP.		
DE Pseudomonas aeruginosa polynucleotide #720.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 25.23%	Mismatches: 98	
Query Match: 7.30%	Indels: 127	
RESULT 60		
ID ABD02056 standard; DNA; 6885 BP.		
DE Pseudomonas aeruginosa polynucleotide #660.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 25.23%	Mismatches: 98	
Query Match: 7.30%	Indels: 127	
RESULT 61		
ID ABD03071 standard; DNA; 1131 BP.		
DE Pseudomonas aeruginosa polynucleotide #1675.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 22.45%	Mismatches: 110	
Query Match: 7.23%	Indels: 121	
RESULT 62		
ID ADN98622 standard; cDNA; 3180 BP.		
DE Novel human cDNA sequence #222.		
PD WO2004038003-A2.		
PD 06-MAY-2004.		
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.		
Best Local Similarity: 22.01%	Mismatches: 124	
Query Match: 7.23%	Indels: 123	
RESULT 63		
ID ADO00191 standard; cDNA; 3180 BP.		
DE Novel human cDNA sequence #1006.		
PD WO2004038003-A2.		
PD 06-MAY-2004.		
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.		
Best Local Similarity: 22.01%	Mismatches: 124	
Query Match: 7.23%	Indels: 123	
RESULT 64		
ID ADC30771 standard; cDNA; 3438 BP.		
DE Human novel cDNA sequence, SEQ ID NO:853.		
PD WO2003029271-A2.		
PD 10-APR-2003.		
PA (HYSE-) HYSEQ INC.		
Best Local Similarity: 22.01%	Mismatches: 124	
Query Match: 7.23%	Indels: 123	
RESULT 65		
ID ABD09457 standard; DNA; 1236 BP.		
DE Pseudomonas aeruginosa polynucleotide #8061.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 23.12%	Mismatches: 114	
Query Match: 7.19%	Indels: 101	
RESULT 66		
ID ABD09598 standard; DNA; 2556 BP.		
DE Pseudomonas aeruginosa polynucleotide #8202.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 23.12%	Mismatches: 114	
Query Match: 7.16%	Indels: 98	
RESULT 67		
ID ABD09598 standard; DNA; 2556 BP.		
DE Pseudomonas aeruginosa polynucleotide #8202.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 23.12%	Mismatches: 114	
Query Match: 7.16%	Indels: 98	
RESULT 68		
ID ABD09598 standard; DNA; 2556 BP.		
DE Pseudomonas aeruginosa polynucleotide #8202.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 23.12%	Mismatches: 114	
Query Match: 7.16%	Indels: 98	
RESULT 69		
ID ADS63367 standard; cDNA; 1101 BP.		
DE Bacterial polynucleotide #15354.		
PD US2003233675-A1.		
PD 18-DEC-2003.		
PA (CAOY/) CAO Y.		
PA (HINK/) HINKLE G J.		
PA (SLAT/) SLATER S C.		
PA (CHEN/) CHEN X.		
PA (GOLD/) GOLDMAN B S.		
Best Local Similarity: 26.70%	Mismatches: 82	
Query Match: 7.12%	Indels: 45	
RESULT 70		
ID ADS63734 standard; cDNA; 1104 BP.		
DE Bacterial polynucleotide #15721.		
PD US2003233675-A1.		
PD 18-DEC-2003.		
PA (CAOY/) CAO Y.		
PA (HINK/) HINKLE G J.		
PA (SLAT/) SLATER S C.		
PA (CHEN/) CHEN X.		
PA (GOLD/) GOLDMAN B S.		
Best Local Similarity: 26.70%	Mismatches: 82	
Query Match: 7.12%	Indels: 45	
RESULT 71		
ID ADS64120 standard; cDNA; 1374 BP.		
DE Bacterial polynucleotide #16107.		
PD US2003233675-A1.		
PD 18-DEC-2003.		
PA (CAOY/) CAO Y.		
PA (HINK/) HINKLE G J.		
PA (SLAT/) SLATER S C.		



PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 26.70% Mismatches: 82  
 Query Match: 7.12% Indels: 45  
 RESULT 72  
 ID ADL46198 standard; DNA; 903 BP.  
 DE Ashbya gossypii GTP cyclohydrolase II-encoding DNA, SEQ ID NO:1.  
 PN WO2004022776-A2.  
 PD 18-MAR-2004.  
 PA (BADI ) BASF AG.  
 Best Local Similarity: 24.36% Mismatches: 100  
 Query Match: 7.09% Indels: 51  
 RESULT 73  
 ID ADK6552 standard; DNA; 1052 BP.  
 DE A gossypii riboflavin synthesis rib1 coding sequence.  
 PN DE10159396-A1.  
 PD 12-JUN-2003.  
 PA (BADI ) BASF AG.  
 Best Local Similarity: 24.36% Mismatches: 100  
 Query Match: 7.09% Indels: 51  
 RESULT 74  
 ID AAT03514 standard; cDNA to mRNA; 1329 BP.  
 DE Ashbya gossypii Rib 1 gene (GTP-cyclohydrolase II).  
 PN DE4420785-A1.  
 PD 05-OCT-1995.  
 PA (BADI ) BASF AG.  
 Best Local Similarity: 24.36% Mismatches: 100  
 Query Match: 7.09% Indels: 51  
 RESULT 75  
 ID ADL46200 standard; DNA; 2528 BP.  
 DE Ashbya gossypii GTP cyclohydrolase II gene (rib1), SEQ ID NO:3.  
 PN WO2004022776-A2.  
 PD 18-MAR-2004.  
 PA (BADI ) BASF AG.  
 Best Local Similarity: 24.36% Mismatches: 100  
 Query Match: 7.09% Indels: 51  
 RESULT 76  
 ID ADI27110 standard; DNA; 3400 BP.  
 DE Human LRP binding family protein DNA #4.  
 PN WO2003106657-A2.  
 PD 24-DEC-2003.  
 PA (STOW-) STOWERS INST MEDICAL RES.  
 Best Local Similarity: 25.65% Mismatches: 85  
 Query Match: 7.09% Indels: 62  
 RESULT 77  
 ID AAA94049 standard; DNA; 5680 BP.  
 DE Human DAN/Cerberus-related protein 6 (hDCR6) gene.  
 PN WO200055193-A2.  
 PD 21-SEP-2000.  
 PA (REG-) REGENERON PHARM INC.  
 Best Local Similarity: 25.65% Mismatches: 85  
 Query Match: 7.09% Indels: 62  
 RESULT 78  
 ID AAD27577 standard; DNA; 7099 BP.  
 DE Human osteolevin gene.  
 PN WO200198491-A2.  
 PD 27-DEC-2001.  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 PA (UVIN-) UNIV INSPELLENT ANTWERPEN UIA.  
 Best Local Similarity: 25.65% Mismatches: 85  
 Query Match: 7.09% Indels: 62  
 RESULT 79  
 ID AAA29064 standard; DNA; 9301 BP.  
 DE Human TGF-beta binding protein (BEER) genomic DNA.  
 PN WO200032773-A1.  
 PD 08-JUN-2000.  
 PA (DARW-) DARWIN DISCOVERY LTD.  
 Best Local Similarity: 25.65% Mismatches: 85  
 Query Match: 7.09% Indels: 62  
 RESULT 80  
 ID ACF79823 standard; DNA; 21501 BP.  
 DE Human SOST gene encoding sclerostin.  
 PN WO2003073991-A2.

PD 12-SEP-2003.  
 PA (CELL-) CELLTech R & D INC.  
 PA (SUTH/) KUNG SUTHERLAND M S.  
 PA (GEOG/) GEOGHEGAN J C.  
 PA (YUCC/) YU C.  
 PA (LATH/) LATHAM J.  
 Best Local Similarity: 25.65% Mismatches: 85  
 Query Match: 7.09% Indels: 62  
 RESULT 81  
 ID ADF11646 standard; DNA; 94752 BP.  
 DE Human chromosome 17 clone HPRC905N1 nucleic acid.  
 PN WO2003087763-A2.  
 PD 23-OCT-2003.  
 PA (CELL-) CELLTech R & D INC.  
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.  
 Best Local Similarity: 25.65% Mismatches: 85  
 Query Match: 7.09% Indels: 62  
 RESULT 82  
 ID ADF11613 standard; DNA; 130320 BP.  
 DE Human sclerostin gene region.  
 PN WO2003087763-A2.  
 PD 23-OCT-2003.  
 PA (CELL-) CELLTech R & D INC.  
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.  
 Best Local Similarity: 25.65% Mismatches: 85  
 Query Match: 7.09% Indels: 62  
 RESULT 83  
 ID ADL45243 standard; DNA; 1810 BP.  
 DE Human ovarian cancer DNA marker #19133.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Best Local Similarity: 27.48% Mismatches: 80  
 Query Match: 7.05% Indels: 64  
 RESULT 84  
 ID ADQ38777 standard; DNA; 2064 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 440.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Best Local Similarity: 28.27% Mismatches: 83  
 Query Match: 7.05% Indels: 65  
 RESULT 85  
 ID ADQ38776 standard; DNA; 2106 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 439.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Best Local Similarity: 28.27% Mismatches: 83  
 Query Match: 7.05% Indels: 65  
 RESULT 86  
 ID ADP65591 standard; DNA; 797 BP.  
 DE Human basic helix-loop-helix binding protein (TWIST) gene, DNA.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Best Local Similarity: 31.02% Mismatches: 79  
 Query Match: 7.02% Indels: 29  
 RESULT 87  
 ID ABT06509 standard; DNA; 1800 BP.  
 DE Twist gene promoter sequence.  
 PN WO200259347-A2.  
 PD 01-AUG-2002.  
 PA (UVJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 Best Local Similarity: 31.63% Mismatches: 79  
 Query Match: 7.02% Indels: 33  
 RESULT 88  
 ID ADC07759 standard; DNA; 2143 BP.  
 DE Rice DNA sequence Seq ID25 related to grain filling.  
 PN WO2003000905-A2.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 22.77% Mismatches: 85

Query Match: 7.02% Indels: 135  
RESULT 89  
ID ACN38185 standard; cDNA; 2213 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA324544, SEQ ID NO:1540.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 23.55% Mismatches: 99  
Query Match: 7.02% Indels: 98  
RESULT 90  
ID ADE54144 standard; cDNA; 5408 BP.  
DE Human prostate cancer cDNA #491.  
PN US2003190640-A1.  
PD 09-OCT-2003.  
PA (FARI/) FARIS M.  
PA (PEAR/) PEARSON C I.  
Best Local Similarity: 24.56% Mismatches: 103  
Query Match: 7.02% Indels: 115  
RESULT 91  
ID ADO26000 standard; DNA; 2285 BP.  
DE Corn chalcone synthase (CHS) polynucleotide seqid 38.  
PN WO2004046336-A2.  
PD 03-JUN-2004.  
PA (MONS) MONSANTO TECHNOLOGY LLC.  
Best Local Similarity: 25.19% Mismatches: 81  
Query Match: 6.98% Indels: 84  
RESULT 92  
ID AAA08834 standard; DNA; 5040 BP.  
DE Murine APC-2 gene.  
PN WO200018913-A1.  
PD 06-APR-2000.  
PA (UYUT-) RIJKSUNIV UTRECHT.  
Best Local Similarity: 24.51% Mismatches: 120  
Query Match: 6.98% Indels: 115  
RESULT 93  
ID AAH18204 standard; cDNA; 6193 BP.  
DE Human cDNA sequence SEQ ID NO:18123.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Best Local Similarity: 25.41% Mismatches: 84  
Query Match: 6.98% Indels: 66  
RESULT 94  
ID ADO07830 standard; cDNA; 6825 BP.  
DE Mouse polynucleotide #43.  
PN US2004071700-A1.  
PD 15-APR-2004.  
PA (LIFE-) LIFE SCI DEV CORP.  
Best Local Similarity: 24.51% Mismatches: 120  
Query Match: 6.98% Indels: 115  
RESULT 95  
ID ADM83716 standard; DNA; 1800 BP.  
DE Human twist promoter.  
PN US2003138783-A1.  
PD 24-JUL-2003.  
PA (SUKU/) SUKUMAR S.  
PA (EVRO/) EVRON E.  
PA (DOOL/) DOOLEY W C.  
PA (SACC/) SACCCHI N.  
PA (DAVI/) DAVIDSON N.  
PA (FACK/) FACKLER M J.  
Best Local Similarity: 31.63% Mismatches: 79  
Query Match: 6.95% Indels: 33  
RESULT 96  
ID ADG91050 standard; DNA; 2120 BP.  
DE Hepatic specific nucleic acid encoding sequence #239.  
PN WO2003066877-A2.  
PD 14-AUG-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 24.17% Mismatches: 111  
Query Match: 6.95% Indels: 53  
RESULT 97  
ID ADG91053 standard; DNA; 2280 BP.  
DE Hepatic specific nucleic acid encoding sequence #242.  
PN WO2003066877-A2.  
PD 14-AUG-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 24.17% Mismatches: 111  
Query Match: 6.95% Indels: 53  
RESULT 98  
ID ADG91049 standard; DNA; 2457 BP.  
DE Hepatic specific nucleic acid encoding sequence #238.  
PN WO2003066877-A2.  
PD 14-AUG-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 24.17% Mismatches: 111  
Query Match: 6.95% Indels: 53  
RESULT 99  
ID ADG91048 standard; DNA; 2489 BP.  
DE Hepatic specific nucleic acid encoding sequence #237.  
PN WO2003066877-A2.  
PD 14-AUG-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 24.17% Mismatches: 111  
Query Match: 6.95% Indels: 53  
RESULT 100  
ID ADG91047 standard; DNA; 2520 BP.  
DE Hepatic specific nucleic acid encoding sequence #236.  
PN WO2003066877-A2.  
PD 14-AUG-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 24.17% Mismatches: 111  
Query Match: 6.95% Indels: 53  
RESULT 101  
ID ADG91054 standard; DNA; 2641 BP.  
DE Hepatic specific nucleic acid encoding sequence #243.  
PN WO2003066877-A2.  
PD 14-AUG-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 24.17% Mismatches: 111  
Query Match: 6.95% Indels: 53  
RESULT 102  
ID ADQ17684 standard; DNA; 2870 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 501.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 31.63% Mismatches: 79  
Query Match: 6.95% Indels: 33  
RESULT 103  
ID ABZ11230 standard; cDNA; 7057 BP.  
DE Human polynucleotide SEQ ID NO 112.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 23.93% Mismatches: 107  
Query Match: 6.95% Indels: 95  
RESULT 104  
ID ADM43748 standard; cDNA; 7057 BP.  
DE Novel human arginine-rich protein cDNA #112.  
PN US2004053250-A1.  
PD 18-MAR-2004.  
PA (TANG/) TANG Y T.  
PA (XUEA/) XUE A.  
PA (DRMA/) DRMANAC R T.  
Best Local Similarity: 23.93% Mismatches: 107  
Query Match: 6.95% Indels: 95  
RESULT 105  
ID ACN45066 standard; DNA; 27189 BP.  
DE Human genomic sequence HCG30694.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 24.16% Mismatches: 117  
Query Match: 6.95% Indels: 89  
RESULT 106

ID AAQ04485 standard; DNA; 1236 BP.  
 DE Plasmid pSEUKS11d encoding UK-S1.  
 PN EP370205-A.  
 PD 30-MAY-1990.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 Best Local Similarity: 27.19% Mismatches: 90  
 Query Match: 6.91% Indels: 44  
 RESULT 107

ID ABD07632 standard; DNA; 1419 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6236.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 23.10% Mismatches: 129  
 Query Match: 6.91% Indels: 123  
 RESULT 108

ID ABD07463 standard; DNA; 1476 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6067.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 23.10% Mismatches: 129  
 Query Match: 6.91% Indels: 123  
 RESULT 109

ID AAC39340 standard; DNA; 1601 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 24273.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 24.51% Mismatches: 74  
 Query Match: 6.91% Indels: 88  
 RESULT 110

ID ABD10451 standard; DNA; 1893 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9055.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 23.36% Mismatches: 121  
 Query Match: 6.88% Indels: 136  
 RESULT 111

ID ABL54590 standard; cDNA; 2242 BP.  
 DE Human CREB conjugated protein 30.8 encoding cDNA SEQ ID NO 1.  
 PN CN1326942-A.  
 PD 19-DEC-2001.  
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 Best Local Similarity: 21.63% Mismatches: 99  
 Query Match: 6.88% Indels: 115  
 RESULT 112

ID ADQ83748 standard; cDNA; 2555 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #562.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Best Local Similarity: 21.63% Mismatches: 99  
 Query Match: 6.88% Indels: 115  
 RESULT 113

ID ABL12402 standard; cDNA; 90104 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31688.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Best Local Similarity: 22.49% Mismatches: 68  
 Query Match: 6.88% Indels: 69  
 RESULT 114

ID ABQ81844 standard; DNA; 349980 BP.  
 DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1100.  
 PN EP1227152-A1.  
 PD 31-JUL-2002.  
 PA (NEST ) SOC PROD NESTLE SA.  
 Best Local Similarity: 27.83% Mismatches: 71  
 Query Match: 6.88% Indels: 58  
 RESULT 115

ID ABK34884 standard; cDNA; 1204 BP.  
 DE Human cDNA encoding secreted protein #22.  
 PN WO200177288-A2.  
 PD 18-OCT-2001.  
 PA (GEMY ) GENETICS INST INC.  
 Best Local Similarity: 28.91% Mismatches: 101  
 Query Match: 6.84% Indels: 52  
 RESULT 116

ID AAC87527 standard; DNA; 1493 BP.  
 DE Human RAP (receptor associated protein) cDNA.  
 PN WO200071714-A2.  
 PD 30-NOV-2000.  
 PA (AMNA-) AMERICAN NAT RED CROSS.  
 Best Local Similarity: 28.27% Mismatches: 83  
 Query Match: 6.84% Indels: 65  
 RESULT 117

ID AAL48893 standard; cDNA; 1493 BP.  
 DE Human receptor-associated protein coding sequence.  
 PN WO200260951-A2.  
 PD 08-AUG-2002.  
 PA (AMNA-) AMERICAN NAT RED CROSS.  
 Best Local Similarity: 28.27% Mismatches: 83  
 Query Match: 6.84% Indels: 65  
 RESULT 118

ID ABR84062 standard; cDNA; 1493 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #633.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Best Local Similarity: 28.27% Mismatches: 83  
 Query Match: 6.84% Indels: 65  
 RESULT 119

ID ADJ74840 standard; DNA; 1493 BP.  
 DE Marker gene SEQ ID NO:92.  
 PN EP1394274-A2.  
 PD 03-MAR-2004.  
 PA (GENO-) GENOX RES INC.  
 Best Local Similarity: 28.27% Mismatches: 83  
 Query Match: 6.84% Indels: 65  
 RESULT 120

ID ADR24896 standard; DNA; 1493 BP.  
 DE Breast cancer prognosis marker #757.  
 PN WO2004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 Best Local Similarity: 28.27% Mismatches: 83  
 Query Match: 6.84% Indels: 65  
 RESULT 121

ID ADP23134 standard; cDNA; 1493 BP.  
 DE PRO polypeptide encoding cDNA SEQ ID NO:228.  
 PN WO2004041170-A2.  
 PD 21-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 28.27% Mismatches: 83  
 Query Match: 6.84% Indels: 65  
 RESULT 122

ID ADA71052 standard; DNA; 2934 BP.  
 DE Rice gene, SEQ ID 4375.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 26.35% Mismatches: 110  
 Query Match: 6.84% Indels: 66  
 RESULT 123

ID ADP23134 standard; cDNA; 1493 BP.  
 DE PRO polypeptide encoding cDNA SEQ ID NO:228.  
 PN WO2004041170-A2.  
 PD 21-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 28.27% Mismatches: 83  
 Query Match: 6.84% Indels: 65  
 RESULT 124

ID ADP23134 standard; cDNA; 1493 BP.  
 DE PRO polypeptide encoding cDNA SEQ ID NO:228.  
 PN WO2004041170-A2.  
 PD 21-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 28.27% Mismatches: 83  
 Query Match: 6.84% Indels: 65  
 RESULT 125

ID ACH89545 standard; DNA; 609 BP.  
 DE Human genome derived single exon probe #22740.

PN US2003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 Best Local Similarity: 32.70%  
 Query Match: 6.81%  
 Mismatches: 67  
 Indels: 23  
 RESULT 126  
 ID AAZ87298 standard; DNA; 11220 BP.  
 DE S. venezuelae macrolide biosynthetic gene pikAII, SEQ ID NO:32.  
 PN WO200000620-A2.  
 PD 06-JAN-2000.  
 PA (MINU) UNIV MINNESOTA.  
 Best Local Similarity: 25.17%  
 Query Match: 6.81%  
 Mismatches: 91  
 Indels: 101  
 RESULT 127  
 ID ADJ91917 standard; DNA; 11220 BP.  
 DE Streptomyces macrolide biosynthetic protein (PikAII) coding sequence.  
 PN US2003194784-A1.  
 PD 16-OCT-2003.  
 PA (SHER/) SHERMAN D H.  
 PA (LIUH/) LIU H.  
 PA (XUEY/) XUE Y.  
 PA (ZHAO/) ZHAO L.  
 Best Local Similarity: 25.17%  
 Query Match: 6.81%  
 Mismatches: 91  
 Indels: 101  
 RESULT 128  
 ID AAZ87318 standard; DNA; 36778 BP.  
 DE S. venezuelae pik (macrolide biosynthesis) gene cluster.  
 PN WO200000620-A2.  
 PD 06-JAN-2000.  
 PA (MINU) UNIV MINNESOTA.  
 Best Local Similarity: 25.17%  
 Query Match: 6.81%  
 Mismatches: 91  
 Indels: 101  
 RESULT 129  
 ID ADJ91933 standard; DNA; 36778 BP.  
 DE Streptomyces venezuelae pik gene cluster coding sequence.  
 PN US2003194784-A1.  
 PD 16-OCT-2003.  
 PA (SHER/) SHERMAN D H.  
 PA (LIUH/) LIU H.  
 PA (XUEY/) XUE Y.  
 PA (ZHAO/) ZHAO L.  
 Best Local Similarity: 25.17%  
 Query Match: 6.81%  
 Mismatches: 91  
 Indels: 101  
 RESULT 130  
 ID AAZ87285 standard; DNA; 37948 BP.  
 DE S. venezuelae pik (macrolide biosynthesis) gene cluster, SEQ ID NO:5.  
 PN WO200000620-A2.  
 PD 06-JAN-2000.  
 PA (MINU) UNIV MINNESOTA.  
 Best Local Similarity: 25.17%  
 Query Match: 6.81%  
 Mismatches: 91  
 Indels: 101  
 RESULT 131  
 ID AAA75633 standard; DNA; 38506 BP.  
 DE Nucleotide sequence of the insert DNA in cosmid pKOS023-27.  
 PN US6117659-A.  
 PD 12-SEP-2000.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Best Local Similarity: 25.17%  
 Query Match: 6.81%  
 Mismatches: 91  
 Indels: 101  
 RESULT 132  
 ID AAZ56001 standard; DNA; 38506 BP.  
 DE Recombinant cosmid pKOS023-27 containing S. venezuelae PKS genes.  
 PN WO9961599-A2.  
 PD 02-DEC-1999.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Best Local Similarity: 25.17%  
 Query Match: 6.81%  
 Mismatches: 91  
 Indels: 101  
 RESULT 133  
 ID ADA09418 standard; DNA; 38506 BP.  
 DE Cosmid pKOS023-27 containing S. venezuelae PKS gene cluster.  
 PN US6509455-B1.

PD 21-JAN-2003.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Best Local Similarity: 25.17%  
 Query Match: 6.81%  
 Mismatches: 91  
 Indels: 101  
 RESULT 134  
 ID ADH53462 standard; DNA; 38506 BP.  
 DE S. venezuelae pKOS023-27 cosmid DNA.  
 PN US2003162262-A1.  
 PD 28-AUG-2003.  
 PA (ASHL/) ASHLEY G.  
 PA (BETL/) BETLACH M C.  
 PA (BETL/) BETLACH M.  
 PA (MCDA/) MCDANIEL R.  
 PA (TANG/) TANG L.  
 Best Local Similarity: 25.17%  
 Query Match: 6.81%  
 Mismatches: 91  
 Indels: 101  
 RESULT 135  
 ID ABS56090 standard; DNA; 38506 BP.  
 DE S. venezuelae DNA inserted into cosmid pKOS023-27.  
 PN WO200297062-A2.  
 PD 05-DEC-2002.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Best Local Similarity: 23.71%  
 Query Match: 6.81%  
 Mismatches: 101  
 Indels: 87  
 RESULT 136  
 ID ABD05377 standard; DNA; 858 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3981.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 26.85%  
 Query Match: 6.77%  
 Mismatches: 91  
 Indels: 50  
 RESULT 137  
 ID ACA26285 standard; DNA; 1347 BP.  
 DE Prokaryotic essential gene #7942.  
 PN WO200271183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 25.38%  
 Query Match: 6.77%  
 Mismatches: 106  
 Indels: 55  
 RESULT 138  
 ID ABD05446 standard; DNA; 1482 BP.  
 DE Pseudomonas aeruginosa polynucleotide #4050.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 26.85%  
 Query Match: 6.77%  
 Mismatches: 91  
 Indels: 50  
 RESULT 139  
 ID AAZ33614 standard; cDNA; 1499 BP.  
 DE Human breast tumour-associated EST 4.  
 PN DE19813839-A1.  
 PD 23-SEP-1999.  
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
 Best Local Similarity: 28.21%  
 Query Match: 6.77%  
 Mismatches: 87  
 Indels: 59  
 RESULT 140  
 ID ABD05293 standard; DNA; 1605 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3897.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 26.85%  
 Query Match: 6.77%  
 Mismatches: 91  
 Indels: 50  
 RESULT 141  
 ID ADD25545 standard; DNA; 3120 BP.  
 DE Binding domain-immunoglobulin fusion protein-associated DNA #57.  
 PN US2003118592-A1.  
 PD 26-JUN-2003.  
 PA (GENE-) GENE-CRAFT INC.  
 Best Local Similarity: 27.19%  
 Query Match: 6.77%  
 Mismatches: 89  
 Indels: 49  
 RESULT 142

ID ADK61414 standard; DNA; 3120 BP.  
 DE Ovarian cancer-related DNA #569 with altered ovarian cancer expression.  
 PN WO2003068054-A2.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PD 21-AUG-2003.  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 PD 13-MAY-2004.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 143  
 ID ADP09696 standard; cDNA; 3120 BP.  
 DE Human IL17R cDNA.  
 PN JP2004135545-A.  
 PD 13-MAY-2004.  
 PA (SUMU ) SUMITOMO SEIYAKU KK.  
 PD 13-MAY-2004.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 144  
 ID ADP13348 standard; DNA; 3120 BP.  
 DE Renal cell carcinoma differentially expressed gene #84.  
 PN WO2004048933-A2.  
 PD 10-JUN-2004.  
 PA (AMHP ) WYETH.  
 PD 10-JUN-2004.  
 PA (TWIN ) TWINE N C.  
 PD 10-JUN-2004.  
 PA (BUREC ) BURCZYNSKI M E.  
 PD 10-JUN-2004.  
 PA (TREP ) TREPICCHIO W L.  
 PD 10-JUN-2004.  
 PA (DORN ) DORNER A.  
 PD 10-JUN-2004.  
 PA (STOV ) STOVER J A.  
 PD 10-JUN-2004.  
 PA (SLON ) SLONI D K.  
 PD 10-JUN-2004.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 145  
 ID AAT33801 standard; cDNA to mRNA; 3223 BP.  
 DE Human interleukin-17 receptor cDNA.  
 PN WO9629408-A1.  
 PD 26-SEP-1996.  
 PA (IMMV ) IMMUNEX CORP.  
 PD 26-SEP-1996.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 146  
 ID AAV27592 standard; cDNA to mRNA; 3223 BP.  
 DE Human interleukin-17 receptor cDNA.  
 PN WO9823284-A1.  
 PD 04-JUN-1998.  
 PA (IMMV ) IMMUNEX CORP.  
 PD 04-JUN-1998.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 147  
 ID AAX01922 standard; cDNA to mRNA; 3223 BP.  
 DE Human IL-17R cDNA.  
 PN US5869286-A.  
 PD 09-FEB-1999.  
 PA (IMMV ) IMMUNEX CORP.  
 PD 09-FEB-1999.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 148  
 ID AAA51988 standard; cDNA to mRNA; 3223 BP.  
 DE Human interleukin-17 receptor coding sequence.  
 PN US6100235-A.  
 PD 08-AUG-2000.  
 PA (IMMV ) IMMUNEX CORP.  
 PD 08-AUG-2000.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 149  
 ID AA52146 standard; cDNA to mRNA; 3223 BP.  
 DE Human interleukin-17 receptor coding sequence.  
 PN US6096305-A.  
 PD 01-AUG-2000.  
 PA (IMMV ) IMMUNEX CORP.  
 PD 01-AUG-2000.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 150  
 ID AAA59871 standard; cDNA; 3223 BP.  
 DE Human interleukin-17 (IL-17) receptor nucleotide sequence.

PN US6072033-A.  
 PD 06-JUN-2000.  
 PA (IMMV ) IMMUNEX CORP.  
 PD 06-JUN-2000.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 151  
 ID AAA61240 standard; cDNA; 3223 BP.  
 DE Human IL-17R cDNA.  
 PN US6072037-A.  
 PD 06-JUN-2000.  
 PA (IMMV ) IMMUNEX CORP.  
 PD 06-JUN-2000.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 152  
 ID AAF57188 standard; cDNA; 3223 BP.  
 DE Human IL-17R (hCTLA-8 receptor) polypeptide encoding cDNA.  
 PN US6197525-B1.  
 PD 06-MAR-2001.  
 PA (IMMV ) IMMUNEX CORP.  
 PD 06-MAR-2001.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 153  
 ID AD02815 standard; DNA; 3223 BP.  
 DE Human Interleukin-17 receptor (IL-17R) or CTLA-8 receptor DNA.  
 PN US6191104-B1.  
 PD 20-FEB-2001.  
 PA (IMMV ) IMMUNEX CORP.  
 PD 20-FEB-2001.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 154  
 ID ADJ88264 standard; cDNA to mRNA; 3223 BP.  
 DE Human IL-17 receptor nucleic acid sequence.  
 PN US6680057-B1.  
 PD 20-JAN-2004.  
 PA (IMMV ) IMMUNEX CORP.  
 PD 20-JAN-2004.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 155  
 ID ADL24268 standard; DNA; 3223 BP.  
 DE Human IL-17 receptor coding sequence.  
 PN WO2004019866-A2.  
 PD 11-MAR-2004.  
 PA (IMMV ) IMMUNEX CORP.  
 PD 11-MAR-2004.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 156  
 ID ADQ91251 standard; cDNA; 3223 BP.  
 DE Human cDNA encoding the interleukin-17 receptor, IL-17R.  
 PN US2004120898-A1.  
 PD 24-JUN-2004.  
 PA (IMMV ) IMMUNEX CORP.  
 PD 24-JUN-2004.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 157  
 ID ADR01307 standard; cDNA to mRNA; 3223 BP.  
 DE Human interleukin-17 receptor, IL-17R, cDNA to mRNA.  
 PN US2004120899-A1.  
 PD 24-JUN-2004.  
 PA (IMMV ) IMMUNEX CORP.  
 PD 24-JUN-2004.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 158  
 ID ADG32974 standard; DNA; 3429 BP.  
 DE Human DNA differentially expressed in patients with SLE SeqID298.  
 PN WO2003090694-A2.  
 PD 06-NOV-2003.  
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
 PD 06-NOV-2003.  
 Best Local Similarity: 27.19% Mismatches: 89  
 Query Match: 6.77% Indels: 49  
 RESULT 159  
 ID ABT08140 standard; DNA; 7438 BP.  
 DE Recombinase domain-containing fusion protein-related vector 1.  
 PN WO200238613-A2.

PD 16-MAY-2002.			
PA (ARTE-) ARTEMIS PHARM GMBH.			
Best Local Similarity: 24.05%	Mismatches: 108		
Query Match: 6.77%	Indels: 57		
RESULT 160			
ID ADB81341 standard; DNA; 7438 BP.			
DE Substrate vector pRK64 with beta-galactosidase under an SV40 promoter.			
PD W02003066867-A2.			
PN W0200238613-A2.			
PD 16-MAY-2002.			
PA (ARTE-) ARTEMIS PHARM GMBH.			
Best Local Similarity: 24.05%	Mismatches: 108		
Query Match: 6.77%	Indels: 57		
RESULT 161			
ID ABT08174 standard; DNA; 7523 BP.			
DE Recombinase domain-containing fusion protein-related vector 17.			
PD W0200238613-A2.			
PD 16-MAY-2002.			
PA (ARTE-) ARTEMIS PHARM GMBH.			
Best Local Similarity: 24.05%	Mismatches: 108		
Query Match: 6.77%	Indels: 57		
RESULT 162			
ID RAD04930 standard; DNA; 7573 BP.			
DE Recombination vector pRK73 used to test C31-Int mediated inversion.			
PN W0200129208-A1.			
PD 26-APR-2001.			
PA (ARTE-) ARTEMIS PHARM GMBH.			
PA (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.			
Best Local Similarity: 24.05%	Mismatches: 108		
Query Match: 6.77%	Indels: 57		
RESULT 163			
ID AAD04944 standard; DNA; 7573 BP.			
DE pRK73-inv vector comprising C31-Int mediated inverted product of pRK73			
PN W0200129208-A1.			
PD 26-APR-2001.			
PA (ARTE-) ARTEMIS PHARM GMBH.			
PA (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.			
Best Local Similarity: 24.05%	Mismatches: 108		
Query Match: 6.77%	Indels: 57		
RESULT 164			
ID ABT08173 standard; DNA; 7608 BP.			
DE Recombinase domain-containing fusion protein-related vector 16.			
PN W0200238613-A2.			
PD 16-MAY-2002.			
PA (ARTE-) ARTEMIS PHARM GMBH.			
Best Local Similarity: 24.05%	Mismatches: 108		
Query Match: 6.77%	Indels: 57		
RESULT 165			
ID ABT08177 standard; DNA; 7803 BP.			
DE Recombinase domain-containing fusion protein-related vector 20.			
PN W0200238613-A2.			
PD 16-MAY-2002.			
PA (ARTE-) ARTEMIS PHARM GMBH.			
Best Local Similarity: 24.05%	Mismatches: 108		
Query Match: 6.77%	Indels: 57		
RESULT 166			
ID ABT08178 standard; DNA; 8167 BP.			
DE Recombinase domain-containing fusion protein-related vector 21.			
PN W0200238613-A2.			
PD 16-MAY-2002.			
PA (ARTE-) ARTEMIS PHARM GMBH.			
Best Local Similarity: 24.05%	Mismatches: 108		
Query Match: 6.77%	Indels: 57		
RESULT 167			
Best Local Similarity: 24.11%	Mismatches: 91		
Query Match: 6.77%	Indels: 56		
RESULT 168			
Best Local Similarity: 22.78%	Mismatches: 111		
Query Match: 6.77%	Indels: 104		
RESULT 169			
Best Local Similarity: 22.78%	Mismatches: 111		
Query Match: 6.77%	Indels: 104		
RESULT 170			
Best Local Similarity: 22.78%	Mismatches: 111		

Query Match:	6.77%	Indels:	104
RESULT 171			
ID ADA44192 standard; DNA; 969 BP.			
DE Maize gene conferring disease resistance in plants.			
FN WO2003000906-A2.			
PD 03-JAN-2003.			
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.			
Best Local Similarity: 26.58%		Mismatches:	70
Query Match: 6.74%		Indels:	74
RESULT 172			
ID ADJ44454 standard; cDNA; 969 BP.			
DE Plant cDNA #5454.			
FN US2004016025-A1.			
PD 22-JAN-2004.			
PA (BUDW/) BUDWORTH P.			
PA (MOWG/) MOUGHAMER T.			
PA (BRIG/) BRIGGS S P.			
PA (COOP/) COOPER B.			
PA (GLAZ/) GLAZEBROOK J.			
PA (GOFF/) GOFF S A.			
PA (KATA/) KATAGIRI F.			
PA (KREP/) KREPS J.			
PA (PROV/) PROVART N.			
PA (RICK/) RIQUE D.			
PA (ZHUT/) ZHU T.			
Best Local Similarity: 26.58%		Mismatches:	70
Query Match: 6.74%		Indels:	74
RESULT 173			
ID ASD07251 standard; DNA; 1311 BP.			
DE Pseudomonas aeruginosa polynucleotide #5855.			
FN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 21.71%		Mismatches:	83
Query Match: 6.74%		Indels:	91
RESULT 174			
ID ADA53443 standard; cDNA; 3278 BP.			
DE Human coding sequence, SEQ ID 1011.			
FN EPI293569-A2.			
PD 19-MAR-2003.			
PA (HELI-) HELIX RES INST.			
PA (REAS-) RES ASSOC BIOTECHNOLOGY.			
Best Local Similarity: 21.20%		Mismatches:	111
Query Match: 6.74%		Indels:	101
RESULT 175			
ID ADG30703 standard; DNA; 3291 BP.			
DE Xanthomonas axonopodis pv citri plant pathology-related XACb0015 DNA.			
FN WO2003089647-A1.			
PD 30-OCT-2003.			
PA (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.			
Best Local Similarity: 23.61%		Mismatches:	121
Query Match: 6.74%		Indels:	61
RESULT 176			
ID AAA38398 standard; DNA; 999 BP.			
DE ORP2-16 encoding Pseudomonas bco gene cluster regulator, SEQ ID NO:18.			
FN JP2000093180-A.			
PD 04-APR-2000.			
PA (TOFU ) TONEN CORP.			
Best Local Similarity: 26.64%		Mismatches:	68
Query Match: 6.70%		Indels:	68
RESULT 177			
ID ACH87698 standard; DNA; 1433 BP.			
DE Human genome derived single exon probe #20893.			
FN US2003194704-A1.			
PD 16-OCT-2003.			
PA (PENN/) PENN S G.			
PA (RANK/) RANK D R.			
PA (HANZ/) HANZEL D K.			
Best Local Similarity: 28.91%		Mismatches:	101
Query Match: 6.70%		Indels:	52
RESULT 178			
ID ACH87093 standard; DNA; 1458 BP.			
DE Human genome derived single exon probe #20288.			



PN US2003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN//) PENN S G.  
 PA (RANK//) RANK D R.  
 PA (HANZ//) HANZEL D K.  
 Best Local Similarity: 28.91%  
 Query Match: 6.70%  
 RESULT 179  
 ID AAL61513 standard; DNA; 1813 BP.  
 DE Human inhibitor-kappa B-R DNA #3.  
 PN WO2003042360-A2.  
 PD 22-MAY-2003.  
 PA (ISIS-) ISIS PHARM INC.  
 Best Local Similarity: 25.31%  
 Query Match: 6.70%  
 RESULT 180  
 ID ADI32145 standard; cDNA; 1813 BP.  
 DE Human cDNA #1471.  
 PN US6607879-B1.  
 PD 19-AUG-2003.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 25.31%  
 Query Match: 6.70%  
 RESULT 181  
 ID ACA31501 standard; DNA; 1831 BP.  
 DE Prokaryotic essential gene #13158.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 29.22%  
 Query Match: 6.70%  
 RESULT 182  
 ID ADN99012 standard; cDNA; 2205 BP.  
 DE Novel human cDNA sequence #612.  
 PN WO2004038003-A2.  
 PD 06-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Best Local Similarity: 28.91%  
 Query Match: 6.70%  
 RESULT 183  
 ID ADO00581 standard; cDNA; 2205 BP.  
 DE Novel human cDNA sequence #1396.  
 PN WO2004038003-A2.  
 PD 06-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Best Local Similarity: 28.91%  
 Query Match: 6.70%  
 RESULT 184  
 ID ADE54125 standard; cDNA; 2661 BP.  
 DE Human prostate cancer cDNA #472.  
 PN US2003190640-A1.  
 PD 09-OCT-2003.  
 PA (FARI//) FARIS M.  
 PA (PEAR//) PEARSON C I.  
 Best Local Similarity: 28.91%  
 Query Match: 6.70%  
 RESULT 185  
 ID ABL67218 standard; DNA; 2678 BP.  
 DE Thyroid cancer related gene sequence SEQ ID NO:5555.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Best Local Similarity: 28.91%  
 Query Match: 6.70%  
 RESULT 186  
 ID ACA56631 standard; cDNA; 2678 BP.  
 DE Human signalling pathway polynucleotide probe SEQ ID NO 1229.  
 PN US6500938-B1.  
 PD 31-DEC-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 28.91%  
 Query Match: 6.70%  
 RESULT 187

ID AD156427 standard; DNA; 2678 BP.  
 DE Human polynucleotide probe #1229.  
 PN US2004010136-A1.  
 PD 15-JAN-2004.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 28.91%  
 Query Match: 6.70%  
 RESULT 188  
 ID ADQ85883 standard; cDNA; 2683 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2755.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH-) GENENTECH INC.  
 PA (WUTD//) WU T D.  
 PA (ZHOU//) ZHOU Y.  
 Best Local Similarity: 28.91%  
 Query Match: 6.70%  
 RESULT 189  
 ID ABL07083 standard; cDNA; 4515 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15731.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE-) PE CORP NY.  
 Best Local Similarity: 24.48%  
 Query Match: 6.70%  
 RESULT 190  
 ID ADQ89769 standard; DNA; 4515 BP.  
 DE Antagonist of cell cycle progression nucleotide sequence #100.  
 PN WO2004063362-A2.  
 PD 29-JUL-2004.  
 PA (CYCL-) CYCLACEL LTD.  
 Best Local Similarity: 24.48%  
 Query Match: 6.70%  
 RESULT 191  
 ID AAA38389 standard; DNA; 11279 BP.  
 DE Pseudomonas sp. WF505 bto gene cluster, SEQ ID NO:1.  
 PN JP2000093180-A.  
 PD 04-APR-2000.  
 PA (TOFU) TONEN CORP.  
 Best Local Similarity: 26.64%  
 Query Match: 6.70%  
 RESULT 192  
 ID ABL07082 standard; cDNA; 26370 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15728.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE-) PE CORP NY.  
 Best Local Similarity: 24.48%  
 Query Match: 6.70%  
 RESULT 193  
 ID ADP64454 standard; DNA; 76994 BP.  
 DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.  
 PN WO2004053065-A2.  
 PD 24-JUN-2004.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Best Local Similarity: 29.69%  
 Query Match: 6.70%  
 RESULT 194  
 ID ADC24078 standard; DNA; 1011 BP.  
 DE DNA sequence (SeqID 345) encoding a nitrilase enzyme.  
 PN WO2003000840-A2.  
 PD 03-JAN-2003.  
 PA (DIVE-) DIVERSA CORP.  
 PA (MADD//) MADDEN D.  
 Best Local Similarity: 23.66%  
 Query Match: 6.67%  
 RESULT 195  
 ID ADH36179 standard; DNA; 1011 BP.  
 DE Chemical process monitoring-related nitrilase gene sequence SeqID345.  
 PN WO2003098187-A2.  
 PD 27-NOV-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Best Local Similarity: 23.66%  
 Query Match: 6.67%  
 RESULT 196

Query Match: 6.67% Indels: 66  
RESULT 196  
ID ADG93879 standard; DNA; 1011 BP.  
DE Nitrilase enzyme gene sequence SeqID345.  
PN WO2003097810-A2.  
PD 27-NOV-2003.  
PA (DIVE-) DIVERSA CORP.  
Best Local Similarity: 23.66% Mismatches: 114  
Query Match: 6.67% Indels: 66  
RESULT 197  
ID ADI62477 standard; DNA; 1011 BP.  
DE DNA encoding nitrilase polypeptide #173.  
PN WO2003106415-A2.  
PD 24-DEC-2003.  
PA (DIVE-) DIVERSA CORP.  
Best Local Similarity: 23.66% Mismatches: 114  
Query Match: 6.67% Indels: 66  
RESULT 198  
ID ADI64598 standard; DNA; 1011 BP.  
DE DNA encoding nitrilase seq id 173.  
PN US2004014195-A1.  
PD 22-JAN-2004.  
PA (DIVE-) DIVERSA CORP.  
Best Local Similarity: 23.66% Mismatches: 114  
Query Match: 6.67% Indels: 66  
RESULT 199  
ID ABL10626 standard; DNA; 1965 BP.  
DE Pseudomonas aeruginosa polynucleotide #9230.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 28.88% Mismatches: 86  
Query Match: 6.67% Indels: 61  
RESULT 200  
ID AAS71429 standard; cDNA; 2253 BP.  
DE DNA encoding novel human diagnostic protein #7233.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 24.05% Mismatches: 113  
Query Match: 6.67% Indels: 70  
RESULT 201  
ID ADC32348 standard; cDNA; 2253 BP.  
DE Human novel cDNA contig sequence, SEQ ID NO:2430.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 24.05% Mismatches: 113  
Query Match: 6.67% Indels: 70  
RESULT 202  
ID ADC32347 standard; cDNA; 2253 BP.  
DE Human novel cDNA contig sequence, SEQ ID NO:2429.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 24.05% Mismatches: 113  
Query Match: 6.67% Indels: 70  
RESULT 203  
ID ACA37877 standard; DNA; 2493 BP.  
DE Prokaryotic essential gene #19534.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 26.96% Mismatches: 91  
Query Match: 6.67% Indels: 52  
RESULT 204  
ID ABD10460 standard; DNA; 2805 BP.  
DE Pseudomonas aeruginosa polynucleotide #9064.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 28.88% Mismatches: 86  
Query Match: 6.67% Indels: 61

RESULT 205  
ID ABD09496 standard; DNA; 3453 BP.  
DE Pseudomonas aeruginosa polynucleotide #8100.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 27.31% Mismatches: 94  
Query Match: 6.67% Indels: 55  
RESULT 206  
ID ADF72496 standard; DNA; 3758 BP.  
DE Osteoclast bicarbonate/chloride exchanger coding sequence, SEQ ID 3.  
PN JP2003334094-A.  
PD 25-NOV-2003.  
PA (SANY ) SANKYO CO LTD.  
Best Local Similarity: 23.96% Mismatches: 106  
Query Match: 6.67% Indels: 115  
RESULT 207  
ID ADF72500 standard; DNA; 3897 BP.  
DE Osteoclast bicarbonate/chloride exchanger coding sequence, SEQ ID 7.  
PN JP2003334094-A.  
PD 25-NOV-2003.  
PA (SANY ) SANKYO CO LTD.  
Best Local Similarity: 23.96% Mismatches: 106  
Query Match: 6.67% Indels: 115  
RESULT 208  
ID ACN38747 standard; cDNA; 3961 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA325047, SEQ ID NO:2455.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.26% Mismatches: 104  
Query Match: 6.67% Indels: 115  
RESULT 209  
ID ADF72498 standard; DNA; 3996 BP.  
DE Osteoclast bicarbonate/chloride exchanger coding sequence, SEQ ID 5.  
PN JP2003334094-A.  
PD 25-NOV-2003.  
PA (SANY ) SANKYO CO LTD.  
Best Local Similarity: 23.96% Mismatches: 106  
Query Match: 6.67% Indels: 115  
RESULT 210  
ID ADK16023 standard; DNA; 64492 BP.  
DE Streptomyces halstedii vincenistatin gene cluster seq id 1.  
PN US2004053274-A1.  
PD 18-MAR-2004.  
PA (TOKD ) TOKYO INST TECHNOLOGY.  
Best Local Similarity: 28.47% Mismatches: 99  
Query Match: 6.67% Indels: 73  
RESULT 211  
ID ACH87373 standard; DNA; 875 BP.  
DE Human genome derived single exon probe #20568.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Best Local Similarity: 27.23% Mismatches: 96  
Query Match: 6.63% Indels: 52  
RESULT 212  
ID AAK53011 standard; cDNA; 1330 BP.  
DE Human polynucleotide SEQ ID NO 2540.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 22.52% Mismatches: 106  
Query Match: 6.63% Indels: 122  
RESULT 213  
ID AAN71338 standard; DNA; 2304 BP.  
DE Modified prourokinase.  
PN EP36040-A.  
PD 09-SEP-1987.  
PA (COLB ) COLLABORATIVE RES INC.  
Best Local Similarity: 24.63% Mismatches: 96

Query Match: 6.63% Indels: 79  
 RESULT 214  
 ID ACN43531 standard; cDNA; 3448 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2406.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 21.92% Mismatches: 99  
 Query Match: 6.63% Indels: 98  
 RESULT 215  
 ID AAS74203 standard; cDNA; 5254 BP.  
 DE DNA encoding novel human diagnostic protein #10007.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 27.23% Mismatches: 96  
 Query Match: 6.63% Indels: 52  
 RESULT 216  
 ID ADR24155 standard; DNA; 5960 BP.  
 DE Breast cancer prognosis marker #16.  
 PN WO2004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 Best Local Similarity: 27.23% Mismatches: 96  
 Query Match: 6.63% Indels: 52  
 RESULT 217  
 ID AAK52019 standard; cDNA; 6044 BP.  
 DE Human polynucleotide SEQ ID NO 564.  
 PN WO200157150-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 27.23% Mismatches: 96  
 Query Match: 6.63% Indels: 52  
 RESULT 218  
 ID AAK53003 standard; cDNA; 6051 BP.  
 DE Human polynucleotide SEQ ID NO 2532.  
 PN WO200157190-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 27.23% Mismatches: 96  
 Query Match: 6.63% Indels: 52  
 RESULT 219  
 ID ACD13189 standard; cDNA; 6075 BP.  
 DE cDNA encoding novel human protein NOV4a.  
 PN WO200298900-A2.  
 PD 12-DEC-2002.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 27.23% Mismatches: 96  
 Query Match: 6.63% Indels: 52  
 RESULT 220  
 ID AAQ73500 standard; DNA; 8438 BP.  
 DE DNA encoding Pseudorabies virus large latency transcript.  
 PN US5352596-A.  
 PD 04-OCT-1994.  
 PA (USDA ) US SEC OF AGRIC.  
 Best Local Similarity: 27.41% Mismatches: 96  
 Query Match: 6.63% Indels: 82  
 RESULT 221  
 ID AAD46790 standard; DNA; 13766 BP.  
 DE pGRN145 plasmid DNA.  
 PN WO200274935-A2.  
 PD 26-SEP-2002.  
 PA (GERO-) GERON CORP.  
 Best Local Similarity: 23.89% Mismatches: 94  
 Query Match: 6.63% Indels: 72  
 RESULT 222  
 ID AA255887 standard; DNA; 68750 BP.  
 DE Sorangium cellulosum 68.75 kb contig.  
 PN WO9966028-A2.  
 PD 23-DEC-1999.  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

Best Local Similarity: 30.49% Mismatches: 91  
 Query Match: 6.63% Indels: 46  
 RESULT 223  
 ID ADJ72363 standard; DNA; 90597 BP.  
 DE Streptomyces roseosporus daptomycin biosynthetic gene cluster DNA.  
 PN WO2003014297-A2.  
 PD 20-FEB-2003.  
 PA (CUBI-) CUBIST PHARM INC.  
 Best Local Similarity: 26.00% Mismatches: 96  
 Query Match: 6.63% Indels: 67  
 RESULT 224  
 ID ADJ72363 standard; DNA; 90597 BP.  
 DE Streptomyces roseosporus daptomycin biosynthetic gene cluster DNA.  
 PN WO2003014297-A2.  
 PD 20-FEB-2003.  
 PA (CUBI-) CUBIST PHARM INC.  
 Best Local Similarity: 24.70% Mismatches: 119  
 Query Match: 6.63% Indels: 97  
 RESULT 225  
 ID ABQ78872 standard; DNA; 90600 BP.  
 DE S. roseosporus daptomycin biosynthetic gene cluster 90kb region.  
 PN WO200259322-A2.  
 PD 01-AUG-2002.  
 PA (MIAO/) MIAO V P W.  
 PA (BRIA/) BRIAN P.  
 PA (BALT/) BALTZ R H.  
 PA (SILV/) SILVA C J.  
 Best Local Similarity: 26.00% Mismatches: 96  
 Query Match: 6.63% Indels: 67  
 RESULT 226  
 ID ABQ78872 standard; DNA; 90600 BP.  
 DE S. roseosporus daptomycin biosynthetic gene cluster 90kb region.  
 PN WO200259322-A2.  
 PD 01-AUG-2002.  
 PA (MIAO/) MIAO V P W.  
 PA (BRIA/) BRIAN P.  
 PA (BALT/) BALTZ R H.  
 PA (SILV/) SILVA C J.  
 Best Local Similarity: 24.70% Mismatches: 119  
 Query Match: 6.63% Indels: 97  
 RESULT 227  
 ID ABX04971 standard; DNA; 103599 BP.  
 DE S. cinnamonensis monensin type I polyketide synthase gene cluster.  
 PN WO200168867-A1.  
 PD 20-SEP-2001.  
 PA (BIOT-) BIOTICA TECHNOLOGY LTD.  
 Best Local Similarity: 21.99% Mismatches: 129  
 Query Match: 6.63% Indels: 99  
 RESULT 228  
 ID AAS08693 standard; DNA; 109519 BP.  
 DE Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.  
 PN WO200049177-A2.  
 PD 24-AUG-2000.  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 Best Local Similarity: 27.90% Mismatches: 81  
 Query Match: 6.60% Indels: 69  
 RESULT 230  
 ID AAL43629 standard; DNA; 1050 BP.  
 DE Rhodococcus picric acid degradation F420-dependent dehydrogenase #2 ORF.  
 PN US2002042117-A1.  
 PD 11-APR-2002.  
 PA (ROUV/) ROUVIERE P E.  
 PA (WALT/) WALTERS D M.  
 PA (RUSS/) RUSS R.  
 Best Local Similarity: 27.90% Mismatches: 81  
 Query Match: 6.60% Indels: 69  
 RESULT 231  
 ID ABK51847 standard; DNA; 1050 BP.

DE R. erythropolis HL PM-1 picric acid degradation gene cluster ORF9.  
PN US6355470-B1.  
PD 12-MAR-2002.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Best Local Similarity: 27.90% Mismatches: 81  
Query Match: 6.60% Indels: 69  
RESULT 232  
ID AAD27248 standard; DNA; 1050 BP.  
DE Rhodococcus erythropolis HL-PM1 picric acid degradation gene ORF8.  
PN US6329151-B1.  
PD 11-DEC-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Best Local Similarity: 27.90% Mismatches: 81  
Query Match: 6.60% Indels: 69  
RESULT 233  
ID ACA26216 standard; DNA; 1629 BP.  
DE Prokaryotic essential gene #7873.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-), ELITRA PHARM INC.  
Best Local Similarity: 21.76% Mismatches: 84  
Query Match: 6.60% Indels: 78  
RESULT 234  
ID ADH71207 standard; DNA; 2268 BP.  
DE Human gene of the invention NOV61 SEQ ID NO:103.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 23.05% Mismatches: 117  
Query Match: 6.60% Indels: 92  
RESULT 235  
ID ACA45234 standard; DNA; 2286 BP.  
DE Prokaryotic essential gene #26891.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-), ELITRA PHARM INC.  
Best Local Similarity: 23.51% Mismatches: 91  
Query Match: 6.60% Indels: 119  
RESULT 236  
ID AAS78878 standard; cDNA; 2653 BP.  
DE DNA encoding novel human diagnostic protein #14682.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 24.89% Mismatches: 61  
Query Match: 6.60% Indels: 83  
RESULT 237  
ID ADO07393 standard; DNA; 7033 BP.  
DE Modified human hepsin plasmid pIRESpuro2W/hepEK.  
PN WO200403630-A2.  
PD 22-APR-2004.  
PA (SCHD) SCHERING AG.  
Best Local Similarity: 22.99% Mismatches: 102  
Query Match: 6.60% Indels: 72  
RESULT 238  
ID AAS3941 standard; DNA; 12508 BP.  
DE 12.5 kb picric acid degradation cluster.  
PN WO200049177-A2.  
PD 24-AUG-2000.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Best Local Similarity: 24.00% Mismatches: 109  
Query Match: 6.60% Indels: 83  
RESULT 239  
ID AAS3941 standard; DNA; 12508 BP.  
DE 12.5 kb picric acid degradation cluster.  
PN WO200049177-A2.  
PD 24-AUG-2000.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Best Local Similarity: 27.90% Mismatches: 81  
Query Match: 6.60% Indels: 69  
RESULT 240  
ID AAD27240 standard; DNA; 12508 BP.  
DE Rhodococcus erythropolis strain HL-PM1 picric acid degradation gene.

PN US6329151-B1.  
PD 11-DEC-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Best Local Similarity: 24.00% Mismatches: 109  
Query Match: 6.60% Indels: 83  
RESULT 241  
ID AAD27240 standard; DNA; 12508 BP.  
DE Rhodococcus erythropolis strain HL-PM1 picric acid degradation gene.  
PN US6329151-B1.  
PD 11-DEC-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Best Local Similarity: 27.90% Mismatches: 81  
Query Match: 6.60% Indels: 69  
RESULT 242  
ID AAL43619 standard; DNA; 12523 BP.  
DE Rhodococcus erythropolis 12kb picric acid degradation gene cluster.  
PN US2002042117-A1.  
PD 11-APR-2002.  
PA (ROUV/) ROUVIERE P E.  
PA (WALT/) WALTERS D M.  
PA (RUSS/) RUSS R.  
Best Local Similarity: 24.00% Mismatches: 109  
Query Match: 6.60% Indels: 83  
RESULT 243  
ID AAL43619 standard; DNA; 12523 BP.  
DE Rhodococcus erythropolis 12kb picric acid degradation gene cluster.  
PN US2002042117-A1.  
PD 11-APR-2002.  
PA (ROUV/) ROUVIERE P E.  
PA (WALT/) WALTERS D M.  
PA (RUSS/) RUSS R.  
Best Local Similarity: 27.90% Mismatches: 81  
Query Match: 6.60% Indels: 69  
RESULT 244  
ID ABK51837 standard; DNA; 12523 BP.  
DE Rhodococcus erythropolis HL PM-1 picric acid degradation gene cluster.  
PN US6355470-B1.  
PD 12-MAR-2002.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Best Local Similarity: 24.00% Mismatches: 109  
Query Match: 6.60% Indels: 83  
RESULT 245  
ID ABK51837 standard; DNA; 12523 BP.  
DE Rhodococcus erythropolis HL PM-1 picric acid degradation gene cluster.  
PN US6355470-B1.  
PD 12-MAR-2002.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Best Local Similarity: 27.90% Mismatches: 81  
Query Match: 6.60% Indels: 69  
RESULT 246  
ID AAL62889 standard; DNA; 88624 BP.  
DE Human alpha-2 macroglobulin genomic DNA.  
Best Local Similarity: 28.95% Mismatches: 30  
Query Match: 6.60% Indels: 29  
RESULT 247  
ID ABD11923 standard; DNA; 891 BP.  
DE Pseudomonas aeruginosa polynucleotide #10527.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 31.48% Mismatches: 45  
Query Match: 6.56% Indels: 16  
RESULT 248  
ID ABD11931 standard; DNA; 1320 BP.  
DE Pseudomonas aeruginosa polynucleotide #10535.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 31.48% Mismatches: 45  
Query Match: 6.56% Indels: 16  
RESULT 249  
ID ABD12035 standard; DNA; 1473 BP.  
DE Pseudomonas aeruginosa polynucleotide #10639.

PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 31.48% Mismatches: 45  
 Query Match: 6.56% Indels: 16  
 RESULT 250  
 ID ABD15515 standard; DNA; 1767 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14119.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 26.72% Mismatches: 108  
 Query Match: 6.56% Indels: 49  
 RESULT 251  
 ID ADH71189 standard; DNA; 2106 BP.  
 DE Human gene of the invention NOV6c SEQ ID NO:85.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 26.16% Mismatches: 125  
 Query Match: 6.56% Indels: 49  
 RESULT 252  
 ID ACA45338 standard; DNA; 2215 BP.  
 DE Prokaryotic essential gene #26995.  
 PN WO200271183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 22.99% Mismatches: 95  
 Query Match: 6.56% Indels: 91  
 RESULT 253  
 ID ADA69752 standard; DNA; 2763 BP.  
 DE Rice gene, SEQ ID 3075.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 26.24% Mismatches: 95  
 Query Match: 6.56% Indels: 82  
 RESULT 254  
 ID ACN43529 standard; cDNA; 3508 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2404.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 23.55% Mismatches: 76  
 Query Match: 6.56% Indels: 78  
 RESULT 255  
 ID ACN43534 standard; cDNA; 3637 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2409.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 23.55% Mismatches: 76  
 Query Match: 6.56% Indels: 78  
 RESULT 256  
 ID ACA42635 standard; DNA; 4248 BP.  
 DE Prokaryotic essential gene #24292.  
 PN WO200271183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 28.14% Mismatches: 109  
 Query Match: 6.56% Indels: 31  
 RESULT 257  
 ID ABD15556 standard; DNA; 4287 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14160.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 26.72% Mismatches: 108  
 Query Match: 6.56% Indels: 49  
 RESULT 258  
 ID ADK41004 standard; DNA; 5159 BP.  
 DE Novel human kinase gene #24.  
 PN WO2003057841-A2.

PD 17-JUL-2003.  
 PA (GRIG/) GRIGORIEV I V.  
 PA (SUDA/) SUDARSANAM S.  
 Best Local Similarity: 25.43% Mismatches: 77  
 Query Match: 6.56% Indels: 75  
 RESULT 259  
 ID ADRI5718 standard; DNA; 5159 BP.  
 DE Kinase 40980 hCT14735 1 coding sequence, SEQ ID 111.  
 PN WO2004069154-A2.  
 PD 19-AUG-2004.  
 PA (GRIG/) GRIGORIEV I V.  
 PA (SUDA/) SUDARSANAM S.  
 Best Local Similarity: 25.43% Mismatches: 77  
 Query Match: 6.56% Indels: 75  
 RESULT 260  
 ID ABD14206 standard; DNA; 1230 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12810.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 29.38% Mismatches: 68  
 Query Match: 6.53% Indels: 51  
 RESULT 261  
 ID AA158354 standard; cDNA; 3542 BP.  
 DE Human polynucleotide SEQ ID NO 557.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 24.23% Mismatches: 94  
 Query Match: 6.53% Indels: 82  
 RESULT 262  
 ID ADQ98563 standard; cDNA; 3542 BP.  
 DE DNA encoding human GPCR-like protein seqid 233.  
 PN US6569662-B1.  
 PD 27-MAY-2003.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 24.23% Mismatches: 94  
 Query Match: 6.53% Indels: 82  
 RESULT 263  
 ID ADB48323 standard; cDNA; 3542 BP.  
 DE Novel human cDNA SEQ ID NO 233.  
 PN US2003104529-A1.  
 PD 05-JUN-2003.  
 PA (ZHOU/) ZHOU P.  
 PA (TANG/) TANG Y T.  
 PA (LIUC/) LIU C.  
 PA (ASUN/) ASUNDI V.  
 PA (DRMA/) DRMANAC R T.  
 Best Local Similarity: 24.23% Mismatches: 94  
 Query Match: 6.53% Indels: 82  
 RESULT 264  
 ID ABL12403 standard; cDNA; 5468 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31691.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 24.74% Mismatches: 123  
 Query Match: 6.53% Indels: 59  
 RESULT 265  
 ID AAV22647 standard; cDNA; 5630 BP.  
 DE Drosophila melanogaster kuzbanian (kuz) gene.  
 PN WO9808933-A1.  
 PD 05-MAR-1998.  
 PA (REGC) UNIV CALIFORNIA.  
 PA (UYIA) UNIV YALE.  
 Best Local Similarity: 24.74% Mismatches: 123  
 Query Match: 6.53% Indels: 59  
 RESULT 266  
 ID AAK51968 standard; cDNA; 6248 BP.  
 DE Human polynucleotide SEQ ID NO 513.  
 PN WO200157190-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.

Best Local Similarity: 26.21% Mismatches: 97  
 Query Match: 6.53% Indels: 86  
 RESULT 267  
 ID AD114148 standard; DNA; 17596 BP.  
 DE M. megalomicea cosmid KOS205-57-2.3B SEQ ID NO:2.  
 PN WO2004003169-A2.  
 PD 08-JAN-2004.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Best Local Similarity: 24.63% Mismatches: 102  
 Query Match: 6.53% Indels: 71  
 RESULT 268  
 ID AAF30757 standard; DNA; 47981 BP.  
 DE Micromonospora megalomicea megalomicin biosynthetic gene cluster.  
 Best Local Similarity: 24.63% Mismatches: 102  
 Query Match: 6.53% Indels: 71  
 RESULT 269  
 ID AAS59515 standard; DNA; 66788 BP.  
 DE Propionibacterium acnes immunogenic protein encoding DNA #10.  
 PN WO200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 24.10% Mismatches: 100  
 Query Match: 6.53% Indels: 80  
 RESULT 270  
 ID ACF6444 standard; DNA; 66788 BP.  
 DE Propionibacterium acnes DNA contig sequence #10.  
 PN WO2003033515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 24.10% Mismatches: 100  
 Query Match: 6.53% Indels: 80  
 RESULT 271  
 Best Local Similarity: 30.00% Mismatches: 29  
 Query Match: 6.53% Indels: 36  
 RESULT 272  
 Best Local Similarity: 30.00% Mismatches: 29  
 Query Match: 6.53% Indels: 36  
 RESULT 273  
 ID ABD02895 standard; DNA; 990 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1499.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 22.19% Mismatches: 103  
 Query Match: 6.49% Indels: 112  
 RESULT 274  
 ID ABD08329 standard; DNA; 1101 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6933.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 31.19% Mismatches: 90  
 Query Match: 6.49% Indels: 36  
 RESULT 275  
 ID ABD08256 standard; DNA; 1320 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6860.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 31.19% Mismatches: 90  
 Query Match: 6.49% Indels: 36  
 RESULT 276  
 ID ABD08161 standard; DNA; 1359 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6765.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 31.19% Mismatches: 90  
 Query Match: 6.49% Indels: 36  
 RESULT 277  
 ID AAF32672 standard; cDNA; 1748 BP.  
 DE Human cDNA encoding intracellular signalling molecule INTRA35.  
 PN WO200077040-A2.

PD 21-DEC-2000.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 28.75% Mismatches: 79  
 Query Match: 6.49% Indels: 63  
 RESULT 278  
 ID ADM87079 standard; cDNA; 1909 BP.  
 DE Human protein encoding cDNA SEQ ID NO:172.  
 PN WO2004009834-A2.  
 PD 29-JAN-2004.  
 PA (NUVE-) NUVELO INC.  
 Best Local Similarity: 25.00% Mismatches: 63  
 Query Match: 6.49% Indels: 88  
 RESULT 279  
 ID AAK74278 standard; DNA; 2388 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29090.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 27.47% Mismatches: 86  
 Query Match: 6.49% Indels: 59  
 RESULT 280  
 ID ADO64606 standard; cDNA; 3554 BP.  
 DE Novel human cDNA sequence #1767.  
 PN EP1440981-A2.  
 PD 28-JUL-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Best Local Similarity: 23.82% Mismatches: 129  
 Query Match: 6.49% Indels: 126  
 RESULT 281  
 ID AAL44297 standard; DNA; 8651 BP.  
 DE Agromyces mediolanus Y1 operon (C50 carotenoid producing operon).  
 PN WO200241833-A2.  
 PD 30-MAY-2002.  
 PA (CRGI ) CARGILL INC.  
 Best Local Similarity: 25.61% Mismatches: 112  
 Query Match: 6.49% Indels: 72  
 RESULT 282  
 ID ADL71890 standard; cDNA; 13068 BP.  
 DE Temperature inducible alphavirus vector pCytts2.1.  
 PN WO2004018506-A2.  
 PD 04-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Best Local Similarity: 23.25% Mismatches: 105  
 Query Match: 6.49% Indels: 75  
 RESULT 283  
 ID ADL71909 standard; cDNA; 15081 BP.  
 DE Expression vector pCytts-Orp.  
 PN WO2004018506-A2.  
 PD 04-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Best Local Similarity: 23.25% Mismatches: 105  
 Query Match: 6.49% Indels: 75  
 RESULT 284  
 ID ADL71910 standard; cDNA; 17753 BP.  
 DE Expression vector pCytts-OPE.  
 PN WO2004018506-A2.  
 PD 04-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Best Local Similarity: 23.25% Mismatches: 105  
 Query Match: 6.49% Indels: 75  
 RESULT 285  
 ID AB033451 standard; DNA; 46338 BP.  
 DE Murine cancer-associated (CA) gene MD07-086.  
 PN WO2004058146-A2.  
 PD 15-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Best Local Similarity: 23.45% Mismatches: 62  
 Query Match: 6.49% Indels: 95  
 RESULT 286  
 ID ADA02798 standard; DNA; 52754 BP.  
 DE Human TNFSF11 carcinoma associated gene, SEQ ID NO:1316.  
 PN WO2003057146-A2.  
 PD 17-JUL-2003.



PA (SAGR-) SAGRES DISCOVERY.		
Best Local Similarity: 22.59%	Mismatches:	113
Query Match: 6.49%	Indels:	95
RESULT 287		
ID ADB72536 standard; DNA; 52754 BP.		
DE Human TNFSF11 gene.		
PN WO2003008583-A2.		
PD 30-JAN-2003.		
PA (SAGR-) SAGRES DISCOVERY.		
Best Local Similarity: 22.59%	Mismatches:	113
Query Match: 6.49%	Indels:	95
RESULT 288		
ID ADC85278 standard; DNA; 52754 BP.		
DE Human TNFSF11 genomic sequence.		
PN WO2003045230-A2.		
PD 05-JUN-2003.		
PA (SAGR-) SAGRES DISCOVERY.		
Best Local Similarity: 22.59%	Mismatches:	113
Query Match: 6.49%	Indels:	95
RESULT 289		
ID ADM74393 standard; DNA; 52754 BP.		
DE Human carcinoma associated (CA) nucleic acid #31.		
PN US2004072154-A1.		
PD 15-APR-2004.		
PA (MORR/) MORRIS D W.		
PA (ENGE/) ENGELHARD E K.		
Best Local Similarity: 22.59%	Mismatches:	113
Query Match: 6.49%	Indels:	95
RESULT 290		
ID AL40781 standard; DNA; 88421 BP.		
DE 88421nt genomic DNA of ramoplanin producing Actinoplanes sp.		
PN WO200231155-A2.		
PD 18-APR-2002.		
PA (ECOP-) ECOPIA BIOSCIENCES INC.		
Best Local Similarity: 26.92%	Mismatches:	84
Query Match: 6.49%	Indels:	66
RESULT 291		
Best Local Similarity: 26.77%	Mismatches:	56
Query Match: 6.49%	Indels:	22
RESULT 292		
Best Local Similarity: 26.77%	Mismatches:	56
Query Match: 6.49%	Indels:	22
RESULT 293		
Best Local Similarity: 26.77%	Mismatches:	56
Query Match: 6.49%	Indels:	22
RESULT 294		
Best Local Similarity: 26.77%	Mismatches:	56
Query Match: 6.49%	Indels:	22
RESULT 295		
Best Local Similarity: 26.77%	Mismatches:	56
Query Match: 6.49%	Indels:	22
RESULT 296		
Best Local Similarity: 26.77%	Mismatches:	56
Query Match: 6.49%	Indels:	22
RESULT 297		
ID ADP74816 standard; DNA; 137560 BP.		
DE Parapoxvirus ovine genome DNA sequence SeqID1.		
Best Local Similarity: 24.85%	Mismatches:	100
Query Match: 6.49%	Indels:	121
RESULT 298		
ID AAQ39088 standard; cDNA; 1659 BP.		
DE XR2 coding sequence.		
PN WO9306215-A1.		
PD 01-APR-1993.		
PA (SALK ) SALK INST BIOLOGICAL STUDIES.		
Best Local Similarity: 24.58%	Mismatches:	70
Query Match: 6.46%	Indels:	91
RESULT 299		
ID ADH71215 standard; DNA; 2368 BP.		
DE Human gene of the invention NOV6p SEQ ID NO:111.		
PN WO2003102155-A2.		
PD 11-DEC-2003.		
PA (CURA-) CURAGEN CORP.		

Best Local Similarity: 23.05%	Mismatches: 117
Query Match: 6.46%	Indels: 92
RESULT 300	
ID ADH71213 standard; DNA; 2268 BP.	
DE Human gene of the invention NOV60 SEQ ID NO:109.	
FN W02003102155-A2.	
PD 11-DEC-2003.	
PA (CURA-) CURAGEN CORP.	
Best Local Similarity: 23.05%	Mismatches: 117
Query Match: 6.46%	Indels: 92
RESULT 301	
ID ADH71185 standard; DNA; 2268 BP.	
DE Human gene of the invention NOV6a SEQ ID NO:81.	
FN W02003102155-A2.	
PD 11-DEC-2003.	
PA (CURA-) CURAGEN CORP.	
Best Local Similarity: 23.05%	Mismatches: 117
Query Match: 6.46%	Indels: 92
RESULT 302	
ID ADH71211 standard; DNA; 2268 BP.	
DE Human gene of the invention NOV6n SEQ ID NO:107.	
FN W02003102155-A2.	
PD 11-DEC-2003.	
PA (CURA-) CURAGEN CORP.	
Best Local Similarity: 23.05%	Mismatches: 117
Query Match: 6.46%	Indels: 92
RESULT 303	
ID ADH71209 standard; DNA; 2268 BP.	
DE Human gene of the invention NOV6m SEQ ID NO:105.	
FN W02003102155-A2.	
PD 11-DEC-2003.	
PA (CURA-) CURAGEN CORP.	
Best Local Similarity: 23.05%	Mismatches: 117
Query Match: 6.46%	Indels: 92
RESULT 304	
ID ADH71187 standard; DNA; 2280 BP.	
DE Human gene of the invention NOV6b SEQ ID NO:83.	
FN W02003102155-A2.	
PD 11-DEC-2003.	
PA (CURA-) CURAGEN CORP.	
Best Local Similarity: 23.05%	Mismatches: 117
Query Match: 6.46%	Indels: 92
RESULT 305	
ID ADS62026 standard; cDNA; 2766 BP.	
DE Bacterial polynucleotide #14013.	
FN US2003233675-A1.	
PD 18-DEC-2003.	
PA (CAOY/) CAO Y.	
PA (HINK/) HINKLE G J.	
PA (SLAT/) SLATER S C.	
PA (CHEN/) CHEN X.	
PA (GOLD/) GOLDMAN B S.	
Best Local Similarity: 21.75%	Mismatches: 91
Query Match: 6.46%	Indels: 117
RESULT 306	
ID ACN44719 standard; cDNA; 2858 BP.	
DE Human mRNA sequence hCT1785697.	
FN W02003073826-A2.	
PD 12-SEP-2003.	
PA (SAGR-) SAGRES DISCOVERY.	
Best Local Similarity: 21.38%	Mismatches: 109
Query Match: 6.46%	Indels: 105
RESULT 307	
ID ABS70366 standard; cDNA; 3030 BP.	
DE Human bone remodelling gene #23.	
FN US6426186-B1.	
PD 30-JUL-2002.	
PA (INCY-) INCYTE GENOMICS INC.	
Best Local Similarity: 21.38%	Mismatches: 109
Query Match: 6.46%	Indels: 105
RESULT 308	
ID AAD59099 standard; DNA; 3389 BP.	
DE Human antiCD3/CD28-RATL 5-h6 contig DNA.	

PN US200314196-A1.  
PD 31-JUL-2003.  
PA (BOWE/) BOWEN M. A.  
PA (FINGER/) FINGER J.  
Best Local Similarity: 21.38% Mismatches: 109  
Query Match: 6.46% Indels: 105  
RESULT 309  
ID ADM86984 standard; cDNA; 3493 BP.  
DE Human protein encoding cDNA SEQ ID NO:77.  
PN WO200400934-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Best Local Similarity: 21.38% Mismatches: 109  
Query Match: 6.46% Indels: 105  
RESULT 310  
ID ADF12845 standard; DNA; 3498 BP.  
DE Reference mRNA sequence #59.  
PN WO2004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Best Local Similarity: 21.38% Mismatches: 109  
Query Match: 6.46% Indels: 105  
RESULT 311  
ID ADS14592 standard; DNA; 3750 BP.  
DE Pseudomonas aeruginosa quorum sensing controlled gene PA2305, SEQ ID 147.  
PN WO2004083385-A2.  
PD 30-SEP-2004.  
PA (IOWA) UNIV IOWA RES FOUND.  
Best Local Similarity: 28.45% Mismatches: 86  
Query Match: 6.46% Indels: 61  
RESULT 312  
ID ADRO7305 standard; cDNA; 4408 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 811.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 25.97% Mismatches: 68  
Query Match: 6.46% Indels: 24  
RESULT 313  
ID ACM44718 standard; DNA; 20478 BP.  
DE Human genomic sequence HCG1747365.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 21.38% Mismatches: 109  
Query Match: 6.46% Indels: 105  
RESULT 314  
ID AAG63350 standard; DNA; 21185 BP.  
DE Streptomyces globisporus C-1027 gene cluster ORF 25-42.  
PN WO200040596-A1.  
PD 13-JUL-2000.  
PA (REGC) UNIV CALIFORNIA.  
Best Local Similarity: 25.65% Mismatches: 76  
Query Match: 6.46% Indels: 67  
RESULT 315  
ID AAV20441 standard; DNA; 35100 BP.  
DE Human c-fos oncogene.  
PN US5734039-A.  
PD 31-MAR-1998.  
PA (UJJE-) UNIV JEFFERSON THOMAS.  
Best Local Similarity: 24.52% Mismatches: 89  
Query Match: 6.46% Indels: 125  
RESULT 316  
ID AAS98633 standard; DNA; 38258 BP.  
DE DNA encoding Colony stimulating factor 1 receptor (CSF1R).  
Best Local Similarity: 24.52% Mismatches: 89  
Query Match: 6.46% Indels: 125  
RESULT 317  
ID AAG63348 standard; DNA; 63164 BP.  
DE Streptomyces globisporus C-1027 gene cluster.  
PN WO200040596-A1.  
PD 13-JUL-2000.  
PA (REGC) UNIV CALIFORNIA.

Best Local Similarity: 25.65% Mismatches: 76  
Query Match: 6.46% Indels: 67  
RESULT 318  
Best Local Similarity: 25.00% Mismatches: 75  
Query Match: 6.48% Indels: 95  
RESULT 319  
ID ADI39160 standard; DNA; 86941 BP.  
DE Streptomyces hygrosopicus herbimycin gene cluster, SEQ ID NO:2.  
PN WO2003106653-A2.  
PD 24-DEC-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
PA (REID/) REID R. C.  
Best Local Similarity: 26.49% Mismatches: 106  
Query Match: 6.46% Indels: 80  
RESULT 320  
Best Local Similarity: 25.00% Mismatches: 75  
Query Match: 6.46% Indels: 95  
RESULT 321  
ID ADH17387 standard; cDNA; 1321 BP.  
DE Human NOV9a cDNA - SEQ ID 77.  
PN WO2003093432-A2.  
PD 13-NOV-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 23.61% Mismatches: 98  
Query Match: 6.42% Indels: 110  
RESULT 322  
ID ABD09161 standard; DNA; 1461 BP.  
DE Pseudomonas aeruginosa polynucleotide #7765.  
PN US551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 22.02% Mismatches: 133  
Query Match: 6.42% Indels: 96  
RESULT 323  
ID ACA42339 standard; DNA; 1608 BP.  
DE Prokaryotic essential gene #23996.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 23.00% Mismatches: 99  
Query Match: 6.42% Indels: 93  
RESULT 324  
ID ADS14623 standard; DNA; 1608 BP.  
DE Pseudomonas aeruginosa quorum sensing controlled gene PA2573, SEQ ID 178.  
PN WO2004083385-A2.  
PD 30-SEP-2004.  
PA (IOWA) UNIV IOWA RES FOUND.  
Best Local Similarity: 23.00% Mismatches: 99  
Query Match: 6.42% Indels: 93  
RESULT 325  
ID ABX70825 standard; cDNA; 1879 BP.  
DE Novel human cDNA sequence #50.  
PN WO200281731-A2.  
PD 17-OCT-2002.  
PA (HYSE-) HYSEQ INC.  
PA (GOOD/) GOODRICH R. W.  
Best Local Similarity: 24.03% Mismatches: 60  
Query Match: 6.42% Indels: 108  
RESULT 326  
ID ADF44669 standard; cDNA; 2094 BP.  
DE Bacterial polynucleotide #19420.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G. J.  
PA (SLAT/) SLATER S. C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B. S.  
Best Local Similarity: 27.91% Mismatches: 108  
Query Match: 6.42% Indels: 30  
RESULT 327  
ID ADB63171 standard; cDNA; 2224 BP.  
DE Human cDNA encoding clone SPLN20073500.

PN EPI308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 26.74% Mismatches: 108  
Query Match: 6.42% Indels: 115  
RESULT 328  
ID ADM02791 standard; cDNA; 3029 BP.  
DE Human cDNA of the invention SEQ ID NO:1476.  
PN EPI347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 24.28% Mismatches: 88  
Query Match: 6.42% Indels: 90  
RESULT 329  
ID AAS27829 standard; DNA; 22452 BP.  
DE DNA encoding novel signal transduction pathway protein, Seq ID 1489.  
PN WO200154733-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 26.62% Mismatches: 88  
Query Match: 6.42% Indels: 88  
RESULT 330  
ID AAS27827 standard; DNA; 22452 BP.  
DE DNA encoding novel signal transduction pathway protein, Seq ID 1487.  
PN WO200154733-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 26.62% Mismatches: 88  
Query Match: 6.42% Indels: 88  
RESULT 331  
ID ADB94632 standard; DNA; 22452 BP.  
DE Novel human protein DNA #241.  
PN US2002168711-A1.  
PD 14-NOV-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Best Local Similarity: 26.62% Mismatches: 88  
Query Match: 6.42% Indels: 88  
RESULT 332  
ID ADB94630 standard; DNA; 22452 BP.  
DE Novel human protein DNA #239.  
PN US2002168711-A1.  
PD 14-NOV-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Best Local Similarity: 26.62% Mismatches: 88  
Query Match: 6.42% Indels: 88  
RESULT 333  
ID ADI00878 standard; DNA; 22773 BP.  
DE Human mucin MUC5B genomic DNA 5' fragment.  
PN US2003096219-A1.  
PD 22-MAY-2003.  
PA (WURR/) WU R.  
PA (CHEN/) CHEN Y.  
Best Local Similarity: 24.09% Mismatches: 106  
Query Match: 6.42% Indels: 126  
RESULT 334  
ID ACN44185 standard; cDNA; 956 BP.  
DE Mouse mRNA sequence mCT18732.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 25.74% Mismatches: 96  
Query Match: 6.39% Indels: 54  
RESULT 335  
ID AAH00902 standard; DNA; 1208 BP.  
DE Sporothrix schenckii nucleotide sequence SEQ ID NO:893.  
PN WO200123604-A2.  
PD 05-APR-2001.  
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

Best Local Similarity: 22.12% Mismatches: 100  
Query Match: 6.39% Indels: 92  
RESULT 336  
ID AAH00502 standard; DNA; 1211 BP.  
DE Sporothrix schenckii nucleotide sequence SEQ ID NO:493.  
PN WO200123604-A2.  
PD 05-APR-2001.  
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.  
Best Local Similarity: 22.12% Mismatches: 100  
Query Match: 6.39% Indels: 92  
RESULT 337  
ID AC449920 standard; DNA; 1425 BP.  
DE Prokaryotic essential gene #31577.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 23.15% Mismatches: 77  
Query Match: 6.39% Indels: 55  
RESULT 338  
ID ACN40783 standard; cDNA; 1600 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326842, SEQ ID NO:5787.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 23.97% Mismatches: 102  
Query Match: 6.39% Indels: 104  
RESULT 339  
ID AAL45648 standard; cDNA; 2064 BP.  
DE Human cancer cell growth inhibitor related cDNA SEQ ID NO: 4.  
PN CN1324819-A.  
PD 05-DEC-2001.  
PA (SHAN-) SHANGHAI CITY INST ONCOLOGY.  
Best Local Similarity: 23.97% Mismatches: 102  
Query Match: 6.39% Indels: 104  
RESULT 340  
ID AAL45649 standard; DNA; 2064 BP.  
DE Human cancer cell growth inhibitor related DNA SEQ ID NO: 6.  
PN CN1324819-A.  
PD 05-DEC-2001.  
PA (SHAN-) SHANGHAI CITY INST ONCOLOGY.  
Best Local Similarity: 23.97% Mismatches: 102  
Query Match: 6.39% Indels: 104  
RESULT 341  
ID ADB62304 standard; cDNA; 2792 BP.  
DE Human cDNA encoding clone FCBBF20059660.  
PN EPI308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 23.97% Mismatches: 102  
Query Match: 6.39% Indels: 104  
RESULT 342  
ID ADM02253 standard; cDNA; 3044 BP.  
DE Human cDNA of the invention SEQ ID NO:938.  
PN EPI347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 23.97% Mismatches: 102  
Query Match: 6.39% Indels: 104  
RESULT 343  
ID AAD51683 standard; cDNA; 3073 BP.  
DE Human nucleic acid associated protein (NAAP)-9 encoding cDNA.  
PN WO200299115-A2.  
PD 12-DEC-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
PA (YUEH/) YUE H.  
Best Local Similarity: 22.50% Mismatches: 125  
Query Match: 6.39% Indels: 124  
RESULT 344  
ID AAD59100 standard; DNA; 3393 BP.  
DE Human RAT1 5h6 DNA.  
PN US2003144196-A1.  
PD 31-JUL-2003.

PA (BOWE/) BOWEN M A.  
 PA (FING/) FINGER J.  
 Best Local Similarity: 21.38% Mismatches: 110  
 Query Match: 6.39% Indels: 105  
 RESULT 345  
 ID AAS92479 standard; cDNA; 4014 BP.  
 DE Human encoding novel human diagnostic protein #28283.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 21.45% Mismatches: 75  
 Query Match: 6.39% Indels: 138  
 RESULT 346  
 ID ABX34460 standard; cDNA; 4709 BP.  
 DE Human mdt cDNA SEQ ID 21.  
 PN WO200279449-A2.  
 PD 10-OCT-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 23.97% Mismatches: 102  
 Query Match: 6.39% Indels: 104  
 RESULT 347  
 ID AAX58463 standard; DNA; 4857 BP.  
 DE Thermophilus thermophilus DNA polymerase dnaE gene.  
 PN WO9913060-A1.  
 PD 18-MAR-1999.  
 PA (ENZY-) ENZYCO INC.  
 Best Local Similarity: 23.51% Mismatches: 99  
 Query Match: 6.39% Indels: 62  
 RESULT 348  
 ID ADI23903 standard; DNA; 8321 BP.  
 DE Streptomyces fradiae A541 locus contig 3.  
 PN US2003198981-A1.  
 PD 23-OCT-2003.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Best Local Similarity: 22.14% Mismatches: 116  
 Query Match: 6.39% Indels: 63  
 RESULT 349  
 ID AAS59517 standard; DNA; 18796 BP.  
 DE Propionibacterium acnes immunogenic protein encoding DNA #12.  
 PN WO200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.87% Mismatches: 134  
 Query Match: 6.39% Indels: 74  
 RESULT 350  
 ID ACP64446 standard; DNA; 18796 BP.  
 DE Propionibacterium acnes DNA contig sequence #12.  
 PN WO2003033515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.87% Mismatches: 134  
 Query Match: 6.39% Indels: 74  
 RESULT 351  
 ID ACN44184 standard; DNA; 20956 BP.  
 DE Mouse genomic sequence mCG15594.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Best Local Similarity: 25.74% Mismatches: 96  
 Query Match: 6.39% Indels: 54  
 RESULT 352  
 ID AAX87248 standard; DNA; 23580 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42060.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.97% Mismatches: 102  
 Query Match: 6.39% Indels: 104  
 RESULT 353  
 ID AAS28556 standard; DNA; 23580 BP.  
 DE Genomic sequence #396 encoding for novel human respiratory antigen.  
 PN WO200155448-A1.  
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.97% Mismatches: 102  
 Query Match: 6.39% Indels: 104  
 RESULT 354  
 ID ADG41752 standard; DNA; 23580 BP.  
 DE Human respiratory system associated genomic DNA seq id 990.  
 PN US2003215893-A1.  
 PD 20-NOV-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.97% Mismatches: 102  
 Query Match: 6.39% Indels: 104  
 RESULT 355  
 ID ADI97526 standard; DNA; 23580 BP.  
 DE Human respiratory system associated polypeptide-related DNA SeqID990.  
 PN US2003077704-A1.  
 PD 24-APR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.97% Mismatches: 102  
 Query Match: 6.39% Indels: 104  
 RESULT 356  
 ID ABQ88164 standard; cDNA; 86080 BP.  
 DE Human osteoblast differentiation related cDNA SEQ ID NO 71.  
 PN WO200250301-A2.  
 PD 27-JUN-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Best Local Similarity: 23.97% Mismatches: 102  
 Query Match: 6.39% Indels: 104  
 RESULT 357  
 ID ABK83561 standard; cDNA; 86080 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #132.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (PROC) PROCTER & GAMBLE CO.  
 Best Local Similarity: 23.97% Mismatches: 102  
 Query Match: 6.39% Indels: 104  
 RESULT 358  
 ID ADQ1054 standard; DNA; 86080 BP.  
 DE Human protective protein for beta-galactosidase gene SEQ ID NO:58.  
 PN WO2003061564-A2.  
 PD 31-JUL-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Best Local Similarity: 23.97% Mismatches: 102  
 Query Match: 6.39% Indels: 104  
 RESULT 359  
 ID ADQ18878 standard; DNA; 86080 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1697.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Best Local Similarity: 23.97% Mismatches: 102  
 Query Match: 6.39% Indels: 104  
 RESULT 360  
 ID ADQ97263 standard; DNA; 100864 BP.  
 DE Mouse cancer associated sequence MD2-08-023, SEQ ID 239.  
 PN WO2004060304-A2.  
 PD 22-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Best Local Similarity: 25.74% Mismatches: 96  
 Query Match: 6.39% Indels: 54  
 RESULT 361  
 ID AAX87248 standard; DNA; 23580 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42060.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.97% Mismatches: 102  
 Query Match: 6.39% Indels: 104  
 RESULT 362  
 ID ABD10328 standard; DNA; 678 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8932.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 28.71% Mismatches: 77  
 Query Match: 6.35% Indels: 54  
 RESULT 363

ID ACA37660 standard; DNA; 1113 BP.  
DE Prokaryotic essential gene #19317.  
PD WO200277183-A2.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 22.92% Mismatches: 101  
Query Match: 6.35% Indels: 104  
RESULT 364  
ID ADJ63193 standard; DNA; 1275 BP.  
DE Human zygote arrest 1 (Zar1) DNA sequence #2.  
PD WO2003091400-A2.  
PA (BAYU) BAYLOR COLLEGE MEDICINE.  
PA (AMHP) WYETH.  
Best Local Similarity: 28.57% Mismatches: 89  
Query Match: 6.35% Indels: 51  
RESULT 365  
ID AAS18432 standard; DNA; 1590 BP.  
DE Contig 143a DNA encoding S. narbonensis polyketide synthase.  
PD US6303767-B1.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Best Local Similarity: 23.38% Mismatches: 111  
Query Match: 6.35% Indels: 103  
RESULT 366  
ID ADJ91888 standard; DNA; 1590 BP.  
DE Streptomyces narbonolide polyketide synthase coding sequence #1.  
PD US2003194784-A1.  
PA (SHER-) SHERMAN D H.  
PA (LIUH-) LIU H.  
PA (XUEY-) XUE Y.  
PA (ZHAO-) ZHAO L.  
Best Local Similarity: 23.38% Mismatches: 111  
Query Match: 6.35% Indels: 103  
RESULT 367  
ID ADC30856 standard; cDNA; 1635 BP.  
DE Human novel cDNA sequence, SEQ ID NO:938.  
PD WO2003029271-A2.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 25.50% Mismatches: 111  
Query Match: 6.35% Indels: 82  
RESULT 368  
ID AAD16105 standard; cDNA; 1908 BP.  
DE Human intracellular regulatory molecule, KWC02 cDNA.  
PD US6274312-B1.  
PA (SCHE) SCHERING CORP.  
Best Local Similarity: 23.87% Mismatches: 87  
Query Match: 6.35% Indels: 58  
RESULT 369  
ID ACA23718 standard; DNA; 2064 BP.  
DE Prokaryotic essential gene #5375.  
PD WO200277183-A2.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 24.22% Mismatches: 92  
Query Match: 6.35% Indels: 45  
RESULT 370  
ID AAN71369 standard; DNA; 2304 BP.  
DE Modified prourokinase (ALA).  
PD EP236040-A.  
PD 09-SEP-1987.  
PA (COUB) COLLABORATIVE RES INC.  
Best Local Similarity: 27.65% Mismatches: 98  
Query Match: 6.35% Indels: 64  
RESULT 371  
ID ADQ86010 standard; cDNA; 2313 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2882.  
PD WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.

PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Best Local Similarity: 23.58% Mismatches: 115  
Query Match: 6.35% Indels: 44  
RESULT 372  
ID ADG63143 standard; cDNA; 2367 BP.  
DE Human cDNA encoding clone SPLEN20024770.  
PD EPI308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 26.38% Mismatches: 118  
Query Match: 6.35% Indels: 80  
RESULT 373  
ID AAK74279 standard; DNA; 2386 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29091.  
PD WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 27.47% Mismatches: 87  
Query Match: 6.35% Indels: 59  
RESULT 374  
ID AAO51488 standard; DNA; 2540 BP.  
DE Ornithine carbamoyl transferase (OCTase) gene.  
PD EP570096-A2.  
PD 18-NOV-1993.  
PA (OJIP) OJI PAPER CO.  
PA (OJIP) NEW OJI PAPER CO LTD.  
Best Local Similarity: 24.28% Mismatches: 98  
Query Match: 6.35% Indels: 62  
RESULT 375  
ID AAL50615 standard; cDNA; 3158 BP.  
DE Human glutamate receptor 14691 coding sequence.  
PD EPI245574-A1.  
PD 02-OCT-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 24.16% Mismatches: 88  
Query Match: 6.35% Indels: 90  
RESULT 376  
ID ADM02252 standard; cDNA; 3241 BP.  
DE Human cDNA of the invention SEQ ID NO:937.  
PD EPI347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 23.91% Mismatches: 88  
Query Match: 6.35% Indels: 90  
RESULT 377  
ID ADL61747 standard; DNA; 3255 BP.  
DE P. aeruginosa pathogenic virulence factor encoding DNA SEQ ID NO:17.  
PD WO2004024937-A2.  
PD 25-MAR-2004.  
PA (GEHO) GEN HOSPITAL CORP.  
Best Local Similarity: 24.45% Mismatches: 86  
Query Match: 6.35% Indels: 89  
RESULT 378  
ID AA222251 standard; DNA; 4257 BP.  
DE Nucleotide sequence of pPur vector.  
PD WO9947921-A1.  
PD 23-SEP-1999.  
PA (PHAR-) PHARMACOEPIA INC.  
Best Local Similarity: 24.05% Mismatches: 109  
Query Match: 6.35% Indels: 57  
RESULT 379  
ID ABT16611 standard; DNA; 4257 BP.  
DE Artificial plant chromosome related plasmid DNA SEQ ID NO 22.  
PD WO200296923-A1.  
PD 05-DEC-2002.  
PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.  
PA (AGRI-) AGRISOMA INC.  
Best Local Similarity: 24.05% Mismatches: 109  
Query Match: 6.35% Indels: 57  
RESULT 380  
ID ACC44641 standard; DNA; 4257 BP.

DE Plasmid pUR nucleotide sequence SEQ ID NO:30.  
 PN WO200297059-A2.  
 PD 05-DEC-2002.  
 PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.  
 Best Local Similarity: 24.05% Mismatches: 109  
 Query Match: 6.35% Indels: 57  
 RESULT 381  
 ID ABR16615 standard; DNA; 4346 BP.  
 DE Artificial plant chromosome related plasmid DNA SEQ ID NO 26.  
 PN WO200296923-A1.  
 PD 05-DEC-2002.  
 PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.  
 PA (AGRI-) AGRISOMA INC.  
 Best Local Similarity: 24.05% Mismatches: 109  
 Query Match: 6.35% Indels: 57  
 RESULT 382  
 ID ACC44716 standard; DNA; 4346 BP.  
 DE Plasmid pSV40193attPeasePUR nucleotide sequence SEQ ID NO:113.  
 PN WO200297059-A2.  
 PD 05-DEC-2002.  
 PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.  
 Best Local Similarity: 24.05% Mismatches: 109  
 Query Match: 6.35% Indels: 57  
 RESULT 383  
 ID ADR24153 standard; DNA; 4608 BP.  
 DE Breast cancer prognosis marker #14.  
 PN WO2004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 Best Local Similarity: 25.88% Mismatches: 99  
 Query Match: 6.35% Indels: 45  
 RESULT 384  
 ID ACM40091 standard; cDNA; 4508 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA326249, SEQ ID NO:4656.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 25.88% Mismatches: 99  
 Query Match: 6.35% Indels: 45  
 RESULT 385  
 ID ADJ63204 standard; DNA; 6002 BP.  
 DE Human zygote arrest 1 (Zar1) DNA sequence #3.  
 PN WO2003091400-A2.  
 PD 06-NOV-2003.  
 PA (BAYU) BAYLOR COLLEGE MEDICINE.  
 PA (AMHP) WYETH.  
 Best Local Similarity: 28.57% Mismatches: 89  
 Query Match: 6.35% Indels: 51  
 RESULT 386  
 ID ADJ63176 standard; DNA; 7405 BP.  
 DE Human zygote arrest 1 (Zar1) DNA sequence #1.  
 PN WO2003091400-A2.  
 PD 06-NOV-2003.  
 PA (BAYU) BAYLOR COLLEGE MEDICINE.  
 PA (AMHP) WYETH.  
 Best Local Similarity: 28.57% Mismatches: 89  
 Query Match: 6.35% Indels: 51  
 RESULT 387  
 ID AAD54223 standard; DNA; 24081 BP.  
 DE Streptomyces platensis subspecies rosaceus dorrigocin ORF6 DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Best Local Similarity: 26.38% Mismatches: 94  
 Query Match: 6.35% Indels: 50  
 RESULT 388  
 ID ADF31997 standard; DNA; 39949 BP.  
 DE Full length cosmid 2A7.  
 PN WO200309993-A2.  
 PD 04-DEC-2003.  
 PA (AVET) AVENTIS PHARM INC.  
 Best Local Similarity: 21.07% Mismatches: 134

Query Match: 6.35% Indels: 39  
 RESULT 389  
 ID ADF31998 standard; DNA; 48200 BP.  
 DE Cosmid 2A7.  
 PN WO200309993-A2.  
 PD 04-DEC-2003.  
 PA (AVET) AVENTIS PHARM INC.  
 Best Local Similarity: 21.07% Mismatches: 134  
 Query Match: 6.35% Indels: 39  
 RESULT 390  
 ID AAD54217 standard; DNA; 52101 BP.  
 DE Streptomyces platensis subspecies rosaceus dorrigocin DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Best Local Similarity: 26.38% Mismatches: 94  
 Query Match: 6.35% Indels: 50  
 RESULT 391  
 ID AD059147 standard; DNA; 70782 BP.  
 DE Angiococcus disciformis tubulysin biosynthesis cluster DNA.  
 PN DE10241152-A1.  
 PD 18-MAR-2004.  
 PA (GBFB) GBS BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 Best Local Similarity: 27.60% Mismatches: 73  
 Query Match: 6.35% Indels: 86  
 RESULT 392  
 ID ADL81732 standard; DNA; 84830 BP.  
 DE P. aeruginosa PA14 large pathogenicity island PAPI-1 DNA SEQ ID NO:2.  
 PN WO2004024937-A2.  
 PD 25-MAR-2004.  
 PA (GEHO) GEN HOSPITAL CORP.  
 Best Local Similarity: 24.45% Mismatches: 86  
 Query Match: 6.35% Indels: 89  
 RESULT 393  
 ID AAS69335 standard; cDNA; 690 BP.  
 DE DNA encoding novel human diagnostic protein #5139.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 31.25% Mismatches: 40  
 Query Match: 6.32% Indels: 37  
 RESULT 394  
 ID ABD15563 standard; DNA; 933 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14167.  
 PN US6551795-81.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 27.11% Mismatches: 93  
 Query Match: 6.32% Indels: 84  
 RESULT 395  
 ID ADC24016 standard; DNA; 1017 BP.  
 DE DNA sequence (SeqID 283) encoding a nitrilase enzyme.  
 PN WO2003000840-A2.  
 PD 03-JAN-2003.  
 PA (DIVE-) DIVERSA CORP.  
 PA (MADD) MADDEN D.  
 Best Local Similarity: 23.16% Mismatches: 109  
 Query Match: 6.32% Indels: 78  
 RESULT 396  
 ID ADH36117 standard; DNA; 1017 BP.  
 DE Chemical process monitoring-related nitrilase gene sequence SeqID283.  
 PN WO2003098187-A2.  
 PD 27-NOV-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Best Local Similarity: 23.16% Mismatches: 109  
 Query Match: 6.32% Indels: 78  
 RESULT 397  
 ID ADG93818 standard; DNA; 1017 BP.  
 DE Nitrilase enzyme gene sequence SeqID283.  
 PN WO2003097810-A2.  
 PD 27-NOV-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Best Local Similarity: 23.16% Mismatches: 109



Query Match: 6.32% Indels: 78  
 RESULT 398  
 ID AD162415 standard; DNA; 1017 BP.  
 DE DNA encoding nitrilase polypeptide #142.  
 PN WO2003106415-A2.  
 PD 24-DEC-2003  
 PA (DIVE-) DIVERSA CORP.  
 Best Local Similarity: 23.16% Mismatches: 109  
 Query Match: 6.32% Indels: 78  
 RESULT 399  
 ID AD164536 standard; DNA; 1017 BP.  
 DE DNA encoding nitrilase seq id 142.  
 PN US2004014195-A1.  
 PD 22-JAN-2004.  
 PA (DIVE-) DIVERSA CORP.  
 Best Local Similarity: 23.16% Mismatches: 109  
 Query Match: 6.32% Indels: 78  
 RESULT 400  
 ID ABD15610 standard; DNA; 1158 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14214.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 27.11% Mismatches: 93  
 Query Match: 6.32% Indels: 84  
 RESULT 401  
 ID ADS45810 standard; cDNA; 1179 BP.  
 DE Bacterial polynucleotide #553.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 26.23% Mismatches: 81  
 Query Match: 6.32% Indels: 66  
 RESULT 402  
 ID ADS56767 standard; cDNA; 1248 BP.  
 DE Bacterial polynucleotide #8754.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 21.52% Mismatches: 115  
 Query Match: 6.32% Indels: 91  
 RESULT 403  
 ID AAX06863 standard; cDNA; 2105 BP.  
 DE Australian banana cv. Mysore-infected badnavirus promoter pmy.  
 PN WO9900492-A1.  
 PD 07-JAN-1999.  
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
 PA (QUEE-) STATE QUEENSLAND DEPT PRIMARY IND.  
 PA (UYQU) UNIV QUEENSLAND.  
 PA (SUGA-) BUREAU SUGAR EXPERIMENT STATIONS.  
 PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.  
 PA (UYLE-) UNIV KATHOLIEKE LEUVEN.  
 Best Local Similarity: 22.33% Mismatches: 90  
 Query Match: 6.32% Indels: 107  
 RESULT 404  
 ID AAN60591 standard; DNA; 2301 BP.  
 DE Sequence encoding modified human pro-urokinase clone.  
 PN WO8604351-A.  
 PD 31-JUL-1986.  
 PA (SAGA) SAGAMI CHEM RES CENTRE.  
 PA (MIYA/) MIYAKE T.  
 PA (HODO) HODOGAYA-CHEM CO LTD.  
 PA (NIPS) NIPPON SODA CO.  
 PA (TOYJ) TOYO SODA MFG CO LTD.  
 PA (NISC) NISSAN CHEM IND LTD.

PA (NIPC) NIPPON CHEM IND CO LTD.  
 PA (NISC) NISSAN CHEM IND LTD.  
 PA (TOYJ) TOYO SODA MFG CO LTD.  
 PA (NIPS) NIPPON SODA CO.  
 Best Local Similarity: 23.81% Mismatches: 100  
 Query Match: 6.32% Indels: 65  
 RESULT 405  
 ID ABD10127 standard; DNA; 2304 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8731.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 23.28% Mismatches: 114  
 Query Match: 6.32% Indels: 118  
 RESULT 406  
 ID AAF93880 standard; cDNA; 2835 BP.  
 DE Human cDNA encoding a membrane or secretory protein clone PSEC0243.  
 PN EP1067182-A2.  
 PD 10-JAN-2001.  
 PA (HELI-) HELIX RES INST.  
 Best Local Similarity: 24.89% Mismatches: 61  
 Query Match: 6.32% Indels: 83  
 RESULT 407  
 ID AB143707 standard; cDNA; 2960 BP.  
 DE Molecule for disease detection and treatment (MDDT)-15 cDNA sequence.  
 PN WO2003052049-A2.  
 PD 26-JUN-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 23.68% Mismatches: 94  
 Query Match: 6.32% Indels: 88  
 RESULT 408  
 ID ABL11633 standard; cDNA; 6036 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29381.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 23.95% Mismatches: 87  
 Query Match: 6.32% Indels: 76  
 RESULT 409  
 ID ABL18880 standard; DNA; 7441 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 8113.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 22.55% Mismatches: 92  
 Query Match: 6.32% Indels: 35  
 RESULT 410  
 ID ABL11632 standard; cDNA; 8223 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29378.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 23.95% Mismatches: 87  
 Query Match: 6.32% Indels: 76  
 RESULT 411  
 ID ADF45448 standard; DNA; 9258 BP.  
 DE Human vasodilator-responsive gene #45.  
 PN JP2003310272-A.  
 PD 05-NOV-2003.  
 PA (TANA/) TANAKA T.  
 PA (ASAH) ASAHI KASEI KK.  
 PA (SUMU) SUMITOMO SEIYAKU KK.  
 Best Local Similarity: 24.34% Mismatches: 91  
 Query Match: 6.32% Indels: 48  
 RESULT 412  
 ID ADQ87183 standard; cDNA; 9260 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #4060.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Best Local Similarity: 24.34% Mismatches: 91

Query Match: 6.32% Indels: 48  
RESULT 413  
ID ADQ84906 standard; cDNA; 9260 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1720.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Best Local Similarity: 24.34% Mismatches: 91  
Query Match: 6.32% Indels: 48  
RESULT 414  
ID ABX76157 standard; DNA; 9272 BP.  
DE Lung cancer-associated polynucleotide #29.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 24.34% Mismatches: 91  
Query Match: 6.32% Indels: 48  
RESULT 415  
ID ADQ18965 standard; DNA; 9272 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1784.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 24.34% Mismatches: 91  
Query Match: 6.32% Indels: 48  
RESULT 416  
ID ABK64501 standard; DNA; 9287 BP.  
DE Human benign prostatic hyperplasia gene #396.  
PN WO200212440-A2.  
PD 14-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (NISB) JAPAN TOBACCO INC.  
Best Local Similarity: 24.34% Mismatches: 91  
Query Match: 6.32% Indels: 48  
RESULT 417  
ID ADQ23327 standard; DNA; 9456 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6147.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 24.34% Mismatches: 91  
Query Match: 6.32% Indels: 48  
RESULT 418  
ID ADQ1703 standard; DNA; 20256 BP.  
DE Polyketide synthase ORF12, SEQ ID 26.  
PN WO2004065401-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Best Local Similarity: 27.70% Mismatches: 105  
Query Match: 6.32% Indels: 85  
RESULT 419  
ID ADD14677 standard; cDNA; 34875 BP.  
DE Human src biomarker polynucleotide SEQ ID NO:71.  
PN WO2003062395-A2.  
PD 31-JUL-2003.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Best Local Similarity: 21.91% Mismatches: 110  
Query Match: 6.32% Indels: 109  
RESULT 420  
ID ADR52965 standard; DNA; 34875 BP.  
DE Drug therapy altered expressed gene #316.  
PN WO2004072285-A2.  
PD 26-AUG-2004.  
PA (AMHP) WYETH.  
PA (BURC/) BURCZYNSKI M.  
PA (TWIN/) TWINE N.  
PA (DORN/) DORNER A J.  
PA (TRFP/) TRFPICCHIO W L.  
Best Local Similarity: 21.91% Mismatches: 110  
Query Match: 6.32% Indels: 109  
RESULT 421

ID ADC00439 standard; DNA; 48423 BP.  
DE Enterohaemorrhagic E. coli 0157:H7-specific nucleic acid SEQ ID NO: 484.  
PN JP2002355074-A.  
PD 10-DEC-2002.  
PA (UTIS-) UNIV TSUKUBA.  
Best Local Similarity: 23.87% Mismatches: 75  
Query Match: 6.32% Indels: 76  
RESULT 422  
ID ACD19124 standard; DNA; 48908 BP.  
DE E. coli 0157 unique DNA sequence OZID\_137.  
PN US2003023075-A1.  
PD 30-JAN-2003.  
PA (BLAT/) BLATTNER F R.  
PA (BURL/) BURLAND V D.  
PA (PERN/) PERNA N T.  
PA (PLUN/) PLUNKETT G.  
PA (WELC/) WELCH R.  
Best Local Similarity: 23.87% Mismatches: 75  
Query Match: 6.32% Indels: 76  
RESULT 423  
ID AA58471 standard; DNA; 58857 BP.  
DE Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30.  
PN WO20040704-A1.  
PD 13-JUL-2000.  
PA (REGC) UNIV CALIFORNIA.  
Best Local Similarity: 26.13% Mismatches: 118  
Query Match: 6.32% Indels: 77  
RESULT 424  
ID ADU15447 standard; DNA; 85915 BP.  
DE Streptomyces bikiniensis NRRL 2737 chalcomycin PKS cluster DNA.  
PN WO2004018703-A2.  
PD 04-MAR-2004.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Best Local Similarity: 26.94% Mismatches: 102  
Query Match: 6.32% Indels: 86  
RESULT 425  
ID ADQ91695 standard; DNA; 164051 BP.  
DE Polyketide synthase related DNA contig 2, SEQ ID 18.  
PN WO2004065401-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Best Local Similarity: 27.70% Mismatches: 105  
Query Match: 6.32% Indels: 85  
RESULT 426  
ID ADP75188 standard; DNA; 276820 BP.  
DE Human ADAMTS2 gene.  
PN WO2003031594-A2.  
PD 17-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 21.85% Mismatches: 83  
Query Match: 6.32% Indels: 98  
RESULT 427  
ID AA96225 standard; cDNA; 1195 BP.  
DE cDNA encoding a maize chitinase polypeptide designated ZmCh9.  
PN WO200056908-A2.  
PD 28-SEP-2000.  
PA (PION-) PIONEER HI-BRED INT INC.  
Best Local Similarity: 26.09% Mismatches: 72  
Query Match: 6.28% Indels: 77  
RESULT 428  
ID ACA23770 standard; DNA; 1212 BP.  
DE Prokaryotic essential gene #5427.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 23.26% Mismatches: 146  
Query Match: 6.28% Indels: 83  
RESULT 429  
ID ABK99935 standard; DNA; 1402 BP.  
DE DNA encoding human secreted protein SCEP-18.  
PN WO200248337-A2.  
PD 20-JUN-2002.  
PA (INCY-) INCYTE GENOMICS INC.

Best Local Similarity: 26.96% Mismatches: 92  
 Query Match: 6.28% Indels: 59  
 RESULT 430  
 ID ADS14792 standard; DNA; 1422 BP.  
 DE Pseudomonas aeruginosa quorum sensing controlled gene PA371, SEQ ID 347.  
 PN WO2004083385-A2.  
 PD 30-SEP-2004.  
 PA (IOWA) UNIV IOWA RES FOUND.  
 Best Local Similarity: 21.41% Mismatches: 136  
 Query Match: 6.28% Indels: 96  
 RESULT 431  
 ID ABD01576 standard; DNA; 1461 BP.  
 DE Pseudomonas aeruginosa polynucleotide #180.  
 PN US651795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 24.28% Mismatches: 133  
 Query Match: 6.28% Indels: 64  
 RESULT 432  
 ID ADQ87560 standard; cDNA; 1868 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #4438.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Best Local Similarity: 23.02% Mismatches: 139  
 Query Match: 6.28% Indels: 123  
 RESULT 433  
 ID ADS14570 standard; DNA; 2055 BP.  
 DE Pseudomonas aeruginosa quorum sensing controlled gene PA2163, SEQ ID 125.  
 PN WO2004083385-A2.  
 PD 30-SEP-2004.  
 PA (IOWA) UNIV IOWA RES FOUND.  
 Best Local Similarity: 27.92% Mismatches: 81  
 Query Match: 6.28% Indels: 31  
 RESULT 434  
 ID AAN71330 standard; DNA; 2304 BP.  
 DE Sequence encoding modified prourokinase.  
 PN EP236040-A.  
 PD 09-SEP-1987.  
 PA (COLB) COLLABORATIVE RES INC.  
 Best Local Similarity: 24.26% Mismatches: 99  
 Query Match: 6.28% Indels: 79  
 RESULT 435  
 ID ADT42110 standard; cDNA; 2442 BP.  
 DE Bacterial polynucleotide #16861.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 26.43% Mismatches: 74  
 Query Match: 6.28% Indels: 65  
 RESULT 436  
 ID AAD48133 standard; DNA; 2878 BP.  
 DE Human chondroitin sulphate proteoglycan BEHAB/brevican DNA.  
 PN WO200276510-A1.  
 PD 03-OCT-2002.  
 PA (AGYT-) AGY THERAPEUTICS INC.  
 Best Local Similarity: 22.50% Mismatches: 108  
 Query Match: 6.28% Indels: 105  
 RESULT 437  
 ID ADN38941 standard; cDNA; 2878 BP.  
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:259.  
 PN WO2003042661-A2.  
 PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Best Local Similarity: 22.50% Mismatches: 108  
 Query Match: 6.28% Indels: 105  
 RESULT 438

ID ADK67783 standard; DNA; 2878 BP.  
 DE Human glycosylation-variant BEHAB isoform coding sequence.  
 PN WO2004013356-A1.  
 PD 12-FEB-2004.  
 PA (UYVA) UNIV YALE.  
 Best Local Similarity: 22.50% Mismatches: 108  
 Query Match: 6.28% Indels: 105  
 RESULT 439  
 ID ADJ80226 standard; cDNA; 3011 BP.  
 DE Novel human nucleic acid-associated protein coding sequence #44.  
 PN WO2003038052-A2.  
 PD 08-MAY-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 23.91% Mismatches: 88  
 Query Match: 6.28% Indels: 90  
 RESULT 440  
 ID ADQ83194 standard; cDNA; 3467 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #8.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Best Local Similarity: 22.50% Mismatches: 108  
 Query Match: 6.28% Indels: 105  
 RESULT 441  
 ID ADQ85107 standard; cDNA; 3467 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #1921.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Best Local Similarity: 22.50% Mismatches: 108  
 Query Match: 6.28% Indels: 105  
 RESULT 442  
 ID ACN42084 standard; cDNA; 4536 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:959.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 22.50% Mismatches: 108  
 Query Match: 6.28% Indels: 105  
 RESULT 443  
 ID ACC49359 standard; DNA; 7282 BP.  
 DE Human NR1 exons 1 and 2 DNA sequence SEQ ID NO:11.  
 PN WO2003018843-A1.  
 PD 06-MAR-2003.  
 PA (SMIK) SMITHKLINE BEECHAM CORP.  
 Best Local Similarity: 25.12% Mismatches: 76  
 Query Match: 6.28% Indels: 66  
 RESULT 444  
 ID ABZ37516 standard; DNA; 59816 BP.  
 DE Streptomyces viridochromogenes Avi gene cluster sense strand.  
 PN WO200268436-A1.  
 PD 06-SEP-2002.  
 PA (COMB-) COMBINATURE BIOPHARM AG.  
 Best Local Similarity: 24.02% Mismatches: 89  
 Query Match: 6.28% Indels: 67  
 RESULT 445  
 ID ABZ37515 standard; DNA; 59816 BP.  
 DE Streptomyces viridochromogenes Avi gene cluster sense strand.  
 PN WO200268436-A1.  
 PD 06-SEP-2002.  
 PA (COMB-) COMBINATURE BIOPHARM AG.  
 Best Local Similarity: 24.02% Mismatches: 89  
 Query Match: 6.28% Indels: 67  
 RESULT 446  
 ID ACN44290 standard; DNA; 59856 BP.  
 DE Human genomic sequence hCG24994.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.

Best Local Similarity: 24.57% Mismatches: 130  
 Query Match: 6.28% Indels: 62  
 RESULT 447  
 ID ADJ33491 standard; DNA; 94001 BP.  
 DE Human LAR related nucleotide sequence SEQ ID NO:20.  
 PN WO2004010956-A2.  
 PD 05-FEB-2004.  
 PA (ISIS-) ISIS PHARM INC.  
 Best Local Similarity: 20.00% Mismatches: 98  
 Query Match: 6.28% Indels: 127  
 RESULT 448  
 Best Local Similarity: 22.60% Mismatches: 117  
 Query Match: 6.28% Indels: 124  
 RESULT 449  
 Best Local Similarity: 22.60% Mismatches: 117  
 Query Match: 6.28% Indels: 124  
 RESULT 450  
 Best Local Similarity: 26.35% Mismatches: 91  
 Query Match: 6.28% Indels: 89  
 RESULT 451  
 Best Local Similarity: 26.35% Mismatches: 91  
 Query Match: 6.28% Indels: 89  
 RESULT 452  
 ID AAS76153 standard; cDNA; 744 BP.  
 DE DNA encoding novel human diagnostic protein #11957.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 26.63% Mismatches: 74  
 Query Match: 6.25% Indels: 35  
 RESULT 453  
 ID ADE63830 standard; DNA; 935 BP.  
 DE Human gene NM\_005194, SEQ ID NO 9774.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GENO-) GEN HOSPITAL CORP.  
 Best Local Similarity: 24.83% Mismatches: 94  
 Query Match: 6.25% Indels: 113  
 RESULT 454  
 ID ABX05207 standard; cDNA; 1074 BP.  
 DE Human novel polynucleotide #222.  
 PN WO200274961-A1.  
 PD 26-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 28.45% Mismatches: 81  
 Query Match: 6.25% Indels: 65  
 RESULT 455  
 ID AAD14511 standard; DNA; 1227 BP.  
 DE Streptomyces clavuligerus ORF10 DNA downstream to pcbC gene.  
 PN US6232106-B1.  
 PD 15-MAY-2001.  
 PA (UYAL-) UNIV ALBERTA.  
 Best Local Similarity: 23.36% Mismatches: 83  
 Query Match: 6.25% Indels: 91  
 RESULT 456  
 ID ADD26452 standard; DNA; 1227 BP.  
 DE Streptomyces clavuligerus ORF10 DNA.  
 PN US6589775-B1.  
 PD 08-JUL-2003.  
 PA (UYAL-) UNIV ALBERTA.  
 Best Local Similarity: 23.36% Mismatches: 83  
 Query Match: 6.25% Indels: 91  
 RESULT 457  
 ID ADG47797 standard; DNA; 1227 BP.  
 DE Streptomyces clavuligerus 15 kb gene ORF10 DNA.  
 PN US2003207411-A1.  
 PD 06-NOV-2003.  
 PA (UYAL-) UNIV ALBERTA.  
 Best Local Similarity: 23.36% Mismatches: 83  
 Query Match: 6.25% Indels: 91  
 RESULT 458  
 ID ACA62934 standard; DNA; 1227 BP.

DE DNA encoding clavulanic acid synthesis associated protein #10.  
 PN US6514735-B1.  
 PD 04-FEB-2003.  
 PA (UYAL-) UNIV ALBERTA.  
 Best Local Similarity: 23.36% Mismatches: 83  
 Query Match: 6.25% Indels: 91  
 RESULT 459  
 ID ADO35847 standard; DNA; 1306 BP.  
 DE Novel mouse gene sequence #520.  
 PN WO2004046310-A2.  
 PD 03-JUN-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Best Local Similarity: 25.68% Mismatches: 81  
 Query Match: 6.25% Indels: 67  
 RESULT 460  
 ID ADS95255 standard; DNA; 1306 BP.  
 DE Murine therapeutic DNA sequence #51, SEQ ID 294.  
 PN WO2004039319-A2.  
 PD 13-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Best Local Similarity: 25.68% Mismatches: 81  
 Query Match: 6.25% Indels: 67  
 RESULT 461  
 ID ADS95254 standard; DNA; 1306 BP.  
 DE Murine therapeutic DNA sequence #50, SEQ ID 293.  
 PN WO2004039319-A2.  
 PD 13-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Best Local Similarity: 25.68% Mismatches: 81  
 Query Match: 6.25% Indels: 67  
 RESULT 462  
 ID ACC62239 standard; cDNA; 1374 BP.  
 DE Human NOVI encoding cDNA SEQ ID NO:7.  
 PN WO2003023001-A2.  
 PD 20-MAR-2003.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 21.79% Mismatches: 110  
 Query Match: 6.25% Indels: 139  
 RESULT 463  
 ID ABD09708 standard; DNA; 1395 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8312.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 25.71% Mismatches: 80  
 Query Match: 6.25% Indels: 61  
 RESULT 464  
 ID ABX06826 standard; DNA; 1422 BP.  
 DE S. pneumoniae type 4 strain coding region #114.  
 PN WO200277021-A2.  
 PD 03-OCT-2002.  
 PA (CHIR-) CHIRON SPA.  
 Best Local Similarity: 23.15% Mismatches: 78  
 Query Match: 6.25% Indels: 55  
 RESULT 465  
 ID AAS62247 standard; cDNA; 1468 BP.  
 DE cDNA sequence #34 encoding novel human secreted protein.  
 PN WO200177231-A2.  
 PD 18-OCT-2001.  
 PA (GENY) GENETICS INST INC.  
 Best Local Similarity: 26.73% Mismatches: 98  
 Query Match: 6.25% Indels: 109  
 RESULT 466  
 ID ABZ42437 standard; DNA; 1470 BP.  
 DE Streptococcus pneumoniae polynucleotide SEQ ID NO 506.  
 PN WO200283855-A2.  
 PD 24-OCT-2002.  
 PA (AMCY) AMERICAN CYANAMID CO.  
 Best Local Similarity: 23.15% Mismatches: 78  
 Query Match: 6.25% Indels: 55  
 RESULT 467  
 ID AAC66917 standard; cDNA; 1478 BP.

DE G-protein modulator GPMII coding sequence.  
 PN WO200068249-A2.  
 PD 16-NOV-2000.  
 PA (MUSC-) MUSC FOUND RES DEV.  
 PA (OSIP-) OSI PHARM INC.  
 Best Local Similarity: 25.71% Mismatches: 53  
 Query Match: 6.25% Indels: 74  
 RESULT 468  
 ID AAV52317 standard; DNA; 1590 BP.  
 DE Streptococcus pneumoniae genome fragment SEQ ID NO:184.  
 PN WO9818931-A2.  
 PD 07-MAY-1998.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.15% Mismatches: 78  
 Query Match: 6.25% Indels: 55  
 RESULT 469  
 ID ABD05065 standard; DNA; 1656 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3669.  
 PN US5551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 27.00% Mismatches: 95  
 Query Match: 6.25% Indels: 45  
 RESULT 470  
 ID AAF54514 standard; DNA; 1797 BP.  
 DE Fructan exohydrolase (FEH) coding sequence.  
 PN WO200068402-A1.  
 PD 16-NOV-2000.  
 PA (LEUV-) LEUVEN RES & DEV.  
 Best Local Similarity: 27.09% Mismatches: 117  
 Query Match: 6.25% Indels: 73  
 RESULT 471  
 ID AAS65351 standard; cDNA; 1848 BP.  
 DE DNA encoding novel human diagnostic protein #1155.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 27.00% Mismatches: 94  
 Query Match: 6.25% Indels: 80  
 RESULT 472  
 ID ABV77856 standard; cDNA; 2061 BP.  
 DE Human Eph receptor protein #1 coding sequence.  
 PN WO200283735-A1.  
 PD 24-OCT-2002.  
 PA (TAKE-) TAKEDA CHEM IND LTD.  
 Best Local Similarity: 27.33% Mismatches: 107  
 Query Match: 6.25% Indels: 77  
 RESULT 473  
 ID ABD06745 standard; DNA; 2469 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5349.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 24.58% Mismatches: 99  
 Query Match: 6.25% Indels: 97  
 RESULT 474  
 ID AAX01559 standard; cDNA to mRNA; 3003 BP.  
 DE Bos taurus stialidase coding sequence.  
 PN WO9853052-A1.  
 PD 26-NOV-1998.  
 PA (MIYA-) MIYAGI-KEN.  
 Best Local Similarity: 27.83% Mismatches: 89  
 Query Match: 6.25% Indels: 58  
 RESULT 475  
 ID ADC13560 standard; cDNA; 3117 BP.  
 DE Human NOVX protein encoding cDNA sequence, SEQ ID No 39.  
 PN WO2003004617-A2.  
 PD 16-JAN-2003.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 23.59% Mismatches: 93  
 Query Match: 6.25% Indels: 105  
 RESULT 476  
 ID AAF74654 standard; DNA; 3186 BP.  
 DE Reporter gene construct vector pTTrap-Puro.

DE Mouse intracellular Na+ receptor GILT nucleotide sequence SEQ ID NO:1.  
 PN WO200112805-A1.  
 PD 22-FEB-2001.  
 PA (UNSY) UNIV SYDNEY.  
 Best Local Similarity: 25.71% Mismatches: 53  
 Query Match: 6.25% Indels: 74  
 RESULT 477  
 ID AAD36958 standard; DNA; 3582 BP.  
 DE Bacillus thuringiensis H04 hybrid toxin DNA #2.  
 PN WO200215701-A2.  
 PD 28-FEB-2002.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 28.14% Mismatches: 84  
 Query Match: 6.25% Indels: 51  
 RESULT 478  
 ID AAD36959 standard; DNA; 3582 BP.  
 DE Bacillus thuringiensis H04 hybrid toxin DNA #3.  
 PN WO200215701-A2.  
 PD 28-FEB-2002.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 28.14% Mismatches: 84  
 Query Match: 6.25% Indels: 51  
 RESULT 479  
 ID ABD06588 standard; DNA; 5103 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5192.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 24.58% Mismatches: 99  
 Query Match: 6.25% Indels: 97  
 RESULT 480  
 ID ACC44692 standard; DNA; 5192 BP.  
 DE Plasmid pIRESpuo2 nucleotide sequence SEQ ID NO:88.  
 PN WO200297059-A2.  
 PD 05-DEC-2002.  
 PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.  
 Best Local Similarity: 23.23% Mismatches: 97  
 Query Match: 6.25% Indels: 72  
 RESULT 481  
 ID ADO47224 standard; DNA; 6280 BP.  
 DE Nucleotide sequence of plasmid pCAR-IRES-puro (pCJ126).  
 PN WO2004029249-A1.  
 PD 08-APR-2004.  
 PA (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI.  
 Best Local Similarity: 23.23% Mismatches: 97  
 Query Match: 6.25% Indels: 72  
 RESULT 482  
 ID ADO47201 standard; DNA; 6502 BP.  
 DE Nucleotide sequence of plasmid pIRES-rtTA-puro.  
 PN WO2004029249-A1.  
 PD 08-APR-2004.  
 PA (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI.  
 Best Local Similarity: 23.23% Mismatches: 97  
 Query Match: 6.25% Indels: 72  
 RESULT 483  
 ID AAC66821 standard; DNA; 6795 BP.  
 DE Reporter gene construct vector pTrapsin-Puro3'5'.  
 PN WO200061809-A2.  
 PD 19-OCT-2000.  
 PA (ICON-) ICONIX PHARM INC.  
 Best Local Similarity: 23.23% Mismatches: 97  
 Query Match: 6.25% Indels: 72  
 RESULT 484  
 ID AAC66822 standard; DNA; 6795 BP.  
 DE Reporter gene construct vector pTrap-Puro 3'5'.  
 PN WO200061809-A2.  
 PD 19-OCT-2000.  
 PA (ICON-) ICONIX PHARM INC.  
 Best Local Similarity: 23.23% Mismatches: 97  
 Query Match: 6.25% Indels: 72  
 RESULT 485  
 ID AAC66817 standard; DNA; 6795 BP.  
 DE Reporter gene construct vector pTTrap-Puro.



Query Match: 6.25% Indels: 89  
 RESULT 505  
 Best Local Similarity: 27.17% Mismatches: 90  
 Query Match: 6.25% Indels: 67  
 RESULT 506  
 Best Local Similarity: 23.15% Mismatches: 78  
 Query Match: 6.25% Indels: 55  
 RESULT 507  
 Best Local Similarity: 25.00% Mismatches: 92  
 Query Match: 6.25% Indels: 80  
 RESULT 508  
 ID ABD04678 standard; DNA; 732 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3282.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 27.18% Mismatches: 68  
 Query Match: 6.22% Indels: 54  
 RESULT 509  
 ID AAF94099 standard; DNA; 744 BP.  
 DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 533.  
 PN EP1067182-A2.  
 PD 10-JAN-2001.  
 PA (HELI-) HELIX RES INST.  
 Best Local Similarity: 35.11% Mismatches: 41  
 Query Match: 6.22% Indels: 10  
 RESULT 510  
 ID ABD04653 standard; DNA; 771 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3257.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 27.18% Mismatches: 68  
 Query Match: 6.22% Indels: 54  
 RESULT 511  
 ID ADA70416 standard; DNA; 849 BP.  
 DE Rice gene, SEQ ID 3739.  
 PN WO200300898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 22.01% Mismatches: 97  
 Query Match: 6.22% Indels: 78  
 RESULT 512  
 ID ABD04612 standard; DNA; 939 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3216.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 27.18% Mismatches: 68  
 Query Match: 6.22% Indels: 54  
 RESULT 513  
 ID ABD04823 standard; DNA; 945 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3427.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 27.18% Mismatches: 68  
 Query Match: 6.22% Indels: 54  
 RESULT 514  
 ID AAA38398 standard; DNA; 999 BP.  
 DE ORF2-16 encoding Pseudomonas bto gene cluster regulator, SEQ ID NO:18.  
 PN JP2000093180-A.  
 PD 04-APR-2000.  
 PA (TOFU) TONEN CORP.  
 Best Local Similarity: 27.90% Mismatches: 90  
 Query Match: 6.22% Indels: 49  
 RESULT 515  
 ID ABD01961 standard; DNA; 1182 BP.  
 DE Pseudomonas aeruginosa polynucleotide #565.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 24.10% Mismatches: 97

Query Match: 6.22% Indels: 83  
 RESULT 516  
 ID ABD01915 standard; DNA; 1206 BP.  
 DE Pseudomonas aeruginosa polynucleotide #519.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 24.10% Mismatches: 97  
 Query Match: 6.22% Indels: 83  
 RESULT 517  
 ID AAQ10168 standard; DNA; 1236 BP.  
 DE Encodes Pro-urokinase derivative UK-T6 with Thr at position 155.  
 PN EP405285-A.  
 PD 02-JAN-1991.  
 PA (KYOW) KYOWA HAKKO KOGYO KK.  
 Best Local Similarity: 25.93% Mismatches: 95  
 Query Match: 6.22% Indels: 42  
 RESULT 518  
 ID ABD04512 standard; DNA; 1365 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3116.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 28.27% Mismatches: 102  
 Query Match: 6.22% Indels: 43  
 RESULT 519  
 ID ADT43155 standard; cDNA; 1407 BP.  
 DE Bacterial polynucleotide #17906.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY) CAO Y.  
 PA (HINK) HINKLE G J.  
 PA (SLAT) SLATER S C.  
 PA (CHEN) CHEN X.  
 PA (GOLD) GOLDMAN B S.  
 Best Local Similarity: 25.61% Mismatches: 96  
 Query Match: 6.22% Indels: 64  
 RESULT 520  
 ID ABD10344 standard; DNA; 1746 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8948.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 25.10% Mismatches: 93  
 Query Match: 6.22% Indels: 58  
 RESULT 521  
 ID AAD33813 standard; cDNA; 1785 BP.  
 DE Human secreted protein-encoding gene 2 cDNA clone HDQF073, SEQ ID NO:12.  
 PN WO200224719-A1.  
 PD 28-MAR-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 26.19% Mismatches: 114  
 Query Match: 6.22% Indels: 78  
 RESULT 522  
 ID ADA48715 standard; DNA; 1821 BP.  
 DE Rice gene conferring disease resistance in plants.  
 PN WO2003000906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 21.74% Mismatches: 112  
 Query Match: 6.22% Indels: 108  
 RESULT 523  
 ID ADA71198 standard; DNA; 1850 BP.  
 DE Rice gene, SEQ ID 4521.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 21.74% Mismatches: 112  
 Query Match: 6.22% Indels: 108  
 RESULT 524  
 ID ABD07145 standard; DNA; 2115 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5749.  
 PN US6551795-B1.



PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP..  
Best Local Similarity: 25.62% Mismatches: 71  
Query Match: 6.22% Indels: 52  
RESULT 525  
ID ABD07103 standard; DNA; 2160 BP.  
DE Pseudomonas aeruginosa polynucleotide #5707.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP..  
Best Local Similarity: 25.62% Mismatches: 71  
Query Match: 6.22% Indels: 52  
RESULT 526  
ID ABD01889 standard; DNA; 2181 BP.  
DE Pseudomonas aeruginosa polynucleotide #493.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP..  
Best Local Similarity: 24.10% Mismatches: 97  
Query Match: 6.22% Indels: 83  
RESULT 527  
ID ABD02005 standard; DNA; 2196 BP.  
DE Pseudomonas aeruginosa polynucleotide #609.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP..  
Best Local Similarity: 24.10% Mismatches: 97  
Query Match: 6.22% Indels: 83  
RESULT 528  
ID ABD16680 standard; DNA; 2319 BP.  
DE Pseudomonas aeruginosa polynucleotide #15284.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP..  
Best Local Similarity: 22.8% Mismatches: 138  
Query Match: 6.22% Indels: 88  
RESULT 529  
ID ABL04363 standard; cDNA; 2349 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7571.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 21.31% Mismatches: 105  
Query Match: 6.22% Indels: 129  
RESULT 530  
ID ABD16792 standard; DNA; 2427 BP.  
DE Pseudomonas aeruginosa polynucleotide #15396.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP..  
Best Local Similarity: 22.8% Mismatches: 138  
Query Match: 6.22% Indels: 88  
RESULT 531  
ID AAF93893 standard; cDNA; 2492 BP.  
DE Human cDNA encoding a membrane or secretory protein clone PSEC0260.  
PN EP1067182-A2.  
PD 10-JAN-2001.  
PA (HELI-) HELIX RES INST.  
Best Local Similarity: 35.11% Mismatches: 41  
Query Match: 6.22% Indels: 10  
RESULT 532  
ID AAG2031 standard; DNA; 2495 BP.  
DE Hydrophobic domain protein cDNA HP03140 isolated from HT-1080 cells.  
PN WO20029448-A2.  
PD 25-MAY-2000.  
PA (SAGA ) SAGAMI CHEM RES CENT.  
PA (PROT-) PROTEGENE INC.  
Best Local Similarity: 35.11% Mismatches: 41  
Query Match: 6.22% Indels: 10  
RESULT 533  
ID ADE07431 standard; DNA; 2503 BP.  
DE Novel coding sequence (useful for identifying genetic disorders) #497.  
PN WO2003054152-A2.

PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 35.11% Mismatches: 41  
Query Match: 6.22% Indels: 10  
RESULT 534  
ID ADS10265 standard; DNA; 2531 BP.  
DE Human therapeutic DNA - SEQ ID 502.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Best Local Similarity: 35.11% Mismatches: 41  
Query Match: 6.22% Indels: 10  
RESULT 535  
ID ABD17466 standard; DNA; 2631 BP.  
DE Pseudomonas aeruginosa polynucleotide #16070.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP..  
Best Local Similarity: 24.89% Mismatches: 99  
Query Match: 6.22% Indels: 45  
RESULT 536  
ID ADG63409 standard; cDNA; 2663 BP.  
DE Novel human cDNA sequence #570.  
PN EPI440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 24.21% Mismatches: 120  
Query Match: 6.22% Indels: 62  
RESULT 537  
ID ADL35972 standard; cDNA; 2707 BP.  
DE Human NOVX cDNA #9.  
PN US2003207800-A1.  
PD 06-NOV-2003.  
PA (MALY/) MALYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (GUOX/) GUO X.  
PA (KEKU/) KEKUDA R.  
PA (GANG/) GANGOLLI E A.  
PA (SHIM/) SHIMKETS R A.  
PA (TAUP/) TAUPIER R J.  
PA (LILL/) LI L.  
PA (PADI/) PADIGARU M.  
Best Local Similarity: 23.91% Mismatches: 90  
Query Match: 6.22% Indels: 98  
RESULT 538  
ID ABS71696 standard; DNA; 2713 BP.  
DE DNA encoding human NOV3 protein.  
PN WO200266643-A2.  
PD 29-AUG-2002.  
PA (CURA-) CURAGEN CORP..  
Best Local Similarity: 23.91% Mismatches: 90  
Query Match: 6.22% Indels: 98  
RESULT 539  
ID AAS84436 standard; cDNA; 2807 BP.  
DE DNA encoding novel human diagnostic protein #20240.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 25.55% Mismatches: 99  
Query Match: 6.22% Indels: 105  
RESULT 540  
ID AAH18697 standard; cDNA; 2947 BP.  
DE Human cDNA sequence SEQ ID NO:18960.  
PN EPI074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Best Local Similarity: 23.91% Mismatches: 90  
Query Match: 6.22% Indels: 98  
RESULT 541  
ID ACN37482 standard; cDNA; 3275 BP.

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DE Tumour-associated antigenic target (TAT) cDNA DNA323924, SEQ ID NO:394.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 542
ID ABD04153 standard; DNA; 3291 BP.
DE Pseudomonas aeruginosa polynucleotide #2757.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 28.21% Mismatches: 102
Query Match: 6.22% Indels: 43
RESULT 543
ID ADT46154 standard; cDNA; 3318 BP.
DE Bacterial polynucleotide #20905.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 24.31% Mismatches: 86
Query Match: 6.22% Indels: 84
RESULT 544
ID ADI28068 standard; cDNA; 3438 BP.
DE ECMCAD gene clone 6755002CB1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 545
ID AAA91017 standard; DNA; 3476 BP.
DE Human secreted protein PRO6018 coding sequence.
PN WO200075317-A2.
PD 14-DEC-2000.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 546
ID ABK69986 standard; DNA; 3476 BP.
DE cDNA encoding human Pro peptide #26.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 547
ID ADA01319 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 548
ID ADA43748 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 549
ID ADA43516 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97

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Query Match: 6.22% Indels: 97
RESULT 550
ID ADA01191 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 551
ID ADA01075 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 552
ID ADA43632 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 553
ID ADA06894 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 554
ID ADA08382 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 555
ID ADH99675 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide SEQ ID 51.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 556
ID ADB86958 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 557
ID ADB66113 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 558
ID ADB99791 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide SEQ ID 51.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97

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RESULT 559  
ID ADB99446 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003082731-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 560  
ID ADB65997 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003082732-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 561  
ID ADC23395 standard; cDNA; 3476 BP.  
DE Human cDNA clone (SeqID 51) encoding the transmembrane PRO protein.  
PN US2003073193-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 562  
ID ADC26088 standard; cDNA; 3476 BP.  
DE Human PRO6018 cDNA.  
PN US2003073194-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 563  
ID ADE04915 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003068778-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 564  
ID ADE11221 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003073191-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 565  
ID ADD88152 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003082733-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 566  
ID ADD95447 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003064473-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 567  
ID ADE06377 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003073195-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 568  
ID ADE37676 standard; cDNA; 3476 BP.

ID ADE38152 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119120-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 569  
ID ADD8268 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003073189-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 570  
ID ADD90849 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003073188-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 571  
ID ADF99404 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003078401-A1.  
PD 24-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 572  
ID ADG06497 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003077742-A1.  
PD 24-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 573  
ID ADG05448 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003077741-A1.  
PD 24-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 574  
ID ADG82449 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003077744-A1.  
PD 24-APR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 575  
ID ADE51702 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104560-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 576  
ID ADE51818 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104561-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 577  
ID ADE37676 standard; cDNA; 3476 BP.

DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104564-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 578  
ID ADE37560 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104565-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 579  
ID ADP95331 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003138901-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 580  
ID ADE38031 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003104566-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 581  
ID ADE76120 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003124665-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 582  
ID ADE39443 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119117-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 583  
ID ADE04247 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003096364-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 584  
ID ADE39844 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138896-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 585  
ID ADE19709 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138903-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 586  
ID ADE77287 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.

PN US2003124666-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 587  
ID ADE65395 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119116-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 588  
ID ADE76004 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003124663-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 589  
ID ADE37915 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119119-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 590  
ID ADE64525 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119114-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 591  
ID ADE38860 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003096363-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 592  
ID ADE51934 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104562-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 593  
ID ADD90965 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003138902-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 594  
ID ADE38744 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003108996-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 595  
ID ADE37444 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104563-A1.

PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 596  
ID ADE06261 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138898-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 597  
ID ADD90120 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003138904-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 598  
ID ADE38628 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119086-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 599  
ID ADE39559 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119118-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 600  
ID ADD89164 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138897-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 601  
ID ADD88931 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138899-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 602  
ID ADE19825 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138900-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 603  
ID ADE77403 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003124667-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 604  
ID ADE65279 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119113-A1.  
PD 26-JUN-2003.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 605  
ID ADE39327 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119115-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 606  
ID ADE38512 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104559-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 607  
ID ADG11065 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003170809-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 608  
ID ADG10949 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003077743-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 609  
ID ADH31477 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 610  
ID ADH38725 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 611  
ID ADH29360 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119137-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 612  
ID ADH23663 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 22.30%  
Query Match: 6.22%  
Mismatches: 100  
Indels: 97  
RESULT 613  
ID ADH26993 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119135-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 614  
ID ADH38261 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119124-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 615  
ID ADH26877 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119134-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 616  
ID ADH38145 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119123-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 617  
ID ADH38841 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119141-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 618  
ID ADH23779 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119142-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 619  
ID ADH40155 standard; cDNA; 3476 BP.  
DE Human PRO6018 cDNA.  
PN US2003119132-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 620  
ID ADH40039 standard; cDNA; 3476 BP.  
DE Human PRO6018 cDNA.  
PN US2003119133-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 621  
ID ADH31361 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119138-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 622  
ID ADH29239 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119136-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97

Query Match: 6.22% Indels: 97  
RESULT 623  
ID ADH49454 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119127-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 624  
ID ADH51918 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119125-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 625  
ID ADH49773 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119128-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 626  
ID ADH52374 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119130-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 627  
ID ADH52490 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119129-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 628  
ID ADH58487 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119121-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 629  
ID ADH51802 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119126-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 630  
ID ADH58363 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97  
RESULT 631  
ID ADH13560 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119131-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 22.30% Mismatches: 100  
Query Match: 6.22% Indels: 97

<b>RESULT 632</b>					
ID	ADK00816 standard; cDNA; 3476 BP.				
DE	Human PRO polynucleotide #26.				
PN	US2003186373-A1.				
PD	02-OCT-2003.				
PA	(GETH) GENENTECH INC.	Mismatches:	100		
Best Local Similarity:	22.30%	Indels:	97		
Query Match:	6.22%				
<b>RESULT 633</b>					
ID	ADL08557 standard; cDNA; 3476 BP.				
DE	Human cDNA encoding secreted/transmembrane polypeptide PRO6018.				
PN	US2003186372-A1.				
PD	02-OCT-2003.				
PA	(GETH) GENENTECH INC.	Mismatches:	100		
Best Local Similarity:	22.30%	Indels:	97		
Query Match:	6.22%				
<b>RESULT 634</b>					
ID	RAN81712 standard; DNA; 3685 BP.				
DE	Clone contg. hom-thrB operon.				
PN	WO8809819-A.				
PD	15-DEC-1988.				
PA	(NASI) MASSACHUSETTS INST TECHNOLOGY.	Mismatches:	115		
Best Local Similarity:	22.71%	Indels:	44		
Query Match:	6.22%				
<b>RESULT 635</b>					
ID	ARK52204 standard; DNA; 3699 BP.				
DE	DNA encoding human phosphoinositide-binding protein SR3.				
PN	WO200218946-A2.				
PD	07-MAR-2002.				
PA	(BABR-) BABRAHAM INST.	Mismatches:	90		
PA	(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.	Indels:	98		
PA	(LIMZ/) LIM Z.				
Best Local Similarity:	23.91%				
Query Match:	6.22%				
<b>RESULT 636</b>					
ID	ABQ93356 standard; cDNA; 5468 BP.				
DE	Human cDNA SEQ ID NO 69.				
PN	WO200218424-A2.				
PD	07-MAR-2002.				
PA	(HYSE-) HYSEQ INC.	Mismatches:	109		
Best Local Similarity:	23.57%	Indels:	64		
Query Match:	6.22%				
<b>RESULT 637</b>					
ID	AAX32024 standard; DNA; 8008 BP.				
DE	Human METH1 related EST X99599.				
PN	WO9937660-A1.				
PD	29-JUL-1999.				
PA	(IRUE/) IRUELA-ARISPE L.				
PA	(HAST/) HASTINGS G A.				
PA	(RUBE/) RUBEN S M.				
Best Local Similarity:	25.71%				
Query Match:	6.22%				
<b>RESULT 638</b>					
ID	AAC90081 standard; DNA; 8009 BP.				
DE	X99599 cDNA clone.				
PN	WO200071577-A1.				
PD	30-NOV-2000.				
PA	(SMIK) SWITHLINE BEECHAM CORP.				
PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.				
PA	(IRUE/) IRUELA-ARISPE L.				
PA	(HAST/) HASTINGS G A.				
PA	(RUBE/) RUBEN S M.				
PA	(JONA/) JONAK Z L.				
PA	(TRUL/) TRULLI S H.				
PA	(FORN/) FORNWALD J A.				
PA	(TERR/) TERRETT J A.				
Best Local Similarity:	25.71%				
Query Match:	6.22%				
<b>RESULT 639</b>					
ID	AAA38389 standard; DNA; 11279 BP.				
DE	Pseudomonas sp. WF505 bto gene cluster, SEQ ID NO:1.				
PN	JP2000093180-A.				



Best Local Similarity: 25.24%	Mismatches: 78	
Query Match: 6.18%	Indels: 61	
RESULT 652		
ID ADT45715 standard; cDNA; 918 BP.		
DE Bacterial polynucleotide #20466.		
PN US2003233675-A1.		
PD 18-DEC-2003.		
PA (CAOY/) CAO Y.		
PA (HINK/) HINKLE G J.		
PA (SLAT/) SLATER S C.		
PA (CHEN/) CHEN X.		
PA (GOLD/) GOLDMAN B S.		
Best Local Similarity: 25.65%	Mismatches: 113	
Query Match: 6.18%	Indels: 48	
RESULT 653		
ID AAS02050 standard; cDNA; 1100 BP.		
DE DNA encoding molecule for disease detection and treatment, mddt15.		
PN WO200123538-A2.		
PD 05-APR-2001.		
PA (INCY-) INCYTE GENOMICS INC.		
Best Local Similarity: 25.24%	Mismatches: 78	
Query Match: 6.18%	Indels: 61	
RESULT 654		
ID AA288362 standard; cDNA; 1296 BP.		
DE Human preprourokinase C792 nucleotide sequence.		
PN WO200006624-A1.		
PD 06-JAN-2000.		
PA (CROP-) CROPTCH DEV CORP.		
Best Local Similarity: 23.35%	Mismatches: 95	
Query Match: 6.18%	Indels: 75	
RESULT 655		
ID ADS61687 standard; cDNA; 1341 BP.		
DE Bacterial polynucleotide #13674.		
PN US2003233675-A1.		
PD 18-DEC-2003.		
PA (CAOY/) CAO Y.		
PA (HINK/) HINKLE G J.		
PA (SLAT/) SLATER S C.		
PA (CHEN/) CHEN X.		
PA (GOLD/) GOLDMAN B S.		
Best Local Similarity: 26.72%	Mismatches: 89	
Query Match: 6.18%	Indels: 50	
RESULT 656		
ID ABD02559 standard; DNA; 1746 BP.		
DE Pseudomonas aeruginosa polynucleotide #1163.		
PN US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 21.69%	Mismatches: 95	
Query Match: 6.18%	Indels: 84	
RESULT 657		
ID ADB61842 standard; DNA; 1795 BP.		
DE Human gene M31222, SEQ ID NO 7771.		
PN WO2003016475-A2.		
PD 27-FEB-2003.		
PA (GEO) GEN HOSPITAL CORP.		
PA (FARB) BAYER AG.		
Best Local Similarity: 26.95%	Mismatches: 107	
Query Match: 6.18%	Indels: 72	
RESULT 658		
ID ADG91045 standard; DNA; 1808 BP.		
DE Hepatic specific nucleic acid encoding sequence #234.		
PN WO2003066877-A2.		
PD 14-AUG-2003.		
PA (DIAD-) DIADEXUS INC.		
Best Local Similarity: 27.18%	Mismatches: 91	
Query Match: 6.18%	Indels: 30	
RESULT 659		
ID AA251001 standard; DNA; 1980 BP.		
DE X. oryzae avrExo repeat domain DNA.		
PN WO200009698-A2.		
PD 24-FEB-2000.		
PA (UNIV) UNIV KANSAS STATE RES FOUND.		
Best Local Similarity: 24.15%		
Query Match: 6.18%		
Mismatches: 107		
Indels: 84		
RESULT 660		
ID AAS72743 standard; cDNA; 2130 BP.		
DE DNA encoding novel human diagnostic protein #8547.		
PN WO200175067-A2.		
PD 11-OCT-2001.		
PA (HYSE-) HYSEQ INC.		
Best Local Similarity: 26.29%	Mismatches: 81	
Query Match: 6.18%	Indels: 24	
RESULT 661		
ID ABD07081 standard; DNA; 2190 BP.		
DE Pseudomonas aeruginosa polynucleotide #5685.		
PN US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 26.64%	Mismatches: 80	
Query Match: 6.18%	Indels: 50	
RESULT 662		
ID AAN92085 standard; DNA; 2579 BP.		
DE ORF of the HCV cDNA in clones 40b, 37b 35, 36, 81, 32, 33b and 25c.		
PN EP318216-A.		
PD 31-MAY-1989.		
PA (CHIR) CHIRON CORP.		
Best Local Similarity: 22.07%	Mismatches: 103	
Query Match: 6.18%	Indels: 45	
RESULT 663		
ID AAN90315 standard; cDNA; 2579 BP.		
DE Hepatitis CDNA virus combined ORF.		
PN GB2212511-A.		
PD 26-JUL-1989.		
PA (CHIR) CHIRON CORP.		
Best Local Similarity: 22.07%	Mismatches: 103	
Query Match: 6.18%	Indels: 45	
RESULT 664		
ID ABQ90126 standard; DNA; 2778 BP.		
DE M. capsulatus gene #111 for DNA array.		
PN WO200255655-A2.		
PD 18-JUL-2002.		
PA (UNIP-) UNIFOB STIFTELSEN UNIV BERGEN.		
PA (TIGR-) TIGR.		
Best Local Similarity: 24.26%	Mismatches: 105	
Query Match: 6.18%	Indels: 73	
RESULT 665		
ID ABD15601 standard; DNA; 2850 BP.		
DE Pseudomonas aeruginosa polynucleotide #14205.		
PN US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 25.74%	Mismatches: 77	
Query Match: 6.18%	Indels: 95	
RESULT 666		
ID ACN92869 standard; DNA; 3072 BP.		
DE Breast cancer related marker, seq id 14019.		
PN US2003099974-A1.		
PD 29-MAY-2003.		
PA (MILL-) MILLENNIUM PHARM INC.		
Best Local Similarity: 28.51%	Mismatches: 102	
Query Match: 6.18%	Indels: 38	
RESULT 667		
ID ADR07958 standard; cDNA; 3329 BP.		
DE Full length human CDNA useful for treating neurological disease Seq 1464.		
PN EP1447413-A2.		
PD 18-AUG-2004.		
PA (REAS-) RES ASSOC BIOTECHNOLOGY.		
Best Local Similarity: 24.31%	Mismatches: 109	
Query Match: 6.18%	Indels: 82	
RESULT 668		
ID AA251000 standard; DNA; 3720 BP.		
DE X. oryzae avrXol gene.		
PN WO200009698-A2.		
PD 24-FEB-2000.		

PA (UNIV ) UNIV KANSAS STATE RES FOUND.  
 Best Local Similarity: 24.15% Mismatches: 107  
 Query Match: 6.18% Indels: 84  
 RESULT 669  
 ID ABL24247 standard; DNA; 4140 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 24214.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Best Local Similarity: 22.50% Mismatches: 80  
 Query Match: 6.18% Indels: 75  
 RESULT 670  
 ID ABD07126 standard; DNA; 4647 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5730.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 26.64% Mismatches: 80  
 Query Match: 6.18% Indels: 50  
 RESULT 671  
 ID AAS75115 standard; cDNA; 5232 BP.  
 DE DNA encoding novel human diagnostic protein #10919.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 21.24% Mismatches: 125  
 Query Match: 6.18% Indels: 89  
 RESULT 672  
 ID AAN92097 standard; DNA; 5300 BP.  
 DE Hepatitis C virus (HCV) cDNA clone.  
 PN EP318216-A.  
 PD 31-MAY-1989.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 673  
 ID AAN90327 standard; cDNA; 5360 BP.  
 DE Hepatitis C virus composite probe.  
 PN GB2212511-A.  
 PD 26-JUL-1989.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 674  
 ID ADI34635 standard; DNA; 5676 BP.  
 DE HCVmodified fusion protein encoding DNA.  
 PN WO2004005473-A2.  
 PD 15-JAN-2004.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 675  
 ID ADO00773 standard; DNA; 5676 BP.  
 DE HCV NS345Core fusion protein encoding DNA SEQ ID NO:7.  
 PN WO2004039950-A2.  
 PD 13-MAY-2004.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 676  
 ID ADS75100 standard; DNA; 6233 BP.  
 DE Plasmid PCR-XL-TOPO-CMV-pur-attB.  
 PN WO2004080162-A2.  
 PD 23-SEP-2004.  
 PA (AVIG-) AVIGENICS INC.  
 Best Local Similarity: 23.27% Mismatches: 103  
 Query Match: 6.18% Indels: 82  
 RESULT 677  
 ID AAN92103 standard; DNA; 5905 BP.  
 DE Combined ORFs of the HCV CDNAs from clones 12f through 15e.  
 PN EP318216-A.  
 PD 31-MAY-1989.

PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 678  
 ID AAN92106 standard; DNA; 7310 BP.  
 DE DE Combined ORFs of the HCV CDNAs from clones K9-1 through 15e.  
 PN EP318216-A.  
 PD 31-MAY-1989.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 679  
 ID AAN90336 standard; DNA; 7310 BP.  
 DE Composite hepatitis C virus (HCV) cDNA.  
 PN GB2212511-A.  
 PD 26-JUL-1989.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 680  
 ID AAQ98221 standard; cDNA to mRNA; 7310 BP.  
 DE Hepatitis C virus clone genome.  
 PN US5443965-A.  
 PD 22-AUG-1995.  
 PA (GENE-) GENELABS INC.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 681  
 ID AAQ05955 standard; cDNA; 8316 BP.  
 DE Hepatitis C virus open reading frame.  
 PN EP388232-A.  
 PD 19-SEP-1990.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 682  
 ID AAA75296 standard; cDNA; 8316 BP.  
 DE cDNA sequence compiled Hepatitis C virus cDNA clones.  
 PN EP1034785-A2.  
 PD 13-SEP-2000.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 683  
 ID ADN35977 standard; cDNA; 8316 BP.  
 DE HCV cDNA clone #1.  
 PN EP1394255-A2.  
 PD 03-MAR-2004.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 684  
 ID AAZ07656 standard; DNA; 9133 BP.  
 DE Nucleotide sequence of HCV-1 ORF.  
 PN EP939128-A2.  
 PD 01-SEP-1999.  
 PA (OVAA/) OVA A.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 685  
 ID AAQ05956 standard; DNA; 9185 BP.  
 DE Sense strand of the compiled Hepatitis C virus cDNA sequence.  
 PN EP388232-A.  
 PD 19-SEP-1990.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 686  
 ID AAQ10566 standard; DNA; 9185 BP.  
 DE Hepatitis C virus strain 1 DNA.

PN EP414475-A.  
 PD 27-FEB-1991.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 687  
 ID AAX00459 standard; DNA; 9185 BP.  
 DE Hepatitis C virus 1 ORF1.  
 PN US5856437-A.  
 PD 05-JAN-1999.  
 PA (NAHE-) NAT INST OF HEALTH JAPAN.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 688  
 ID AAX26737 standard; DNA; 9185 BP.  
 DE Nucleotide sequence of the ORF of HCV1.  
 PN US5871503-A.  
 PD 16-FEB-1999.  
 PA (NAHE-) NAT INST OF HEALTH JAPAN.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 689  
 ID ADF66068 standard; DNA; 9185 BP.  
 DE Hepatitis C virus 1 ORF nucleotide sequence.  
 PN US5959092-A.  
 PD 28-SEP-1999.  
 PA (CHIR ) CHIRON CORP.  
 PA (NAHE-) NAT INST OF HEALTH JAPAN.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 690  
 ID AAA75297 standard; cDNA; 9185 BP.  
 DE Sense strand of HCV encoding a polyprotein.  
 PN EP1034785-A2.  
 PD 13-SEP-2000.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 691  
 ID ADN35979 standard; cDNA; 9185 BP.  
 DE HCV cDNA clone #2.  
 PN EP1394255-A2.  
 PD 03-MAR-2004.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 692  
 ID AAQ36209 standard; DNA; 9379 BP.  
 DE Composite cDNA for Hepatitis C virus (HCV) type 1.  
 PN WO9300365-A2.  
 PD 07-JAN-1993.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 693  
 ID AAQ21744 standard; DNA; 9400 BP.  
 DE Compiled HCV cDNA.  
 PN WO9202642-A.  
 PD 20-FEB-1992.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 694  
 ID AAT12710 standard; cDNA; 9401 BP.  
 DE Hepatitis C virus polyprotein.  
 PN EP693687-A1.  
 PD 24-JAN-1996.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 695

ID AAT99981 standard; DNA; 9401 BP.  
 DE HCV polyprotein coding sequence.  
 PN US5683864-A.  
 PD 04-NOV-1997.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 696  
 ID AAV09989 standard; DNA; 9401 BP.  
 DE HCV polyprotein coding sequence DNA.  
 PN US5712087-A.  
 PD 27-JAN-1998.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 697  
 ID AAD35043 standard; cDNA; 9401 BP.  
 DE Hepatitis C virus (HCV) polyprotein cDNA.  
 PN US6312889-B1.  
 PD 06-NOV-2001.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 698  
 ID ADU23106 standard; DNA; 9401 BP.  
 DE Hepatitis C virus genomic DNA sequence SeqID 1.  
 PN WO2004003141-A2.  
 PD 08-JAN-2004.  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 699  
 ID ADR29358 standard; DNA; 9401 BP.  
 DE Hepatitis C virus polyprotein precursor encoding DNA SEQ ID NO:2.  
 PN WO2004071414-A2.  
 PD 26-AUG-2004.  
 PA (GENZ ) GENZYME CORP.  
 PA (GRHO ) GEN HOSPITAL CORP DBA MASSACHUSETTS GEN.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 700  
 ID ADN33102 standard; DNA; 9618 BP.  
 DE Hepatitis C virus detection method-related gene.  
 PN KR2002034759-A.  
 PD 09-MAY-2002.  
 PA (DONG-) DONG WHA PHARM IND CO LTD.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 701  
 ID AAF83667 standard; DNA; 9620 BP.  
 DE HCV delNS35 ORF comprising pCMV-delNS35 nucleic acid sequence.  
 PN WO200138360-A2.  
 PD 31-MAY-2001.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 702  
 ID AAF83666 standard; DNA; 9620 BP.  
 DE HCV NS35 ORF comprising pCMV-NS35 nucleic acid sequence.  
 PN WO200138360-A2.  
 PD 31-MAY-2001.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.18% Indels: 45  
 RESULT 703  
 ID ADF44493 standard; cDNA; 10655 BP.  
 DE Mouse kinase protein encoding cDNA SEQ ID NO:11.  
 PN WO2003084992-A1.  
 PD 16-OCT-2003.  
 PA (RIKE ) RIKEN KK.  
 PA (DNAP-) DNAFORM KK.  
 PA (MITU ) MITSUBISHI CHEM CORP.  
 Best Local Similarity: 28.69% Mismatches: 77

Query Match:	6.18%	Indels:	69
RESULT 704			
ID AAV59364 standard; cDNA; 12980 BP.			
DE Hepatitis C virus clone p90/HCVFlong pu cDNA.			
PN WO9839031-A1.			
PD 11-SEP-1998.			
PA (UNIW ) UNIV WASHINGTON.			
Best Local Similarity: 22.07%		Mismatches:	102
Query Match:	6.18%	Indels:	45
RESULT 705			
ID ABK67286 standard; cDNA; 12980 BP.			
DE Hepatitis C virus plasmid p90/HCVFlongpu cDNA sequence.			
PN US6392028-B1.			
PD 21-MAY-2002.			
PA (UNIW ) UNIV WASHINGTON.			
Best Local Similarity: 22.07%		Mismatches:	102
Query Match:	6.18%	Indels:	45
RESULT 706			
ID ACA62469 standard; DNA; 12980 BP.			
DE DNA encoding p90/HCVFlong pu.			
PN US2003028010-A1.			
PD 06-FEB-2003.			
PA (UNIW ) UNIV WASHINGTON.			
Best Local Similarity: 22.07%		Mismatches:	102
Query Match:	6.18%	Indels:	45
RESULT 707			
ID ADS75098 standard; DNA; 17402 BP.			
DE Plasmid pOMIFN-Ins-CMV-pur-attB.			
PN WO2004080162-A2.			
PD 23-SEP-2004.			
PA (AVIG-) AVIGENICS INC.			
Best Local Similarity: 23.27%		Mismatches:	103
Query Match:	6.18%	Indels:	82
RESULT 708			
ID ADS75097 standard; DNA; 18116 BP.			
DE Plasmid p12.0-lys-LSPINNM-CMV-pur-attB.			
PN WO2004080162-A2.			
PD 23-SEP-2004.			
PA (AVIG-) AVIGENICS INC.			
Best Local Similarity: 23.27%		Mismatches:	103
Query Match:	6.18%	Indels:	82
RESULT 709			
ID AAF83671 standard; DNA; 19798 BP.			
DE Nucleic acid sequence of pd.deltans3NS5.pj.			
PN WO200138360-A2.			
PD 31-MAY-2001.			
PA (CHIR ) CHIRON CORP.			
Best Local Similarity: 22.07%		Mismatches:	103
Query Match:	6.18%	Indels:	45
RESULT 710			
ID AAF83670 standard; DNA; 19912 BP.			
DE Nucleic acid sequence of pd.deltans3NS5.			
PN WO200138360-A2.			
PD 31-MAY-2001.			
PA (CHIR ) CHIRON CORP.			
Best Local Similarity: 22.07%		Mismatches:	103
Query Match:	6.18%	Indels:	45
RESULT 711			
ID AAF83672 standard; DNA; 20160 BP.			
DE Nucleic acid sequence of pd.deltans3NS5.pj.corei21.			
PN WO200138360-A2.			
PD 31-MAY-2001.			
PA (CHIR ) CHIRON CORP.			
Best Local Similarity: 22.07%		Mismatches:	103
Query Match:	6.18%	Indels:	45
RESULT 712			
ID AAF83674 standard; DNA; 20217 BP.			
DE Nucleic acid sequence of pd.deltans3NS5.pj.corei40.			
PN WO200138360-A2.			
PD 31-MAY-2001.			
PA (CHIR ) CHIRON CORP.			
Best Local Similarity: 22.07%		Mismatches:	103
Query Match:	6.18%	Indels:	45
RESULT 713			
ID AAF83675 standard; DNA; 20247 BP.			
DE Nucleic acid sequence of pd.deltans3NS5.pj.corei50.			
PN WO200138360-A2.			
PD 31-MAY-2001.			
PA (CHIR ) CHIRON CORP.			
Best Local Similarity: 22.07%		Mismatches:	103
Query Match:	6.18%	Indels:	45
RESULT 714			
ID AAF83673 standard; DNA; 20316 BP.			
DE Nucleic acid sequence of pd.deltans3NS5.pj.corei73.			
PN WO200138360-A2.			
PD 31-MAY-2001.			
PA (CHIR ) CHIRON CORP.			
Best Local Similarity: 22.07%		Mismatches:	103
Query Match:	6.18%	Indels:	45
RESULT 715			
ID ABQ72998 standard; cDNA; 27754 BP.			
DE Human transporter protein encoding DNA SEQ ID NO:3.			
PN WO20025703-A2.			
PD 18-JUL-2002.			
PA (PEKE ) PE CORP NY.			
Best Local Similarity: 24.55%		Mismatches:	81
Query Match:	6.18%	Indels:	54
RESULT 716			
ID AAQ46806 standard; DNA; 29879 BP.			
DE eryA region of S. erythraea chromosome.			
PN WO9313663-A1.			
PD 22-JUL-1993.			
PA (ABBO ) ABBOTT LAB.			
Best Local Similarity: 21.58%		Mismatches:	104
Query Match:	6.18%	Indels:	47
RESULT 717			
ID ADL27113 standard; DNA; 31631 BP.			
DE Mouse genomic sequence for RORC.			
PN US2003216558-A1.			
PD 20-NOV-2003.			
PA (MORR/) MORRIS D W.			
Best Local Similarity: 26.20%		Mismatches:	91
Query Match:	6.18%	Indels:	80
RESULT 718			
ID AAX23517 standard; DNA; 50000 BP.			
DE Human kidney aminopeptidase P genomic DNA fragment 1.			
PN WO9911799-A2.			
PD 11-MAR-1999.			
PA (MEDI-) MEDICAL COLLEGE GEORGIA RES INST.			
Best Local Similarity: 23.39%		Mismatches:	77
Query Match:	6.18%	Indels:	88
RESULT 719			
ID ABL62723 standard; DNA; 66109 BP.			
DE Colon adenocarcinoma related gene sequence SEQ ID NO:1060.			
PN WO200194629-A2.			
PD 13-DEC-2001.			
PA (AVAL-) AVALON PHARM.			
Best Local Similarity: 27.03%		Mismatches:	95
Query Match:	6.18%	Indels:	70
RESULT 720			
ID ABN97273 standard; DNA; 66109 BP.			
DE Gene #3771 used to diagnose liver cancer.			
PN WO200229103-A2.			
PD 11-APR-2002.			
PA (GENE-) GENE LOGIC INC.			
Best Local Similarity: 27.03%		Mismatches:	95
Query Match:	6.18%	Indels:	70
RESULT 721			
ID ADR52892 standard; DNA; 151152 BP.			
DE Drug therapy altered expressed gene #243.			
PN WO2004072265-A2.			
PD 26-AUG-2004.			
PA (AMHP ) WYETH.			
PA (BURC/) BURCZYNSKI M.			
PA (TWIN/) TWINE N.			

PA (DORN/) DORNER A. J.  
 PA (TREP/) TREPICCHIO W. L.  
 Best Local Similarity: 23.3% Mismatches: 77  
 Query Match: 6.1% Indels: 88  
 RESULT 722  
 ID ABX84699 standard; CDNA; 198285 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #1270.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Best Local Similarity: 27.0% Mismatches: 95  
 Query Match: 6.1% Indels: 70  
 RESULT 723  
 ID ABN97319 standard; DNA; 198285 BP.  
 DE Gene #3817 used to diagnose liver cancer.  
 PN WO200229103-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Best Local Similarity: 27.0% Mismatches: 95  
 Query Match: 6.1% Indels: 70  
 RESULT 724  
 ID ADR52987 standard; DNA; 198285 BP.  
 DE Drug therapy altered expressed gene #338.  
 PN WO200407265-A2.  
 PD 26-AUG-2004.  
 PA (AMHP) WYETH.  
 PA (BURC/) BURCZYNSKI M.  
 PA (TWIN/) TWINE N.  
 PA (DORN/) DORNER A. J.  
 PA (TREP/) TREPICCHIO W. L.  
 Best Local Similarity: 27.0% Mismatches: 95  
 Query Match: 6.1% Indels: 70  
 RESULT 725  
 ID ADR65058 standard; CDNA; 729 BP.  
 DE Cotton cDNA sequence, SEQ ID 5839.  
 PN US200418130-A1.  
 PD 16-SEP-2004.  
 PA (KOVA/) KOVALIC D. K.  
 PA (ZHOU/) ZHOU Y.  
 PA (CAOY/) CAO Y.  
 Best Local Similarity: 24.3% Mismatches: 104  
 Query Match: 6.1% Indels: 41  
 RESULT 726  
 ID ACA25241 standard; DNA; 909 BP.  
 DE Prokaryotic essential gene #698.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 24.5% Mismatches: 81  
 Query Match: 6.1% Indels: 61  
 RESULT 727  
 ID AAV15072 standard; DNA; 922 BP.  
 DE Hybrid DNA comprising a family 45 cellulase core region.  
 PN WO9743409-A2.  
 PD 20-NOV-1997.  
 PA (NOVO) NOVO-NORDISK AS.  
 Best Local Similarity: 21.6% Mismatches: 88  
 Query Match: 6.1% Indels: 52  
 RESULT 728  
 ID ADE64174 standard; DNA; 981 BP.  
 DE Human gene L36318, SEQ ID NO 10126.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEO) GEN HOSPITAL CORP.  
 Best Local Similarity: 26.9% Mismatches: 70  
 Query Match: 6.1% Indels: 70  
 RESULT 729  
 ID ADE64170 standard; DNA; 981 BP.  
 DE Human gene L36318, SEQ ID NO 10122.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.  
 Best Local Similarity: 26.9% Mismatches: 70  
 Query Match: 6.1% Indels: 70  
 RESULT 730  
 ID ABD11890 standard; DNA; 993 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10494.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 26.1% Mismatches: 88  
 Query Match: 6.1% Indels: 50  
 RESULT 731  
 ID AAS68339 standard; CDNA; 1128 BP.  
 DE DNA encoding novel human diagnostic protein #4143.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 18.5% Mismatches: 78  
 Query Match: 6.1% Indels: 88  
 RESULT 732  
 ID ACA43475 standard; DNA; 1140 BP.  
 DE Prokaryotic essential gene #25132.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 26.1% Mismatches: 91  
 Query Match: 6.1% Indels: 47  
 RESULT 733  
 ID AAZ88364 standard; CDNA; 1239 BP.  
 DE Human prourokinase CT97 nucleotide sequence.  
 PN WO200000624-A1.  
 PD 06-JAN-2000.  
 PA (CROP-) CROPTTECH DEV CORP.  
 Best Local Similarity: 24.3% Mismatches: 87  
 Query Match: 6.1% Indels: 62  
 RESULT 734  
 ID AAZ88363 standard; CDNA; 1305 BP.  
 DE Patatin signal peptide and prourokinase CT111 nucleotide sequence.  
 PN WO200000624-A1.  
 PD 06-JAN-2000.  
 PA (CROP-) CROPTTECH DEV CORP.  
 Best Local Similarity: 24.3% Mismatches: 87  
 Query Match: 6.1% Indels: 62  
 RESULT 735  
 ID ADS55918 standard; CDNA; 1488 BP.  
 DE Bacterial polynucleotide #7905.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G. J.  
 PA (SLAT/) SLATER S. C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B. S.  
 Best Local Similarity: 25.3% Mismatches: 100  
 Query Match: 6.1% Indels: 53  
 RESULT 736  
 ID AAH14085 standard; CDNA; 1771 BP.  
 DE Human cDNA sequence SEQ ID NO:11244.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Best Local Similarity: 28.3% Mismatches: 89  
 Query Match: 6.1% Indels: 55  
 RESULT 737  
 ID ADT44736 standard; CDNA; 1788 BP.  
 DE Bacterial polynucleotide #19487.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G. J.  
 PA (SLAT/) SLATER S. C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B. S.

Best Local Similarity: 24.69% Mismatches: 67  
Query Match: 6.15% Indels: 78  
RESULT 738  
ID AAX23753 standard; DNA; 1821 BP.  
DE Rice anthranilate synthase second isozyme alpha-subunit DNA.  
PD WO9511800-A1.  
PD 11-MAR-1999.  
PA (HOKK) HOKKO CHEM IND CO LTD.  
PA (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.  
Best Local Similarity: 21.74% Mismatches: 112  
Query Match: 6.15% Indels: 108  
RESULT 739  
ID AD50711 standard; DNA; 1821 BP.  
DE Rice anthranilate synthase DNA.  
PD WO200290497-A2.  
PD 14-NOV-2002.  
PA (RENE-) RENESSEN LLC.  
PA (MONS) MONSANTO CO.  
PA (WEAV-) WEAVER L M.  
PA (LIAN-) LIANG J.  
PA (CHEN-) CHEN R.  
PA (JEON-) JEONG S S.  
PA (MITS-) MITSKY T.  
PA (SLAT-) SLATER S.  
PA (RAPP-) RAPP W.  
Best Local Similarity: 21.74% Mismatches: 112  
Query Match: 6.15% Indels: 108  
RESULT 740  
ID ADO05512 standard; DNA; 1821 BP.  
DE Rice anthranilate synthase DNA, SEQ:94.  
PD WO2003092363-A2.  
PD 13-NOV-2003.  
PA (MONS) MONSANTO TECHNOLOGY LLC.  
Best Local Similarity: 21.74% Mismatches: 112  
Query Match: 6.15% Indels: 108  
RESULT 741  
ID ABD13200 standard; DNA; 1866 BP.  
DE Pseudomonas aeruginosa polynucleotide #11804.  
PD US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 24.92% Mismatches: 83  
Query Match: 6.15% Indels: 114  
RESULT 742  
ID ADQ87560 standard; cDNA; 1868 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4438.  
PD WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH-) GENENTECH INC.  
PA (WUTD-) WU T D.  
PA (ZHOU-) ZHOU Y.  
Best Local Similarity: 26.97% Mismatches: 75  
Query Match: 6.15% Indels: 84  
RESULT 743  
ID ABN59958 standard; cDNA; 1915 BP.  
DE Novel human coding sequence SEQ ID NO: 369.  
PD WO20022660-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 28.38% Mismatches: 89  
Query Match: 6.15% Indels: 55  
RESULT 744  
ID ADG32679 standard; DNA; 1940 BP.  
DE Human DNA differentially expressed in patients with SLE SeqID3.  
PD WO2003090694-A2.  
PD 06-NOV-2003.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Best Local Similarity: 25.23% Mismatches: 92  
Query Match: 6.15% Indels: 41  
RESULT 745  
ID ADG33091 standard; DNA; 1940 BP.  
DE Human DNA differentially expressed in patients with SLE SeqID415.  
PD WO2003090694-A2.

PD 06-NOV-2003.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Best Local Similarity: 25.23% Mismatches: 92  
Query Match: 6.15% Indels: 41  
RESULT 746  
ID ADJ74893 standard; DNA; 1940 BP.  
DE Marker gene SEQ ID NO:145.  
PD EPI394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Best Local Similarity: 25.23% Mismatches: 92  
Query Match: 6.15% Indels: 41  
RESULT 747  
ID ADJ74967 standard; DNA; 1940 BP.  
DE Marker gene SEQ ID NO:219.  
PD EPI394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Best Local Similarity: 25.23% Mismatches: 92  
Query Match: 6.15% Indels: 41  
RESULT 748  
ID ADJ83069 standard; cDNA; 1940 BP.  
DE Human PRO3673 cDNA, SEQ ID 271.  
PD WO2004024097-A2.  
PD 25-MAR-2004.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 25.23% Mismatches: 92  
Query Match: 6.15% Indels: 41  
RESULT 749  
ID ADN04326 standard; cDNA; 1940 BP.  
DE Antipsoriatic cDNA sequence #363.  
PD WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 25.23% Mismatches: 92  
Query Match: 6.15% Indels: 41  
RESULT 750  
ID ADP24097 standard; cDNA; 1940 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:1275.  
PD WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 25.23% Mismatches: 92  
Query Match: 6.15% Indels: 41  
RESULT 751  
ID ABD13031 standard; DNA; 1941 BP.  
DE Pseudomonas aeruginosa polynucleotide #11635.  
PD US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 24.92% Mismatches: 83  
Query Match: 6.15% Indels: 114  
RESULT 752  
ID ACN41685 standard; cDNA; 2381 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:560.  
PD WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 25.23% Mismatches: 92  
Query Match: 6.15% Indels: 41  
RESULT 753  
ID ADQ63792 standard; cDNA; 2438 BP.  
DE Novel human cDNA sequence #953.  
PD EPI440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 21.20% Mismatches: 89  
Query Match: 6.15% Indels: 99  
RESULT 754  
ID ACN41683 standard; cDNA; 2606 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:559.  
PD WO2004023973-A2.  
PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 24.54% Mismatches: 110  
 Query Match: 6.15% Indels: 62  
 RESULT 755  
 ID ACN41682 standard; cDNA; 2608 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:557.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 24.54% Mismatches: 110  
 Query Match: 6.15% Indels: 62  
 RESULT 756  
 ID AAQ0631 standard; DNA; 2614 BP.  
 DE Gene conferring teicoplanin resistance.  
 PN EP39328-A.  
 PD 28-NOV-1990.  
 PA (LEPE) GRUPPO LEPETIT SPA.  
 Best Local Similarity: 27.40% Mismatches: 82  
 Query Match: 6.15% Indels: 54  
 RESULT 757  
 ID ADC72232 standard; DNA; 2691 BP.  
 DE Human NR3B gene SEQ ID NO:9.  
 PN WO2003016479-A2.  
 PD 27-FEB-2003.  
 PA (BURN-) BURNHAM INST.  
 PA (UYVA) UNIV YALE.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 758  
 ID ADN49187 standard; cDNA; 2691 BP.  
 DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) EST cDNA.  
 PN US2004033500-A1.  
 PD 19-FEB-2004.  
 PA (BURN-) BURNHAM INST.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 759  
 ID AAL47419 standard; cDNA; 2706 BP.  
 DE Human N-methyl-D-aspartate receptor coding sequence.  
 PN WO200240538-A2.  
 PD 23-MAY-2002.  
 PA (FARB) BAYER AG.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 760  
 ID ACC47899 standard; cDNA; 2706 BP.  
 DE Human NR3B subunit receptor polypeptide coding sequence.  
 PN WO2003033672-A2  
 PD 24-APR-2003.  
 PA (RIKE) RIKEN KK.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 761  
 ID ADM02343 standard; cDNA; 2715 BP.  
 DE Human cDNA of the invention SEQ ID NO:1028.  
 PN EP1347046-A1.  
 PD 24-SEP-2003.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Best Local Similarity: 23.49% Mismatches: 99  
 Query Match: 6.15% Indels: 105  
 RESULT 762  
 ID ADS59378 standard; cDNA; 2781 BP.  
 DE Bacterial polynucleotide #11365.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY) CAO Y.  
 PA (HINK) HINKLE G J.  
 PA (SLAT) SLATER S C.  
 PA (CHEN) CHEN X.  
 PA (GOLD) GOLDMAN B S.  
 Best Local Similarity: 25.00% Mismatches: 111

Query Match: 6.15% Indels: 45  
 RESULT 763  
 ID ADS62861 standard; cDNA; 2781 BP.  
 DE Bacterial polynucleotide #14848.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY) CAO Y.  
 PA (HINK) HINKLE G J.  
 PA (SLAT) SLATER S C.  
 PA (CHEN) CHEN X.  
 PA (GOLD) GOLDMAN B S.  
 Best Local Similarity: 25.00% Mismatches: 111  
 Query Match: 6.15% Indels: 45  
 RESULT 764  
 ID ADS63051 standard; cDNA; 2781 BP.  
 DE Bacterial polynucleotide #15038.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY) CAO Y.  
 PA (HINK) HINKLE G J.  
 PA (SLAT) SLATER S C.  
 PA (CHEN) CHEN X.  
 PA (GOLD) GOLDMAN B S.  
 Best Local Similarity: 25.00% Mismatches: 111  
 Query Match: 6.15% Indels: 45  
 RESULT 765  
 ID ADN49407 standard; DNA; 2898 BP.  
 DE Human glutamate receptor (MEM2) DNA.  
 PN US2004086931-A1.  
 PD 06-MAY-2004.  
 PA (SPAD) SPADERNA S K.  
 PA (QUIN) QUINN K E.  
 PA (SHIM) SHIMKETS R A.  
 PA (PADI) PADIGARU M.  
 PA (SPYT) SPYTEK K A.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 766  
 ID AAS06334 standard; cDNA; 2916 BP.  
 DE DNA encoding human glutamate receptor-like protein, MEM3.  
 PN WO200144473-A2.  
 PD 21-JUN-2001.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 767  
 ID ADN49409 standard; DNA; 2916 BP.  
 DE Human glutamate receptor (MEM3) DNA.  
 PN US2004086931-A1.  
 PD 06-MAY-2004.  
 PA (SPAD) SPADERNA S K.  
 PA (QUIN) QUINN K E.  
 PA (SHIM) SHIMKETS R A.  
 PA (PADI) PADIGARU M.  
 PA (SPYT) SPYTEK K A.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 768  
 ID ADC7232 standard; DNA; 3096 BP.  
 DE Human NR3B gene SEQ ID NO:5.  
 PN WO2003016479-A2.  
 PD 27-FEB-2003.  
 PA (BURN-) BURNHAM INST.  
 PA (UYVA) UNIV YALE.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 769  
 ID ADN49183 standard; cDNA; 3096 BP.  
 DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) cDNA #1.  
 PN US2004033500-A1.  
 PD 19-FEB-2004.  
 PA (BURN-) BURNHAM INST.



PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 770  
 ID ADC72287 standard; DNA; 3097 BP.  
 DE Human NR3B gene SEQ ID NO:61.  
 PN WO2003016479-A2.  
 PD 27-FEB-2003.  
 PA (BURN-) BURNHAM INST.  
 PA (UYIA) UNIV YALE.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 771  
 ID ADN49238 standard; cDNA; 3097 BP.  
 DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) cDNA #2.  
 PN US2004033500-A1.  
 PD 19-FEB-2004.  
 PA (BURN-) BURNHAM INST.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 772  
 ID AAS06335 standard; cDNA; 3132 BP.  
 DE DNA encoding human glutamate receptor-like protein, MEM4.  
 PN WO200144473-A2.  
 PD 21-JUN-2001.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 773  
 ID AB233750 standard; cDNA; 3132 BP.  
 DE Human TRICH encoding cDNA SEQ ID NO 56.  
 PN WO200246415-A2.  
 PD 13-JUN-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 774  
 ID ADN49411 standard; DNA; 3132 BP.  
 DE Human glutamate receptor (MEM4) DNA.  
 PN US2004086931-A1.  
 PD 06-MAY-2004.  
 PA (SPAD-) SPADERNA S K.  
 PA (QUIN-) QUINN K E.  
 PA (SHIM-) SHIMKETS R A.  
 PA (PADI-) PADIGARU M.  
 PA (SPYT-) SPYTEK K A.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 775  
 ID AAC76703 standard; cDNA; 3207 BP.  
 DE Human ORFX ORF2258 polynucleotide sequence SEQ ID NO:4515.  
 PN WO200058473-A2.  
 PD 05-OCT-2000.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 23.64% Mismatches: 88  
 Query Match: 6.15% Indels: 96  
 RESULT 776  
 ID ADP98744 standard; DNA; 6051 BP.  
 DE C. albicans specific gene, orf19.1084, DNA sequence.  
 PN WO2004056965-A2.  
 PD 08-JUL-2004.  
 PA (ELIT-) ELITRA PHARM INC.  
 PA (ELIT-) ELITRA CANADA LTD.  
 Best Local Similarity: 26.06% Mismatches: 88  
 Query Match: 6.15% Indels: 28  
 RESULT 777  
 ID ADQ24692 standard; DNA; 6961 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7512.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.

Best Local Similarity: 22.09% Mismatches: 100  
 Query Match: 6.15% Indels: 139  
 RESULT 778  
 ID ABQ76621 standard; cDNA; 8496 BP.  
 DE C. albicans BAX-associated cDNA fragment SEQ ID 667.  
 PN WO200264766-A2.  
 PD 22-AUG-2002.  
 PA (JANC) JANSSEN PHARM NV.  
 Best Local Similarity: 26.06% Mismatches: 88  
 Query Match: 6.15% Indels: 28  
 RESULT 779  
 ID ACA37617 standard; DNA; 10232 BP.  
 DE Prokaryotic essential gene #19274.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 24.88% Mismatches: 116  
 Query Match: 6.15% Indels: 86  
 RESULT 780  
 ID ABL56921 standard; DNA; 10283 BP.  
 DE Human immediate early interleukin-four induced protein genomic DNA.  
 PN WO200218574-A2.  
 PD 07-MAR-2002.  
 PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
 Best Local Similarity: 22.09% Mismatches: 100  
 Query Match: 6.15% Indels: 139  
 RESULT 781  
 ID AAK73194 standard; DNA; 12050 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28006.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 27.08% Mismatches: 72  
 Query Match: 6.15% Indels: 75  
 RESULT 782  
 ID AAV52831 standard; DNA; 16836 BP.  
 DE Acetobacter xylinum cellulose synthetase complex encoding gene.  
 PN WO9839455-A1.  
 PD 11-SEP-1998.  
 PA (BIOP-) BIO-POLYMER RES CO LTD.  
 Best Local Similarity: 20.69% Mismatches: 112  
 Query Match: 6.15% Indels: 98  
 RESULT 783  
 ID ACC00503 standard; DNA; 23434 BP.  
 DE Human histone deacetylase HDAC10 genomic DNA sequence, SEQ ID NO:4.  
 PN WO2003014340-A2.  
 PD 20-FEB-2003.  
 PA (NOVS) NOVARTIS AG.  
 PA (NOVS) NOVARTIS PHARMA GMBH.  
 Best Local Similarity: 24.02% Mismatches: 70  
 Query Match: 6.15% Indels: 92  
 RESULT 784  
 ID ADL27170 standard; DNA; 29040 BP.  
 DE Human genomic sequence for LFNG.  
 PN US2003216558-A1.  
 PD 20-NOV-2003.  
 PA (MORR-) MORRIS D W.  
 PA (ENGE-) ENGELHARD E K.  
 Best Local Similarity: 22.57% Mismatches: 104  
 Query Match: 6.15% Indels: 76  
 RESULT 785  
 ID ADQ59147 standard; DNA; 70782 BP.  
 DE Angiococcus disciformis tubulysin biosynthesis cluster DNA.  
 PN DE10241152-A1.  
 PD 18-MAR-2004.  
 PA (GBPF) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 Best Local Similarity: 23.05% Mismatches: 129  
 Query Match: 6.15% Indels: 81  
 RESULT 786  
 ID ADO56274 standard; DNA; 99100 BP.  
 DE Human cyclin-dependent kinase 10, CDK10, genomic sequence.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.

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RESULT 787
ID ABL55601 standard; DNA; 625 BP.
DE HCV bait polypeptide 17 encoding sequence.
PN EP1178116-A1.
PD 06-FEB-2002.
PA (HYBR-) HYBRIGENICS SA.
Best Local Similarity: 21.11% Mismatches: 104
Query Match: 6.11% Indels: 45
RESULT 788
ID ADJR99934 standard; DNA; 1220 BP.
DE Immune Response Associated Protein, IRAP-10, coding sequence, SEQ ID 42.
PN WO2004081157-A2.
PD 23-SEP-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 25.68% Mismatches: 94
Query Match: 6.11% Indels: 41
RESULT 789
ID ABD10671 standard; DNA; 1263 BP.
DE Pseudomonas aeruginosa polynucleotide #9275.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 25.73% Mismatches: 78
Query Match: 6.11% Indels: 76
RESULT 790
ID AAX90993 standard; cDNA; 1512 BP.
DE cDNA encoding modified interferon regulatory factor-7 (IRF-7).
PN WO9951737-A1.
PD 14-OCT-1999.
PA (DAVI-) DAVIS-JEWISH GEN HOSPITAL MORTIMER B.
Best Local Similarity: 26.04% Mismatches: 67
Query Match: 6.11% Indels: 37
RESULT 791
ID ABD05238 standard; DNA; 1617 BP.
DE Pseudomonas aeruginosa polynucleotide #3842.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 27.47% Mismatches: 93
Query Match: 6.11% Indels: 45
RESULT 792
ID AAX90994 standard; cDNA; 1629 BP.
DE cDNA encoding chimeric protein IRF-7(1-246)/IRF-3(132-427).
PN WO9951737-A1.
PD 14-OCT-1999.
PA (DAVI-) DAVIS-JEWISH GEN HOSPITAL MORTIMER B.
Best Local Similarity: 26.04% Mismatches: 67
Query Match: 6.11% Indels: 37
RESULT 793
ID ADJ74892 standard; DNA; 1646 BP.
DE Marker gene SEQ ID NO:144.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Best Local Similarity: 25.00% Mismatches: 85
Query Match: 6.11% Indels: 58
RESULT 794
ID ADJ74966 standard; DNA; 1646 BP.
DE Marker gene SEQ ID NO:218.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Best Local Similarity: 25.00% Mismatches: 85
Query Match: 6.11% Indels: 58
RESULT 795
ID ADRI4354 standard; DNA; 1646 BP.
DE Human NF-kappaB pathway-associated gene SeqID355.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Best Local Similarity: 25.00% Mismatches: 85
Query Match: 6.11% Indels: 58
RESULT 796
ID ABL68654 standard; DNA; 1816 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6991.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Best Local Similarity: 26.04% Mismatches: 67
Query Match: 6.11% Indels: 37
RESULT 797
ID ADJ74891 standard; DNA; 1816 BP.
DE Marker gene SEQ ID NO:143.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Best Local Similarity: 26.04% Mismatches: 67
Query Match: 6.11% Indels: 37
RESULT 798
ID ADJ74965 standard; DNA; 1816 BP.
DE Marker gene SEQ ID NO:217.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Best Local Similarity: 26.04% Mismatches: 67
Query Match: 6.11% Indels: 37
RESULT 799
ID ADS64449 standard; DNA; 1816 BP.
DE Human interferon regulatory factor 7 (IRF-7) gene.
PN US2004185489-A1.
PD 23-SEP-2004.
PA (CERT/) CERTA U.
PA (FOSE/) FOSER S.
PA (WEYE/) WEYER K.
Best Local Similarity: 26.04% Mismatches: 67
Query Match: 6.11% Indels: 37
RESULT 800
ID ACN41686 standard; cDNA; 1843 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:561.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 26.04% Mismatches: 67
Query Match: 6.11% Indels: 37
RESULT 801
ID ACA56563 standard; cDNA; 1864 BP.
DE Human signalling pathway polynucleotide probe SEQ ID NO 1161.
PN US6500938-B1.
PD 31-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 26.04% Mismatches: 67
Query Match: 6.11% Indels: 37
RESULT 802
ID ADI56359 standard; DNA; 1864 BP.
DE Human polynucleotide probe #1161.
PN US2004010136-A1.
PD 15-JAN-2004.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 26.04% Mismatches: 67
Query Match: 6.11% Indels: 37
RESULT 803
ID ABN96893 standard; DNA; 1890 BP.
DE Gene #3391 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 26.04% Mismatches: 67
Query Match: 6.11% Indels: 37
RESULT 804
ID ADJ74890 standard; DNA; 1890 BP.
DE Marker gene SEQ ID NO:142.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Best Local Similarity: 26.04% Mismatches: 67
Query Match: 6.11% Indels: 37

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RESULT 805  
ID ADJ74964 standard; DNA; 1890 BP.  
DE Marker gene SEQ ID NO:216.  
PN EPI394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Best Local Similarity: 26.04%  
Query Match: 6.11%  
Mismatches: 67  
Indels: 37

RESULT 806  
ID ADB80136 standard; DNA; 1956 BP.  
DE Mycobacterium tuberculosis nutrient starvation-inducible gene #82.  
PN WO2003004520-A2.  
PD 16-JAN-2003.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Best Local Similarity: 20.68%  
Query Match: 6.11%  
Mismatches: 103  
Indels: 126

RESULT 807  
ID ABX56503 standard; cDNA; 2102 BP.  
DE Human protein modification and maintenance molecule (PMOD) cDNA #5.  
PN WO200281636-A2.  
PD 17-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 24.42%  
Query Match: 6.11%  
Mismatches: 86  
Indels: 121

RESULT 808  
ID ADG77055 standard; cDNA; 2286 BP.  
DE Human nucleic acid associated polypeptide (NAAP) 30 cDNA sequence.  
PN WO2003076586-A2.  
PD 18-SEP-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 26.04%  
Query Match: 6.11%  
Mismatches: 67  
Indels: 37

RESULT 809  
ID ADR99935 standard; DNA; 2418 BP.  
DE Immune Response Associated Protein, IRAP-11, coding sequence, SEQ ID 43.  
PN WO2004081197-A2.  
PD 23-SEP-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 26.04%  
Query Match: 6.11%  
Mismatches: 67  
Indels: 37

RESULT 810  
ID ACN41684 standard; cDNA; 2436 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:559.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 25.68%  
Query Match: 6.11%  
Mismatches: 94  
Indels: 41

RESULT 811  
ID ACN41681 standard; cDNA; 2609 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:556.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 26.04%  
Query Match: 6.11%  
Mismatches: 67  
Indels: 37

RESULT 812  
ID ABD17785 standard; DNA; 3744 BP.  
DE Pseudomonas aeruginosa polynucleotide #16389.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 23.67%  
Query Match: 6.11%  
Mismatches: 92  
Indels: 97

RESULT 813  
ID ADD78275 standard; DNA; 4801 BP.  
DE Human CGDD-17 coding sequence.  
PN WO2003077875-A2.  
PD 25-SEP-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 25.72%  
Query Match: 6.11%  
Mismatches: 110  
Indels: 64

RESULT 814  
ID AAD57243 standard; cDNA; 4884 BP.  
DE Human CGDD-23 cDNA.  
PN WO2003050253-A2.  
PD 19-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 25.72%  
Query Match: 6.11%  
Mismatches: 110  
Indels: 64

RESULT 815  
ID ACD13338 standard; cDNA; 4933 BP.  
DE Human DNA encoding a p53 modifier, SEQ ID 7.  
PN WO200299122-A1.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Best Local Similarity: 25.72%  
Query Match: 6.11%  
Mismatches: 110  
Indels: 64

RESULT 816  
ID ADP13275 standard; DNA; 5047 BP.  
DE Renal cell carcinoma differentially expressed gene #11.  
PN WO2004048933-A2.  
PD 10-JUN-2004.  
PA (AMHP) WYETH.  
PA (TWIN) TWINE N C.  
PA (BURC) BURCZYNSKI M E.  
PA (TREP) TREPICCHIO W L.  
PA (DORN) DORNER A.  
PA (STOV) STOVER J A.  
PA (SLON) SLONI D K.  
Best Local Similarity: 24.23%  
Query Match: 6.11%  
Mismatches: 66  
Indels: 90

RESULT 817  
ID ADQ84256 standard; cDNA; 5047 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1070.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD) WU T D.  
PA (ZHOU) ZHOU Y.  
Best Local Similarity: 24.23%  
Query Match: 6.11%  
Mismatches: 66  
Indels: 90

RESULT 818  
ID ADQ85638 standard; cDNA; 5047 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2452.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD) WU T D.  
PA (ZHOU) ZHOU Y.  
Best Local Similarity: 24.23%  
Query Match: 6.11%  
Mismatches: 66  
Indels: 90

RESULT 819  
ID ADQ86737 standard; cDNA; 5047 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3612.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD) WU T D.  
PA (ZHOU) ZHOU Y.  
Best Local Similarity: 24.23%  
Query Match: 6.11%  
Mismatches: 66  
Indels: 90

RESULT 820  
ID AAD57244 standard; cDNA; 5079 BP.  
DE Human CGDD-24 cDNA.  
PN WO2003050253-A2.  
PD 19-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 25.72%  
Query Match: 6.11%  
Mismatches: 110  
Indels: 64

RESULT 821  
ID ABV72514 standard; cDNA; 5139 BP.  
DE Nucleotide sequence of a human intracellular signalling molecule.  
PN WO200277235-A2.  
PD 03-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.

Best Local Similarity: 25.72% Mismatches: 110  
 Query Match: 6.11% Indels: 64  
 RESULT 822  
 ID ADO34015 standard; cDNA; 5153 BP.  
 DE Human MBCT (modifier of beta-catenin) SCRIB cDNA, SEQ ID NO:5.  
 PN WO2004047761-A2.  
 PD 10-JUN-2004.  
 PA (EXEL-) EXELIXIS INC.  
 Best Local Similarity: 25.72% Mismatches: 110  
 Query Match: 6.11% Indels: 64  
 RESULT 823  
 ID ABS78655 standard; DNA; 5811 BP.  
 DE S. macromyceticus DNA encoding PKSE protein macromomycin.  
 PN CA2387401-A1.  
 PD 04-SEP-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Best Local Similarity: 26.48% Mismatches: 91  
 Query Match: 6.11% Indels: 73  
 RESULT 824  
 ID AAL54423 standard; DNA; 6609 BP.  
 DE Hepatitis C virus DNA, SEQ ID NO 1.  
 PN FR2824072-A1.  
 PD 31-OCT-2002.  
 PA (CNRS) CNRS CENT NAT RECH SCI.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.11% Indels: 45  
 RESULT 825  
 ID ADD93727 standard; DNA; 7993 BP.  
 DE Hepatitis C virus genotype 1a replicon.  
 PN WO2003085084-A2.  
 PD 16-OCT-2003.  
 PA (SMIK) SMITHKLINE BEECHAM CORP.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Query Match: 6.11% Indels: 45  
 RESULT 826  
 ID ADD93722 standard; DNA; 7989 BP.  
 DE Hepatitis C virus strain H77 (BB7-F1) replicon.  
 PN WO2003085084-A2.  
 PD 16-OCT-2003.  
 PA (SMIK) SMITHKLINE BEECHAM CORP.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Query Match: 6.11% Indels: 45  
 RESULT 827  
 ID ADP38453 standard; DNA; 7990 BP.  
 DE DNA encoding Hepatitis C virus strain H77 NS3-NS5B polyprotein Seq 4.  
 PN WO2004074507-A2.  
 PD 02-SEP-2004.  
 PA (MERI) MERCK & CO INC.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.11% Indels: 45  
 RESULT 828  
 ID ADD93723 standard; DNA; 7992 BP.  
 DE Hepatitis C virus strain H77 (BB7-F1/F2) replicon.  
 PN WO2003085084-A2.  
 PD 16-OCT-2003.  
 PA (SMIK) SMITHKLINE BEECHAM CORP.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Query Match: 6.11% Indels: 45  
 RESULT 829  
 ID AAL54425 standard; DNA; 8451 BP.  
 DE Hepatitis C virus DNA, SEQ ID NO 3.  
 PN FR2824072-A1.  
 PD 31-OCT-2002.  
 PA (CNRS) CNRS CENT NAT RECH SCI.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.11% Indels: 45  
 RESULT 830  
 ID AAT41882 standard; cDNA; 9401 BP.  
 DE Hepatitis C virus protease NS3-NS4 cDNA.  
 PN WO9634976-A1.  
 PD 07-NOV-1996.  
 PA (VERT-) VERTEX PHARM INC.  
 Best Local Similarity: 22.07% Mismatches: 103

Query Match: 6.11% Indels: 45  
 RESULT 831  
 ID AAV59378 standard; cDNA; 9416 BP.  
 DE Hepatitis C virus H-CMR cDNA.  
 PN WO9839031-A1.  
 PD 11-SEP-1998.  
 PA (UNIW) UNIV WASHINGTON.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.11% Indels: 45  
 RESULT 832  
 ID ABK87300 standard; cDNA; 9416 BP.  
 DE cDNA encoding hepatitis C virus (HCV) HCV protein.  
 PN US6392028-B1.  
 PD 21-MAY-2002.  
 PA (UNIW) UNIV WASHINGTON.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.11% Indels: 45  
 RESULT 833  
 ID ACA62483 standard; cDNA; 9416 BP.  
 DE HEV-H cDNA.  
 PN US2003028010-A1.  
 PD 06-FEB-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Query Match: 6.11% Indels: 45  
 RESULT 834  
 ID AAD03778 standard; cDNA; 9518 BP.  
 DE Hepatitis C virus envelope 2 protein lacking hypervariable region 1 cDNA.  
 PN WO200121807-A1.  
 PD 29-MAR-2001.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Query Match: 6.11% Indels: 45  
 RESULT 835  
 ID AAD03808 standard; cDNA; 9518 BP.  
 DE Hepatitis C virus H77C cDNA lacking HVRI region from chimpanzee #96A008.  
 PN WO200121807-A1.  
 PD 29-MAR-2001.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Query Match: 6.11% Indels: 45  
 RESULT 836  
 ID AAD03807 standard; cDNA; 9518 BP.  
 DE Hepatitis C virus H77C cDNA lacking HVRI region from chimpanzee 1590.  
 PN WO200121807-A1.  
 PD 29-MAR-2001.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Query Match: 6.11% Indels: 45  
 RESULT 837  
 ID AAX24833 standard; DNA; 9599 BP.  
 DE Infectious hepatitis C virus genotype 1a/1b chimera genome.  
 PN WO9904008-A2.  
 PD 28-JAN-1999.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Query Match: 6.11% Indels: 45  
 RESULT 838  
 ID AAX24832 standard; DNA; 9599 BP.  
 DE Infectious hepatitis C virus genotype 1a strain H77C genome.  
 PN WO9904008-A2.  
 PD 28-JAN-1999.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Query Match: 6.11% Indels: 45  
 RESULT 839  
 ID AAF23491 standard; DNA; 9599 BP.  
 DE Infectious Hepatitis C virus 1a genotype.  
 PN WO200075337-A1.  
 PD 14-DEC-2000.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Query Match: 6.11% Indels: 45

RESULT 840  
 ID AAC86638 standard; DNA; 9599 BP.  
 DE Nucleotide sequence of a hepatitis C virus (HCV) clone genotype 1a.  
 PN WO200075352-A2.  
 PD 14-DEC-2000.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Indels: 45  
 Query Match: 6.11%  
 RESULT 841  
 ID ADJ56743 standard; DNA; 9599 BP.  
 DE Hepatitis C virus DNA SeqID 13.  
 PN WO2004005498-A1.  
 PD 15-JAN-2004.  
 PA (TEXA) UNIV TEXAS SYSTEM.  
 PA (INSP) INST PASTEUR.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Indels: 45  
 Query Match: 6.11%  
 RESULT 842  
 ID ADJ64255 standard; DNA; 9599 BP.  
 DE Hepatitis C virus polynucleotide.  
 PN US2004039187-A1.  
 PD 26-FEB-2004.  
 PA (TEXA) UNIV TEXAS SYSTEM.  
 PA (INSP) INST PASTEUR.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Indels: 45  
 Query Match: 6.11%  
 RESULT 843  
 ID AAC86646 standard; DNA; 9611 BP.  
 DE Nucleotide sequence of chimeric Hepatitis C virus clone pH77(p7)-CV-J6S.  
 PN WO200075338-A2.  
 PD 14-DEC-2000.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Indels: 45  
 Query Match: 6.11%  
 RESULT 844  
 ID AAC86645 standard; DNA; 9611 BP.  
 DE Nucleotide sequence of chimeric Hepatitis C virus clone pH77(p7)-CV-J6S.  
 PN WO200075338-A2.  
 PD 14-DEC-2000.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Indels: 45  
 Query Match: 6.11%  
 RESULT 845  
 ID AAC86647 standard; DNA; 9611 BP.  
 DE Nucleotide sequence of chimeric Hepatitis C virus clone J6S.  
 PN WO200075338-A2.  
 PD 14-DEC-2000.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Indels: 45  
 Query Match: 6.11%  
 RESULT 846  
 ID AAC86648 standard; DNA; 9611 BP.  
 DE Nucleotide sequence of chimeric Hepatitis C virus clone pH77(p7)-J6S.  
 PN WO200075338-A2.  
 PD 14-DEC-2000.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Indels: 45  
 Query Match: 6.11%  
 RESULT 847  
 ID AAL54424 standard; DNA; 9622 BP.  
 DE Hepatitis C virus DNA, SEQ ID NO 2.  
 PN FR2824072-A1.  
 PD 31-OCT-2002.  
 PA (CNRS) CNRS CENT NAT RECH SCI.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Indels: 45  
 Query Match: 6.11%  
 RESULT 848  
 ID AAV59361 standard; cDNA; 9646 BP.  
 DE Hepatitis C virus H77 consensus sequence.  
 PN WO9839031-A1.  
 PD 11-SEP-1998.  
 PA (UNIW) UNIV WASHINGTON.  
 Best Local Similarity: 22.07% Mismatches: 103

Query Match: 6.11% Indels: 45  
 RESULT 849  
 ID ABX87285 standard; cDNA; 9646 BP.  
 DE cDNA encoding hepatitis C virus (HCV) H77 consensus protein.  
 PN US6392028-B1.  
 PD 21-MAY-2002.  
 PA (UNIW) UNIV WASHINGTON.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Indels: 45  
 Query Match: 6.11%  
 RESULT 850  
 ID ACA62466 standard; cDNA; 9646 BP.  
 DE HCV H77 consensus sequence cDNA.  
 PN US2003028010-A1.  
 PD 06-FEB-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Best Local Similarity: 22.07% Mismatches: 103  
 Indels: 45  
 Query Match: 6.11%  
 RESULT 851  
 ID ADD67945 standard; DNA; 10803 BP.  
 DE Modified hepatitis C virus (HCV) RNA seqid 17.  
 PN US2003125541-A1.  
 PD 03-JUL-2003.  
 PA (TEXA) UNIV TEXAS SYSTEM.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Indels: 45  
 Query Match: 6.11%  
 RESULT 852  
 ID ABX10617 standard; DNA; 10803 BP.  
 DE MKO-Z nucleotide sequence encoding viral polypeptides.  
 PN US2002155582-A1.  
 PD 24-OCT-2002.  
 PA (LEMO) LEMON S M.  
 PA (YIMM) YI M.  
 Best Local Similarity: 21.17% Mismatches: 104  
 Indels: 45  
 Query Match: 6.11%  
 RESULT 853  
 ID ACD19239 standard; DNA; 12848 BP.  
 DE E. coli 0157 unique DNA sequence OZID\_252.  
 PN US2003023075-A1.  
 PD 30-JAN-2003.  
 PA (BLAT) BLATTNER F R.  
 PA (BURL) BURLAND V D.  
 PA (PERN) PERNA N T.  
 PA (PLON) PLUNKETT G.  
 PA (WELC) WELCH R.  
 Best Local Similarity: 23.20% Mismatches: 111  
 Indels: 87  
 Query Match: 6.11%  
 RESULT 854  
 ID ABU28892 standard; DNA; 21407 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38149.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 20.45% Mismatches: 103  
 Indels: 141  
 Query Match: 6.11%  
 RESULT 855  
 ID ADC00831 standard; DNA; 39824 BP.  
 DE Enterohaemorrhagic E. coli 0157:H7-specific nucleic acid SEQ ID NO: 876.  
 PN JP2002355074-A.  
 PD 10-DEC-2002.  
 PA (UYTS) UNIV TSUKUBA.  
 Best Local Similarity: 23.20% Mismatches: 111  
 Indels: 87  
 Query Match: 6.11%  
 RESULT 856  
 ID AAT80413 standard; DNA; 43280 BP.  
 DE Tyactone synthase gene cluster.  
 PN EP791655-A2.  
 PD 27-AUG-1997.  
 PA (ELIL) LILLY & CO ELI.  
 Best Local Similarity: 24.08% Mismatches: 102  
 Indels: 101  
 Query Match: 6.11%  
 RESULT 857  
 ID AAZ23902 standard; DNA; 49999 BP.  
 DE Human LOBO homologue genomic DNA fragment 4.

PA WO9950284-A2.  
 PD 07-OCT-1999.  
 PA (ROSE/) ROSENTHAL A.  
 Best Local Similarity: 22.97% Mismatches: 114  
 Query Match: 6.11% Indels: 86  
 RESULT 858  
 ID AA223904 standard; DNA; 49999 BP.  
 DE Human LOBO homologue genomic DNA fragment 6.  
 PN WO9950284-A2.  
 PD 07-OCT-1999.  
 PA (ROSE/) ROSENTHAL A.  
 Best Local Similarity: 28.85% Mismatches: 78  
 Query Match: 6.11% Indels: 51  
 RESULT 859  
 ID ACN44438 standard; DNA; 73967 BP.  
 DE Human genomic sequence hCG27607.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Best Local Similarity: 22.18% Mismatches: 105  
 Query Match: 6.11% Indels: 87  
 RESULT 860  
 ID ADP64454 standard; DNA; 76994 BP.  
 DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.  
 PN WO2004053065-A2.  
 PD 24-JUN-2004.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Best Local Similarity: 26.81% Mismatches: 118  
 Query Match: 6.11% Indels: 75  
 RESULT 861  
 ID AAL50814 standard; DNA; 79528 BP.  
 DE Human cancer status prediction method-related DNA sequence #6.  
 PN WO200272828-A1.  
 PD 19-SEP-2002.  
 PA (DNAC-) DNA CHIP RES INC.  
 (HISP) HITACHI SOFTWARE ENG CO LTD.  
 Best Local Similarity: 24.51% Mismatches: 119  
 Query Match: 6.11% Indels: 74  
 RESULT 862  
 ID ADQ19802 standard; DNA; 79528 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2621.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Best Local Similarity: 24.51% Mismatches: 119  
 Query Match: 6.11% Indels: 74  
 RESULT 863  
 ID ADQ56274 standard; DNA; 99100 BP.  
 DE Human cyclin-dependent kinase 10, CDK10, genomic sequence.  
 Best Local Similarity: 28.31% Mismatches: 74  
 Query Match: 6.11% Indels: 58  
 RESULT 864  
 Best Local Similarity: 20.68% Mismatches: 103  
 Query Match: 6.11% Indels: 126  
 RESULT 865  
 Best Local Similarity: 20.68% Mismatches: 103  
 Query Match: 6.11% Indels: 126  
 RESULT 866  
 ID AAC42335 standard; DNA; 816 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35161.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Best Local Similarity: 24.31% Mismatches: 80  
 Query Match: 6.08% Indels: 103  
 RESULT 867  
 ID ABR65240 standard; cDNA; 1037 BP.  
 DE Arabidopsis cDNA encoding a transcription factor #92.  
 PN WO200215675-A1.  
 PD 28-FEB-2002.  
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
 (PILG) PILGRIM M.  
 (CREE) CREELMAN R.  
 (DUBE/) DUBELL A J.  
 PA (HEAR/) HEARD J.  
 (JIAN/) JIANG C.  
 (KEDD/) KEDDIE J.  
 (ADAM/) ADAM L.  
 (RATC/) RATCLIFF O.  
 (REUB/) REUBER J L.  
 (RIEC/) RIECHMANN J L.  
 (YUGG/) YU G.  
 (PINE/) PINEDA O.  
 Best Local Similarity: 24.31% Mismatches: 80  
 Query Match: 6.08% Indels: 103  
 RESULT 868  
 ID ADO61718 standard; DNA; 1037 BP.  
 DE Transcription factor G1142 coding sequence, SEQ ID 185.  
 PN WO2004031349-A2.  
 PD 15-APR-2004.  
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
 Best Local Similarity: 24.31% Mismatches: 80  
 Query Match: 6.08% Indels: 103  
 RESULT 869  
 ID ADF57640 standard; cDNA; 1041 BP.  
 DE Human polynucleotide sequence SEQ ID NO:7.  
 PN WO2003080795-A2.  
 PD 02-OCT-2003.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 25.00% Mismatches: 81  
 Query Match: 6.08% Indels: 107  
 RESULT 870  
 ID ADM80103 standard; DNA; 1179 BP.  
 DE Spiramycin biosynthesis orf18, SEQ ID 70.  
 PN FR2845394-A1.  
 PD 09-APR-2004.  
 PA (AVET) AVENTIS PHARMA SA.  
 (CNRS) CNRS CENT NAT RECH SCI.  
 Best Local Similarity: 25.91% Mismatches: 106  
 Query Match: 6.08% Indels: 97  
 RESULT 871  
 ID ADN97619 standard; DNA; 1179 BP.  
 DE S ambofaciens spiramycin biosynthetic gene ORF18.  
 PN WO2004033689-A2.  
 PD 22-APR-2004.  
 PA (AVET) AVENTIS PHARMA SA.  
 (CNRS) CNRS.  
 Best Local Similarity: 25.91% Mismatches: 106  
 Query Match: 6.08% Indels: 97  
 RESULT 872  
 ID ABD17265 standard; DNA; 1366 BP.  
 DE Pseudomonas aeruginosa polynucleotide #15869.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 22.87% Mismatches: 124  
 Query Match: 6.08% Indels: 100  
 RESULT 873  
 ID ABD04654 standard; DNA; 1362 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3258.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 25.95% Mismatches: 75  
 Query Match: 6.08% Indels: 108  
 RESULT 874  
 ID ADG33747 standard; DNA; 1383 BP.  
 DE Actinomycetes dual condensation/epimerisation NRPS domain DNA ID 6.  
 PN WO2003089641-A2.  
 PD 30-OCT-2003.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Best Local Similarity: 25.78% Mismatches: 93  
 Query Match: 6.08% Indels: 72  
 RESULT 875  
 ID ADS6770 standard; cDNA; 1383 BP.  
 DE Bacterial polynucleotide #8757.  
 PN US2003233675-A1.

PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 28.20% Mismatches: 106  
 Query Match: 6.08% Indels: 95  
 RESULT 876  
 ID ADA70910 standard; DNA; 1506 BP.  
 DE Rice gene, SEQ ID 4233.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 27.32% Mismatches: 74  
 Query Match: 6.08% Indels: 47  
 RESULT 877  
 ID ABD04613 standard; DNA; 1551 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3217.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 25.95% Mismatches: 75  
 Query Match: 6.08% Indels: 108  
 RESULT 878  
 ID ABL1891 standard; DNA; 1692 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 8116.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Best Local Similarity: 23.59% Mismatches: 85  
 Query Match: 6.08% Indels: 36  
 RESULT 879  
 ID ABA21353 standard; DNA; 1703 BP.  
 DE Human nervous system related polynucleotide SEQ ID NO 13684.  
 PN WO200159063-A2.  
 PD 16-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 24.62% Mismatches: 116  
 Query Match: 6.08% Indels: 109  
 RESULT 880  
 ID ADQ85038 standard; cDNA; 1972 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #1852.  
 PN WO2004050270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Best Local Similarity: 27.31% Mismatches: 104  
 Query Match: 6.08% Indels: 60  
 RESULT 881  
 ID ADQ87342 standard; cDNA; 1972 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #4219.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Best Local Similarity: 27.31% Mismatches: 104  
 Query Match: 6.08% Indels: 60  
 RESULT 882  
 ID ABD12917 standard; DNA; 1995 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11521.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 22.98% Mismatches: 102  
 Query Match: 6.08% Indels: 48  
 RESULT 883  
 ID ACA23717 standard; DNA; 2097 BP.  
 DE Prokaryotic essential gene #5374.  
 PN WO200271183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 23.19% Mismatches: 102  
 Query Match: 6.08% Indels: 72  
 RESULT 884  
 ID ADB63573 standard; cDNA; 2258 BP.  
 DE Human cDNA encoding clone THYMU20018250.  
 PN EP1308459-A2.  
 PD 07-MAY-2003.  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Best Local Similarity: 26.64% Mismatches: 102  
 Query Match: 6.08% Indels: 57  
 RESULT 885  
 ID AAA95821 standard; cDNA; 2346 BP.  
 DE Human metalloproteinase ADAMTS-2 cDNA.  
 PN WO200053774-A2.  
 PD 14-SEP-2000.  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 Best Local Similarity: 21.47% Mismatches: 107  
 Query Match: 6.08% Indels: 139  
 RESULT 886  
 ID AAH20226 standard; DNA; 2670 BP.  
 DE Human ADAM-type metalloprotease-related probe, SEQ ID NO:3.  
 PN JP2001017183-A.  
 PD 23-JAN-2001.  
 PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
 Best Local Similarity: 21.23% Mismatches: 104  
 Query Match: 6.08% Indels: 147  
 RESULT 887  
 ID AAF82166 standard; cDNA; 2670 BP.  
 DE Human ADAM type metal protease MDT53 encoding cDNA SEQ ID NO:21.  
 PN JP2001008687-A.  
 PD 16-JAN-2001.  
 PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
 Best Local Similarity: 21.23% Mismatches: 104  
 Query Match: 6.08% Indels: 147  
 RESULT 888  
 ID ADA71138 standard; DNA; 2960 BP.  
 DE Rice gene, SEQ ID 4461.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 25.25% Mismatches: 88  
 Query Match: 6.08% Indels: 98  
 RESULT 889  
 ID ADK70389 standard; cDNA; 3327 BP.  
 DE Respiratory disease differentially expressed cDNA #125.  
 PN WO2003101283-A2.  
 PD 11-DEC-2003.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 21.23% Mismatches: 104  
 Query Match: 6.08% Indels: 147  
 RESULT 890  
 ID ADL62057 standard; DNA; 3964 BP.  
 DE Human ovarian cancer DNA marker #20269.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Best Local Similarity: 26.64% Mismatches: 102  
 Query Match: 6.08% Indels: 57  
 RESULT 891  
 ID ADQ22564 standard; DNA; 4006 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5384.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Best Local Similarity: 24.92% Mismatches: 124  
 Query Match: 6.08% Indels: 97  
 RESULT 892  
 ID ABN59988 standard; cDNA; 4164 BP.  
 DE Novel human coding sequence SEQ ID NO: 399.  
 PN WO200222660-A2.  
 PD 21-MAR-2002.



PA (HYSE-) HYSEQ INC. 102  
 Best Local Similarity: 26.64% Mismatches:  
 Query Match: 6.08% Indels: 57  
 RESULT 893  
 ID ADP10534 standard; DNA; 4239 BP.  
 DE Reference mRNA sequences for marker probe #211.  
 PN WO20004042346-A2.  
 PD 21-MAY-2004.  
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC. 102  
 Best Local Similarity: 26.64% Mismatches:  
 Query Match: 6.08% Indels: 57  
 RESULT 894  
 ID ADQ64705 standard; cDNA; 4293 BP.  
 DE Novel human cDNA sequence #1866.  
 PN EP1440981-A2.  
 PD 28-JUL-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY. 102  
 Best Local Similarity: 26.64% Mismatches:  
 Query Match: 6.08% Indels: 57  
 RESULT 895  
 ID ACF04824 standard; DNA; 5244 BP.  
 DE M lichenicola melithiazol synthesis gene Mel G.  
 PN WO2003080828-A2.  
 PD 02-OCT-2003.  
 PA (GBFB) GBF GES BIOTECH FORSCHUNG GMBH. 83  
 Best Local Similarity: 26.79% Mismatches:  
 Query Match: 6.08% Indels: 56  
 RESULT 896  
 ID ABX72552 standard; cDNA; 5465 BP.  
 DE Human CAL25 cDNA encoding the amino terminal domain.  
 PN WO200283866-A2.  
 PD 24-OCT-2002.  
 PA (UYAR-) UNIV ARKANSAS. 119  
 Best Local Similarity: 21.92% Mismatches:  
 Query Match: 6.08% Indels: 72  
 RESULT 897  
 ID ABS78696 standard; DNA; 5802 BP.  
 DE S. kaniharaensis DNA encoding PKSE.  
 PN CA2387401-A1.  
 PD 04-SEP-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC. 122  
 Best Local Similarity: 21.82% Mismatches:  
 Query Match: 6.08% Indels: 88  
 RESULT 898  
 ID AAV45225 standard; DNA; 5960 BP.  
 DE Human nerve growth factor promoter plasmid pGL3-neo.  
 PN WO9835027-A2.  
 PD 13-AUG-1998.  
 PA (HMRI) HOECHST MARION ROUSSEL INC. 97  
 Best Local Similarity: 20.62% Mismatches:  
 Query Match: 6.08% Indels: 118  
 RESULT 899  
 ID ABX71177 standard; cDNA; 5967 BP.  
 DE Novel human cDNA sequence #402.  
 PN WO200281731-A2.  
 PD 17-OCT-2002.  
 PA (HYSE-) HYSEQ INC. 112  
 PA (GOOD/) GOODRICH R W. Mismatches:  
 Best Local Similarity: 23.25% Indels: 101  
 Query Match: 6.08%  
 RESULT 900  
 ID AAV62154 standard; DNA; 21034 BP.  
 DE HSV-2 strain SB5 Contig ID 10 DNA sequence.  
 PN WO9820016-A1.  
 PD 14-MAY-1998.  
 PA (SMIK) SMITHKLINE BEECHAM CORP. 111  
 Best Local Similarity: 22.59% Mismatches:  
 Query Match: 6.08% Indels: 121  
 RESULT 901  
 ID ADJ53165 standard; DNA; 25681 BP.  
 DE Saccharothrix aerocolonigenes rebeccamycin biosynthetic gene cluster.  
 PN WO200303706-A1.  
 PD 24-APR-2003.

PA (UYOV-) UNIV OVIEDO. 78  
 Best Local Similarity: 25.69% Mismatches:  
 Query Match: 6.08% Indels: 50  
 RESULT 902  
 ID ADM80034 standard; DNA; 30943 BP.  
 DE Spiramycin biosynthesis related DNA, SEQ ID 1.  
 PN FR2845394-A1.  
 PD 09-APR-2004.  
 PA (AVET) AVENTIS PHARMA SA. 106  
 Best Local Similarity: 25.91% Mismatches:  
 Query Match: 6.08% Indels: 97  
 RESULT 903  
 ID ADN97550 standard; DNA; 30943 BP.  
 DE S ambofaciens spiramycin biosynthetic enzyme genomic region.  
 PN WO2004033689-A2.  
 PD 22-APR-2004.  
 PA (AVET) AVENTIS PHARMA SA. 106  
 Best Local Similarity: 25.91% Mismatches:  
 Query Match: 6.08% Indels: 97  
 RESULT 904  
 ID ADA03020 standard; DNA; 38764 BP.  
 DE Human RAC2 carcinoma associated gene, SEQ ID NO:1538.  
 PN WO2003057146-A2.  
 PD 17-JUL-2003.  
 PA (SAGR-) SAGRES DISCOVERY. 117  
 Best Local Similarity: 24.75% Mismatches:  
 Query Match: 6.08% Indels: 73  
 RESULT 905  
 ID ADB72758 standard; DNA; 38764 BP.  
 DE Human RAC2 gene.  
 PN WO2003008583-A2.  
 PD 30-JAN-2003.  
 PA (SAGR-) SAGRES DISCOVERY. 117  
 Best Local Similarity: 24.75% Mismatches:  
 Query Match: 6.08% Indels: 73  
 RESULT 906  
 ID ADC85500 standard; DNA; 38764 BP.  
 DE Human Rac2 genomic sequence.  
 PN WO2003045230-A2.  
 PD 03-JUN-2003.  
 PA (SAGR-) SAGRES DISCOVERY. 117  
 Best Local Similarity: 24.75% Mismatches:  
 Query Match: 6.08% Indels: 73  
 RESULT 907  
 ID ADM74615 standard; DNA; 38764 BP.  
 DE Human carcinoma associated (CA) nucleic acid #142.  
 PN US2004072154-A1.  
 PD 15-APR-2004.  
 PA (MORR/) MORRIS D W. 117  
 Best Local Similarity: 24.75% Mismatches:  
 Query Match: 6.08% Indels: 73  
 RESULT 908  
 ID ABE88150 standard; cDNA; 40668 BP.  
 DE Human osteoblast differentiation related cDNA SEQ ID NO 57.  
 PN WO200250301-A2.  
 PD 27-JUN-2002.  
 PA (GENE-) GENE LOGIC INC. 59  
 PA (PROC) PROCTER & GAMBLE CO. Mismatches:  
 Best Local Similarity: 32.57% Indels: 78  
 Query Match: 6.08%  
 RESULT 909  
 ID ACF04818 standard; DNA; 51855 BP.  
 DE Melithiazol biosynthetic gene cluster.  
 PN WO2003080828-A2.  
 PD 02-OCT-2003.  
 PA (GBFB) GBF GES BIOTECH FORSCHUNG GMBH. 95  
 Best Local Similarity: 26.61% Mismatches:  
 Query Match: 6.08% Indels: 63  
 RESULT 910  
 ID ADP84151 standard; DNA; 57082 BP.

PN	US6551795-B1.			
PD	22-APR-2003.			
PA	(GENO-) GENOME THERAPEUTICS CORP.		Mismatches:	87
Best Local Similarity:	27.51%		Indels:	53
Query Match:	6.04%			
RESULT 923				
ID	ACA90158 standard; cDNA; 717 BP.			
DE	cDNA encoding novel human protein NOV1b.			
DN	WO2003031571-A2.			
PD	17-APR-2003.			
PA	(CURA-) CURAGEN CORP.			
Best Local Similarity:	25.54%		Mismatches:	73
Query Match:	6.04%		Indels:	77
RESULT 924				
ID	ABD05881 standard; DNA; 963 BP.			
DE	Pseudomonas aeruginosa polynucleotide #4485.			
DN	US6551795-B1.			
PD	22-APR-2003.			
PA	(GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity:	25.23%		Mismatches:	58
Query Match:	6.04%		Indels:	82
RESULT 925				
ID	ADS14617 standard; DNA; 1023 BP.			
DE	Pseudomonas aeruginosa quorum sensing controlled gene PA2514, SEQ ID 172.			
DN	WO2004083385-A2.			
PD	30-SEP-2004.			
PA	(IOWA) UNIV IOWA RES FOUND.			
Best Local Similarity:	27.85%		Mismatches:	100
Query Match:	6.04%		Indels:	42
RESULT 926				
ID	ACA53049 standard; DNA; 1086 BP.			
DE	Prokaryotic essential gene #34706.			
DN	WO200277183-A2.			
PD	03-OCT-2002.			
PA	(ELIT-) ELITRA PHARM INC.			
Best Local Similarity:	28.49%		Mismatches:	55
Query Match:	6.04%		Indels:	51
RESULT 927				
ID	ACA37717 standard; DNA; 1098 BP.			
DE	Prokaryotic essential gene #19374.			
DN	WO200277183-A2.			
PD	03-OCT-2002.			
PA	(ELIT-) ELITRA PHARM INC.			
Best Local Similarity:	25.76%		Mismatches:	70
Query Match:	6.04%		Indels:	48
RESULT 928				
ID	ABD02700 standard; DNA; 1098 BP.			
DE	Pseudomonas aeruginosa polynucleotide #1304.			
DN	US6551795-B1.			
PD	22-APR-2003.			
PA	(GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity:	21.76%		Mismatches:	93
Query Match:	6.04%		Indels:	80
RESULT 929				
ID	ABD10087 standard; DNA; 1149 BP.			
DE	Pseudomonas aeruginosa polynucleotide #8691.			
DN	US6551795-B1.			
PD	22-APR-2003.			
PA	(GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity:	24.24%		Mismatches:	97
Query Match:	6.04%		Indels:	107
RESULT 930				
ID	ADT42293 standard; cDNA; 1191 BP.			
DE	Bacterial polynucleotide #17044.			
DN	US2003233675-A1.			
PD	18-DEC-2003.			
PA	(CAOY) CAO Y.			
PA	(HINK) HINKLE G J.			
PA	(SLAT) SLATER S C.			
PA	(CHEN) CHEN X.			
PA	(GOLD) GOLDMAN B S.			
Best Local Similarity:	23.70%		Mismatches:	86
Query Match:	6.04%		Indels:	86

RESULT 931  
 ID ADH77842 standard; DNA; 1218 BP.  
 DE Hepatitis B virus surface antigen, HBsAgL coding sequence, SEQ ID 1.  
 PN WO2004002459-A1.  
 PD 08-JAN-2004.  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 Best Local Similarity: 27.54% Mismatches: 41  
 Query Match: 6.04% Indels: 68  
 RESULT 932  
 ID ADO48158 standard; DNA; 1218 BP.  
 DE Hepatitis B virus pre-S1 protein gene SeqID1.  
 PN WO2004047812-A1.  
 PD 10-JUN-2004.  
 PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.  
 Best Local Similarity: 27.54% Mismatches: 41  
 Query Match: 6.04% Indels: 68  
 RESULT 933  
 ID ADS91503 standard; DNA; 1218 BP.  
 DE Nucleotide sequence of a HBV surface antigen protein.  
 PN WO2004082720-A1.  
 PD 30-SEP-2004.  
 PA (BEAC-) BEACLE INC.  
 PA (VIBV-) VIB VLAAMS INTERUNIVERSITAIR INST BIOTEC.  
 PA (COLL-) COLLEN RES FOUND VZW ONDERWIJZEN NAVORSI.  
 Best Local Similarity: 27.54% Mismatches: 41  
 Query Match: 6.04% Indels: 68  
 RESULT 934  
 ID ABL08663 standard; cDNA; 1235 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 20471.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE-) PE CORP NY.  
 Best Local Similarity: 27.05% Mismatches: 100  
 Query Match: 6.04% Indels: 55  
 RESULT 935  
 ID AAC40581 standard; DNA; 1270 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 28826.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Best Local Similarity: 26.40% Mismatches: 54  
 Query Match: 6.04% Indels: 25  
 RESULT 936  
 ID AAQ06049 standard; DNA; 1296 BP.  
 DE plasmid pUK1 pro-Urokinase sequence.  
 PN EP390592-A.  
 PD 03-OCT-1990.  
 PA (KYOW) KYOWA HAKKO KOGYO KK.  
 PA (EXPE-) CENT INST EXPER ANIMALS.  
 PA (JIKK-) JIKKEN DOBUTSU CHUU KENK.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 937  
 ID AAQ55772 standard; cDNA to mRNA; 1296 BP.  
 DE Pro-urokinase derivative.  
 PN JP05336965-A.  
 PD 21-DEC-1993.  
 PA (KYOW) KYOWA HAKKO KOGYO KK.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 938  
 ID ABK86598 standard; cDNA; 1296 BP.  
 DE Human plasminogen activator, urokinase (PLAU) cDNA.  
 PN WO200240503-A2.  
 PD 23-MAY-2002.  
 PA (GENA-) GENA/ISSANCE PHARM INC.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 939  
 ID ABA00207 standard; cDNA; 1296 BP.  
 DE sc-UPA coding sequence.  
 PN EP1232755-A2.  
 PD 21-AUG-2002.  
 PA (JCRP-) JCR PHARM CO LTD.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 940  
 ID ADF28768 standard; cDNA; 1296 BP.  
 DE Human urokinase-type plasminogen activator (uPA) encoding cDNA.  
 PN WO2003082072-A2.  
 PD 09-OCT-2003.  
 PA (HARB/) HARBECK N.  
 PA (KATE/) KATES R E.  
 PA (SCHM/) SCHMITT M.  
 PA (FOEK/) FOEKENS J A.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 941  
 ID ABD03649 standard; DNA; 1323 BP.  
 DE Pseudomonas aeruginosa polynucleotide #2253.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 24.14% Mismatches: 100  
 Query Match: 6.04% Indels: 90  
 RESULT 942  
 ID ABD03827 standard; DNA; 1389 BP.  
 DE Pseudomonas aeruginosa polynucleotide #2431.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 24.14% Mismatches: 100  
 Query Match: 6.04% Indels: 90  
 RESULT 943  
 ID ABD05663 standard; DNA; 1428 BP.  
 DE Pseudomonas aeruginosa polynucleotide #4267.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 25.23% Mismatches: 58  
 Query Match: 6.04% Indels: 82  
 RESULT 944  
 ID AAS67372 standard; cDNA; 1470 BP.  
 DE DNA encoding novel human diagnostic protein #3176.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 25.10% Mismatches: 70  
 Query Match: 6.04% Indels: 89  
 RESULT 945  
 ID AAN92037 standard; DNA; 1473 BP.  
 DE Sequence of variant human prourokinase.  
 PN JP01252283-A.  
 PD 06-OCT-1989.  
 PA (GREC) GREEN CROSS CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 946  
 ID AAN50138 standard; DNA; 1474 BP.  
 DE Sequence of the signal sequence and noncoding region of the pro-UK structural gene (Sequence II).  
 PN EP154272-A.  
 PD 11-SEP-1985.  
 PA (GREC) GREEN CROSS CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 947  
 ID AAN81558 standard; DNA; 1475 BP.  
 DE Pro-UK structural gene, signal sequence and non-coding region.  
 PN EP265874-A.  
 PD 04-MAY-1988.  
 PA (GREC) GREEN CROSS CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 948  
 ID AA224619 standard; cDNA; 1475 BP.  
 DE Human lung tumor associated polynucleotide.

PN WO9947674-A2.  
 PD 23-SEP-1999.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Indels: 73  
 Query Match:  
 RESULT 949  
 ID AAC65858 standard; cDNA; 1475 BP.  
 DE Human lung cancer-associated cDNA for contig 10.  
 PN WO200061612-A2.  
 PD 19-OCT-2000.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Indels: 73  
 Query Match:  
 RESULT 950  
 ID AB235047 standard; cDNA; 1475 BP.  
 DE Human gene expression profile polynucleotide SEQ ID NO 159.  
 PN WO200274979-A2.  
 PD 26-SEP-2002.  
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Indels: 73  
 Query Match:  
 RESULT 951  
 ID AB149077 standard; cDNA; 1475 BP.  
 DE Human lung tumour cDNA sequence for contig 10 SEQ ID NO:122.  
 PN WO200200174-A2.  
 PD 03-JAN-2002.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Indels: 73  
 Query Match:  
 RESULT 952  
 ID ABO92263 standard; cDNA; 1475 BP.  
 DE Human lung cancer associated cDNA sequence SEQ ID NO:122.  
 PN WO200247534-A2.  
 PD 20-JUN-2002.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Indels: 73  
 Query Match:  
 RESULT 953  
 ID ADA28212 standard; cDNA; 1475 BP.  
 DE Human lung tumour associated cDNA contig 10.  
 PN US2003064947-A1.  
 PD 03-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Indels: 73  
 Query Match:  
 RESULT 954  
 ID ADE53417 standard; cDNA; 1475 BP.  
 DE Human lung tumour protein cDNA sequence #119.  
 PN US2003119763-A1.  
 PD 26-JUN-2003.  
 PA (WANG/) WANG T.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Indels: 73  
 Query Match:  
 RESULT 955  
 ID ADH36776 standard; cDNA; 1475 BP.  
 DE Human lung cancer-related cDNA sequence #119.  
 PN WO2003086175-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Indels: 73  
 Query Match:  
 RESULT 956  
 ID ACC78885 standard; DNA; 1475 BP.  
 DE Human urokinase encoding DNA.  
 PN WO2003031464-A2.  
 PD 17-APR-2003.  
 PA (NEOS-) NEOSE TECHNOLOGIES INC.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Indels: 73  
 Query Match:  
 RESULT 957  
 ID ADM56579 standard; cDNA; 1475 BP.  
 DE Human lung tumour cDNA #119.  
 PN US2003138438-A1.

PD 24-JUL-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Indels: 73  
 Query Match:  
 RESULT 958  
 ID ADN89623 standard; cDNA; 1475 BP.  
 DE Human lung squamous cell carcinoma cDNA seqid 122.  
 PN US5660838-B1.  
 PD 09-DEC-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Indels: 73  
 Query Match:  
 RESULT 959  
 ID ADN49705 standard; DNA; 1475 BP.  
 DE Human urokinase DNA SeqID 33.  
 PN WO2004033651-A2.  
 PD 22-APR-2004.  
 PA (NEOS-) NEOSE TECHNOLOGIES INC.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Indels: 73  
 Query Match:  
 RESULT 960  
 ID AAN91617 standard; DNA; 1500 BP.  
 DE Sequence of entire prourokinase (PKU) gene from PKU-producing tumour cell line ATCC CCL138 clone PUC20.  
 PN EP312941-A.  
 PD 26-APR-1989.  
 PA (BADI) BASF AG.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Indels: 73  
 Query Match:  
 RESULT 961  
 ID AAN91618 standard; cDNA to mRNA; 1500 BP.  
 DE Human pro-urokinase coding sequence plus untranslated regions.  
 PN EP312942-A.  
 PD 26-APR-1989.  
 PA (BADI) BASF AG.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Indels: 73  
 Query Match:  
 RESULT 962  
 ID ABD16344 standard; DNA; 1713 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14948.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 26.01% Mismatches: 127  
 Indels: 56  
 Query Match:  
 RESULT 963  
 ID ADQ83498 standard; cDNA; 1740 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #312.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Best Local Similarity: 23.00% Mismatches: 103  
 Indels: 80  
 Query Match:  
 RESULT 964  
 ID ADQ85633 standard; cDNA; 1740 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2447.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Best Local Similarity: 23.00% Mismatches: 103  
 Indels: 80  
 Query Match:  
 RESULT 965  
 ID ADD69669 standard; DNA; 1779 BP.  
 DE Chimeric IFN beta/HBsAg L DNA - SEQ ID 17.  
 PN WO2003082345-A1.  
 PD 09-OCT-2003.  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 Best Local Similarity: 27.54% Mismatches: 41  
 Indels: 68  
 Query Match:

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RESULT 966
ID  ADF81657 standard; DNA; 1781 BP.
DE  Leukemia-related DNA sequence #2213.
PN  WO2003039443-A2.
PD  15-MAY-2003.
PA  (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA  (UYIU-) UNIV LUDWIG MAXIMILIANS.
PA  (HAFE/) HAFERLACH T.
PA  (SCHO/) SCHOCH C.
PA  (KERN/) KERN W.
Best Local Similarity: 23.00%      Mismatches: 103
Query Match: 6.04%      Indels: 80
RESULT 967
ID  ABD17236 standard; DNA; 1782 BP.
DE  Pseudomonas aeruginosa polynucleotide #15840.
PN  US6551795-B1.
PD  22-APR-2003.
PA  (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 25.56%      Mismatches: 139
Query Match: 6.04%      Indels: 58
RESULT 968
ID  ADD69667 standard; DNA; 1803 BP.
DE  Chimeric IFN omega/HBsAg L DNA - SEQ ID 15.
PN  WO2003082345-A1.
PD  09-OCT-2003.
PA  (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Best Local Similarity: 27.54%      Mismatches: 41
Query Match: 6.04%      Indels: 68
RESULT 969
ID  ABD05993 standard; DNA; 1836 BP.
DE  Pseudomonas aeruginosa polynucleotide #4587.
PN  US6551795-B1.
PD  22-APR-2003.
PA  (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 25.23%      Mismatches: 58
Query Match: 6.04%      Indels: 82
RESULT 970
ID  ADM98693 standard; DNA; 1884 BP.
DE  HMG-CoA reductase DNA #28.
PN  US2004072323-A1.
PD  15-APR-2004.
PA  (MATS/) MATSUDA S P T.
PA  (HART/) HART E A.
Best Local Similarity: 23.15%      Mismatches: 107
Query Match: 6.04%      Indels: 87
RESULT 971
ID  AAH48560 standard; DNA; 1896 BP.
DE  Human fascin DNA fragment SEQ ID 10.
PN  WO200151631-A2.
PD  19-JUL-2001.
PA  (RESK/) RESKE-KUNZ A.
PA  (ROSS/) ROSS X.
PA  (ROSS/) ROSS R.
PA  (BROS/) BROS M.
Best Local Similarity: 27.65%      Mismatches: 91
Query Match: 6.04%      Indels: 42
RESULT 972
ID  AAH28220 standard; DNA; 1964 BP.
DE  Nucleotide sequence of urokinase plasminogen activator.
PN  WO200149309-A2.
PD  12-JUL-2001.
PA  (PFIZ ) PFIZER LTD.
PA  (PFIZ ) PFIZER INC.
Best Local Similarity: 23.05%      Mismatches: 96
Query Match: 6.04%      Indels: 73
RESULT 973
ID  AAD27855 standard; cDNA; 1964 BP.
DE  Human uPA cDNA.
PN  WO200196606-A2.
PD  20-DEC-2001.
PA  (NYXI-) NYXIS NEURO THERAPIES INC.
Best Local Similarity: 23.05%      Mismatches: 96
Query Match: 6.04%      Indels: 73

RESULT 974
ID  ADD69687 standard; DNA; 2013 BP.
DE  Chimeric GFP/HBsAg L DNA - SEQ ID 13.
PN  WO2003082345-A1.
PD  09-OCT-2003.
PA  (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Best Local Similarity: 27.54%      Mismatches: 41
Query Match: 6.04%      Indels: 68
RESULT 975
ID  ADS45868 standard; cDNA; 2058 BP.
DE  Bacterial polynucleotide #611.
PN  US2003233675-A1.
PD  18-DEC-2003.
PA  (CAOY/) CAO Y.
PA  (HINK/) HINKLE G J.
PA  (SLAT/) SLATER S C.
PA  (CHEN/) CHEN X.
PA  (GOLD/) GOLDMAN B S.
Best Local Similarity: 27.20%      Mismatches: 103
Query Match: 6.04%      Indels: 46
RESULT 976
ID  ABD17273 standard; DNA; 2121 BP.
DE  Pseudomonas aeruginosa polynucleotide #15877.
PN  US6551795-B1.
PD  22-APR-2003.
PA  (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 25.56%      Mismatches: 139
Query Match: 6.04%      Indels: 58
RESULT 977
ID  ABZ18317 standard; cDNA; 2161 BP.
DE  Group III cDNA cancer related clone SEQ ID NO:743.
PN  WO200278516-A2.
PD  10-OCT-2002.
PA  (CORI-) CORIXA CORP.
Best Local Similarity: 24.74%      Mismatches: 97
Query Match: 6.04%      Indels: 89
RESULT 978
ID  AAN93079 standard; DNA; 2266 BP.
DE  Sequence encoding prourokinase.
PN  EP299706-A.
PD  18-JAN-1989.
PA  (COLB ) COLLABORATIVE RES INC.
Best Local Similarity: 23.05%      Mismatches: 96
Query Match: 6.04%      Indels: 73
RESULT 979
ID  AA224620 standard; cDNA; 2281 BP.
DE  Human lung tumor associated polynucleotide.
PN  WO9947674-A2.
PD  23-SEP-1999.
PA  (CORI-) CORIXA CORP.
Best Local Similarity: 23.05%      Mismatches: 96
Query Match: 6.04%      Indels: 73
RESULT 980
ID  AAC65859 standard; cDNA; 2294 BP.
DE  Human lung cancer-associated cDNA for contig 12.
PN  WO200061612-A2.
PD  19-OCT-2000.
PA  (CORI-) CORIXA CORP.
Best Local Similarity: 23.05%      Mismatches: 96
Query Match: 6.04%      Indels: 73
RESULT 981
ID  ABL49078 standard; cDNA; 2294 BP.
DE  Human lung tumour cDNA sequence for contig 12 SEQ ID NO:123.
PN  WO200200174-A2.
PD  03-JAN-2002.
PA  (CORI-) CORIXA CORP.
Best Local Similarity: 23.05%      Mismatches: 96
Query Match: 6.04%      Indels: 73
RESULT 982
ID  ABQ92264 standard; cDNA; 2294 BP.
DE  Human lung cancer associated cDNA sequence SEQ ID NO:123.
PN  WO200247534-A2.
PD  20-JUN-2002.

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PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 983  
 ID ADA28213 standard; cDNA; 2294 BP.  
 DE Human lung tumour associated cDNA contig 12.  
 PN US2003064947-A1.  
 PD 03-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 984  
 ID ADE53418 standard; cDNA; 2294 BP.  
 DE Human lung tumour protein cDNA sequence #120.  
 PN US2003119763-A1.  
 PD 26-JUN-2003.  
 PA (WANG/) WANG T.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 985  
 ID ADH36777 standard; cDNA; 2294 BP.  
 DE Human lung cancer-related cDNA sequence #120.  
 PN WO2003086175-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 986  
 ID ADK61310 standard; cDNA; 2294 BP.  
 DE Ovarian cancer-related DNA #465 with altered ovarian cancer expression.  
 PN WO2003068054-A2.  
 PD 21-AUG-2003.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 PA (SLOK) SLOAN KETTERING INST CANCER RES.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 987  
 ID ADI31891 standard; cDNA; 2294 BP.  
 DE Human cDNA #1217.  
 PN US6607879-B1.  
 PD 19-AUG-2003.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 988  
 ID ADM56580 standard; cDNA; 2294 BP.  
 DE Human lung tumour cDNA #120.  
 PN US2003138438-A1.  
 PD 24-JUL-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 989  
 ID ADN89624 standard; cDNA; 2294 BP.  
 DE Human lung squamous cell carcinoma cDNA seqid 123.  
 PN US6660838-B1.  
 PD 09-DEC-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 990  
 ID ACN44243 standard; cDNA; 2297 BP.  
 DE Human mRNA sequence hCT11616.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 991  
 ID AAN80981 standard; cDNA; 2298 BP.  
 DE Sequence of the single chain urokinase plasminogen activator (SCU-PA)  
 DE cDNA insert prepared from human Hep3 cells.  
 PN EP288435-A.

PD 26-OCT-1988.  
 PA (CIBA) CIBA GEIGY AG.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 992  
 ID AAN60703 standard; cDNA; 2299 BP.  
 DE Sequence encoding human urokinase.  
 PN JP61181377-A.  
 PD 14-AUG-1986.  
 PA (NISC) NISSAN CHEM IND LTD.  
 PA (HODO) HODOGAYA CHEM IND CO LTD.  
 PA (SAGA) SAGAMI CHEM RES CENTRE.  
 PA (CENG) CENTRAL GLASS CO LTD.  
 PA (NIPS) NIPPON SODA CO.  
 PA (TOYJ) TOYO SODA MFG CO LTD.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 993  
 ID AAN70390 standard; cDNA; 2301 BP.  
 DE cDNA encoding human prourokinase in plasmid pKU22.  
 PN EP231883-A.  
 PD 12-AUG-1987.  
 PA (SAGA) SAGAMI CHEM RES CENTRE.  
 PA (NIPS) NIPPON SODA CO.  
 PA (CENG) CENTRAL GLASS CO LTD.  
 PA (TOYJ) TOYO SODA MFG CO LTD.  
 PA (NISC) NISSAN CHEM IND LTD.  
 PA (NISC) NISSAN CHEMICAL INDS KK.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 994  
 ID AAN91075 standard; cDNA; 2301 BP.  
 DE cDNA encoding natural human prourokinase and 5' UTR and 3' UTR.  
 PN WO9901513-A.  
 PD 23-FEB-1989.  
 PA (SAGA) SAGAMI CHEM RES CENTRE.  
 PA (CENG) CENTRAL GLASS CO LTD.  
 PA (HODO) HODOGAYA CHEM KK.  
 PA (NIPS) NIPPON SODA CO.  
 PA (NISC) NISSAN CHEM IND LTD.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 995  
 ID AAN91740 standard; cDNA; 2303 BP.  
 DE Sequence of prourokinase cDNA.  
 PN EP316068-A.  
 PD 17-MAY-1989.  
 PA (COLB) COLLABORATIVE RES INC.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 996  
 ID AA073483 standard; cDNA; 2303 BP.  
 DE Full length human urokinase protein cDNA.  
 PN EP620279-A1.  
 PD 19-OCT-1994.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 997  
 ID AAN30030 standard; cDNA; 2304 BP.  
 DE Sequence encoding full length urokinase.  
 PN EP92182-A.  
 PD 26-OCT-1983.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 998  
 ID ABL59543 standard; cDNA; 2304 BP.  
 DE Human pro-urokinase (uPA) cDNA SEQ ID NO:43.  
 PN WO200207028-A1.  
 PD 04-APR-2002.  
 PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.  
 Best Local Similarity: 23.05% Mismatches: 96

Query Match:	6.04%	Indels:	73
RESULT 999			
ID ABX76437 standard; DNA; 2304 BP.			
DE Lung cancer-associated polynucleotide #301.			
PN WO200286443-A2.			
PD 31-OCT-2002.			
PA (EOSB-) EOS BIOTECHNOLOGY INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1000			
ID ABX76275 standard; DNA; 2304 BP.			
DE Lung cancer-associated polynucleotide #140.			
PN WO200286443-A2.			
PD 31-OCT-2002.			
PA (EOSB-) EOS BIOTECHNOLOGY INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1001			
ID ABX17681 standard; DNA; 2304 BP.			
DE DNA encoding Human urokinase plasminogen activator #1.			
PN WO200279515-A1.			
PD 10-OCT-2002.			
PA (ISIS-) ISIS PHARM INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1002			
ID ACF12920 standard; cDNA; 2304 BP.			
DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:183.			
PN WO2002101075-A2.			
PD 19-DEC-2002.			
PA (MILL-) MILLENNIUM PHARM INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1003			
ID ADG89387 standard; DNA; 2304 BP.			
DE Cancer detection method related gene #50.			
PN WO2003078662-A1.			
PD 25-SEP-2003.			
PA (GENO-) GENOMIC HEALTH INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1004			
ID ADN39095 standard; cDNA; 2304 BP.			
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:413.			
PN WO2003042661-A2.			
PD 22-MAY-2003.			
PA (EOSB-) EOS BIOTECHNOLOGY INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1005			
ID ADN39740 standard; cDNA; 2304 BP.			
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C112.			
PN WO2003042661-A2.			
PD 22-MAY-2003.			
PA (EOSB-) EOS BIOTECHNOLOGY INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1006			
ID ADN95543 standard; DNA; 2304 BP.			
DE Human BEC/LEC-related gene sequence SeqID466.			
PN WO2003080640-A1.			
PD 02-OCT-2003.			
PA (LUDW-) LUDWIG INST CANCER RES.			
PA (LICN) LICENTIA LTD.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1007			
ID ADL70594 standard; cDNA; 2304 BP.			
DE Cervical cancer marker M58, urokinase, cDNA.			
PN WO2004018999-A2.			
PD 04-MAR-2004.			
PA (MILL-) MILLENNIUM PHARM INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1008			
ID ADP07333 standard; DNA; 2304 BP.			
DE Human UPA DNA.			
PN DE10255104-A1.			
PD 11-MAR-2004.			
PA (BFIG-) EPIGENOMICS AG.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1009			
ID ADP23870 standard; cDNA; 2304 BP.			
DE PRO polypeptide encoding cDNA SEQ ID NO:1048.			
PN WO2004041170-A2.			
PD 21-MAY-2004.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1010			
ID ADE25630 standard; cDNA; 2328 BP.			
DE Human gene differentially expressed in foam cells #34.			
PN US2003194721-A1.			
PD 16-OCT-2003.			
PA (INCY-) INCYTE GENOMICS INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1011			
ID ABZ35347 standard; cDNA; 2336 BP.			
DE Human gene expression profile polynucleotide SEQ ID NO 458.			
PN WO200274979-A2.			
PD 26-SEP-2002.			
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1012			
ID ADE47346 standard; cDNA; 2336 BP.			
DE Human cDNA upregulated in dendritic cells SEQ ID NO 46.			
PN US2003134283-A1.			
PD 17-JUL-2003.			
PA (PETE/) PETERSON D P.			
PA (PEAR/) PEARSON C I.			
PA (COCK/) COCKS B G.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1013			
ID ADE54011 standard; cDNA; 2336 BP.			
DE Human prostate cancer cDNA #358.			
PN US2003190640-A1.			
PD 09-OCT-2003.			
PA (FARI/) FARIS M.			
PA (PEAR/) PEARSON C I.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1014			
ID ACH03958 standard; cDNA; 2341 BP.			
DE Human cDNA differentially expressed in lung cancer #163.			
PN US2003065157-A1.			
PD 03-APR-2003.			
PA (LASE/) LASEK A W.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1015			
ID ADO62846 standard; cDNA; 2352 BP.			
DE Novel human cDNA sequence #7.			
PN EPI440981-A2.			
PD 28-JUL-2004.			
PA (REAS-) RES ASSOC BIOTECHNOLOGY.			
Best Local Similarity: 24.79%		Mismatches:	110
Query Match: 6.04%		Indels:	44
RESULT 1016			
ID AAQ20360 standard; cDNA; 2377 BP.			
DE Human pro-urokinase cDNA.			
PN DE4122688-A.			
PD 16-JAN-1992.			



PA (FARM ) FARMITALIA ERBA SRL CARLO.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 1017  
 ID AAQ04107 standard; cDNA; 2427 BP.  
 DE Human pro-urokinase cDNA of clone pcUK176.  
 PN EP365894-A.  
 PD 02-MAY-1990.  
 PA (FARM ) FARMITALIA ERBA SPA CARLO.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 1018  
 ID ABQ54872 standard; cDNA; 2484 BP.  
 DE Human ovarian antigen HVCB79 cDNA, SEQ ID NO:752.  
 PN WO200200677-A1.  
 PD 03-JAN-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 1019  
 ID AAH34897 standard; cDNA; 2486 BP.  
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:1979.  
 PN WO200122920-A2.  
 PD 05-APR-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 1020  
 ID AAS75261 standard; cDNA; 2511 BP.  
 DE DNA encoding novel human diagnostic protein #11065.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 25.84% Mismatches: 68  
 Query Match: 6.04% Indels: 42  
 RESULT 1021  
 ID ADN61537 standard; cDNA; 2554 BP.  
 DE Human KPP-47 encoding cDNA SEQ ID NO:103.  
 PN WO2004042022-A2.  
 PD 21-MAY-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 27.33% Mismatches: 107  
 Query Match: 6.04% Indels: 77  
 RESULT 1022  
 ID ADQ22641 standard; DNA; 2655 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5461.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 6.04% Indels: 73  
 RESULT 1023  
 ID ADS6316 standard; cDNA; 2855 BP.  
 DE Bacterial polynucleotide #8303.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAQY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 27.44% Mismatches: 89  
 Query Match: 6.04% Indels: 79  
 RESULT 1024  
 ID AAK53269 standard; cDNA; 2976 BP.  
 DE Human polynucleotide SEQ ID NO 2798.  
 PN WO200157190-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 25.96% Mismatches: 81  
 Query Match: 6.04% Indels: 68  
 RESULT 1025  
 ID ABD11116 standard; DNA; 3006 BP.

DE Pseudomonas aeruginosa polynucleotide #9720.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 25.38% Mismatches: 93  
 Query Match: 6.04% Indels: 70  
 RESULT 1026  
 ID AAC98992 standard; cDNA; 3094 BP.  
 DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:220.  
 PN WO200055320-A1.  
 PD 21-SEP-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 25.19% Mismatches: 117  
 Query Match: 6.04% Indels: 47  
 RESULT 1027  
 ID ABD16084 standard; DNA; 3144 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14688.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 26.01% Mismatches: 127  
 Query Match: 6.04% Indels: 56  
 RESULT 1028  
 ID AAS51474 standard; DNA; 3189 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #59.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 26.01% Mismatches: 127  
 Query Match: 6.04% Indels: 56  
 RESULT 1029  
 ID ACA19473 standard; DNA; 3189 BP.  
 DE Prokaryotic essential gene #1130.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 26.01% Mismatches: 127  
 Query Match: 6.04% Indels: 56  
 RESULT 1030  
 ID ABD16462 standard; DNA; 3198 BP.  
 DE Pseudomonas aeruginosa polynucleotide #15066.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 26.01% Mismatches: 127  
 Query Match: 6.04% Indels: 56  
 RESULT 1031  
 ID AAS34856 standard; cDNA; 3220 BP.  
 DE cDNA encoding novel human neoplastic disease associated polypeptide #90.  
 PN WO200155163-A1.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 25.96% Mismatches: 81  
 Query Match: 6.04% Indels: 68  
 RESULT 1032  
 ID ADC46014 standard; cDNA; 3220 BP.  
 DE Human neoplastic disease-associated gene 90 cDNA #1.  
 PN US2003082758-A1.  
 PD 01-MAY-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 25.96% Mismatches: 81  
 Query Match: 6.04% Indels: 68  
 RESULT 1033  
 ID ADD69671 standard; DNA; 3359 BP.  
 DE Chimeric HGP/HBSng L DNA - SEQ ID 19.  
 PN WO2003082345-A1.  
 PD 09-OCT-2003.  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 Best Local Similarity: 27.54% Mismatches: 41  
 Query Match: 6.04% Indels: 68  
 RESULT 1034  
 ID ABV21315 standard; cDNA; 3440 BP.  
 DE Human prostate expression marker cDNA 21306.

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PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 25.96% Mismatches: 81
Query Match: 6.04% Indels: 68
RESULT 1035
ID ABV27134 standard; cDNA; 3440 BP.
DE Human prostate expression marker cDNA 27125.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 25.96% Mismatches: 81
Query Match: 6.04% Indels: 68
RESULT 1036
ID ABV22159 standard; cDNA; 3440 BP.
DE Human prostate expression marker cDNA 22150.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 25.96% Mismatches: 81
Query Match: 6.04% Indels: 68
RESULT 1037
ID ABV27998 standard; cDNA; 3440 BP.
DE Human prostate expression marker cDNA 27989.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 25.96% Mismatches: 81
Query Match: 6.04% Indels: 68
RESULT 1038
ID ADS59759 standard; cDNA; 3462 BP.
DE Bacterial polynucleotide #11746.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 25.32% Mismatches: 84
Query Match: 6.04% Indels: 61
RESULT 1039
ID AAA97456 standard; cDNA; 3585 BP.
DE Human RalGDS (hralGDS) cDNA.
PN CN1257923-A.
PD 28-JUN-2000.
PA (UYFU-) UNIV FUDAN.
Best Local Similarity: 25.96% Mismatches: 81
Query Match: 6.04% Indels: 68
RESULT 1040
ID ABN67289 standard; DNA; 3632 BP.
DE Streptococcus polynucleotide SEQ ID NO 2491.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Best Local Similarity: 23.66% Mismatches: 123
Query Match: 6.04% Indels: 41
RESULT 1041
ID ADR07359 standard; cDNA; 3690 BP.
DE Full length human cDNA useful for treating neurological disease Seq 865.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 25.96% Mismatches: 81
Query Match: 6.04% Indels: 68
RESULT 1042
ID ABX93554 standard; cDNA; 3691 BP.
DE Human cDNA encoding GTP releasing factor 15368.
PN US2002187138-A1.
PD 12-DEC-2002.
PA (MEYE/) MEYERS R.
Best Local Similarity: 25.96% Mismatches: 81
Query Match: 6.04% Indels: 68
RESULT 1043
ID ADJ67856 standard; DNA; 3729 BP.
DE T. thermophilus dnaE gene.
PN US2004038289-A1.
PD 26-FEB-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
Best Local Similarity: 24.60% Mismatches: 97
Query Match: 6.04% Indels: 63
RESULT 1044
ID ADJ68068 standard; DNA; 3729 BP.
DE T. thermophilus dnaE gene.
PN US2004038290-A1.
PD 26-FEB-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
Best Local Similarity: 24.60% Mismatches: 97
Query Match: 6.04% Indels: 63
RESULT 1045
ID ADK01146 standard; DNA; 3729 BP.
DE DNA polymerase III-type enzyme subunit DNA #6.
PN US2004043415-A1.
PD 04-MAR-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
Best Local Similarity: 24.60% Mismatches: 97
Query Match: 6.04% Indels: 63
RESULT 1046
ID ADJ79365 standard; DNA; 3729 BP.
DE T. thermophilus dnaE gene.
PN US2004043414-A1.
PD 04-MAR-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
Best Local Similarity: 24.60% Mismatches: 97
Query Match: 6.04% Indels: 63
RESULT 1047
ID ADJ84805 standard; DNA; 3729 BP.
DE T. thermophilus DNA polymerase III alpha subunit gene.
PN US2004048309-A1.
PD 11-MAR-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
Best Local Similarity: 24.60% Mismatches: 97
Query Match: 6.04% Indels: 63
RESULT 1048
ID ADM77593 standard; DNA; 3729 BP.
DE DNA polymerase III-type enzyme related polynucleotide #4.
PN US2004077012-A1.
PD 22-APR-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.

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PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Best Local Similarity: 24.60%  
 Query Match: 6.04%  
 Mismatches: 97  
 Indels: 63  
 RESULT 1049  
 ID ADM66260 standard; DNA; 3729 BP.  
 DE T. thermophilus dnaE gene.  
 PN US2004081995-A1.  
 PD 29-APR-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Best Local Similarity: 24.60%  
 Query Match: 6.04%  
 Mismatches: 97  
 Indels: 63  
 RESULT 1050  
 ID AD004313 standard; DNA; 3729 BP.  
 DE T. thermophilus DNA polymerase III dnaE gene.  
 PN US2004106137-A1.  
 PD 03-JUN-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Best Local Similarity: 24.60%  
 Query Match: 6.04%  
 Mismatches: 97  
 Indels: 63  
 RESULT 1051  
 ID ADP82390 standard; DNA; 3729 BP.  
 DE Thermus thermophilus dnaE gene.  
 PN US2004110210-A1.  
 PD 10-JUN-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Best Local Similarity: 24.60%  
 Query Match: 6.04%  
 Mismatches: 97  
 Indels: 63  
 RESULT 1052  
 ID ABD14910 standard; DNA; 4401 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13514.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 24.77%  
 Query Match: 6.04%  
 Mismatches: 82  
 Indels: 66  
 RESULT 1053  
 ID ABL22547 standard; DNA; 4674 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 19114.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 22.14%  
 Query Match: 6.04%  
 Mismatches: 93  
 Indels: 87  
 RESULT 1054  
 ID AAK52952 standard; cDNA; 5537 BP.  
 DE Human polynucleotide SEQ ID NO 2481.  
 PN WO200157190-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 25.52%  
 Query Match: 6.04%  
 Mismatches: 97  
 Indels: 86  
 RESULT 1055  
 ID AAD28151 standard; DNA; 5628 BP.  
 DE Human secretion and trafficking DNA-6 (SAT-6).  
 PN WO200202610-A2.

PD 10-JAN-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 25.52%  
 Query Match: 6.04%  
 Mismatches: 97  
 Indels: 86  
 RESULT 1056  
 ID ABS78666 standard; DNA; 5871 BP.  
 DE S. ghanaensis DNA encoding PKSE.  
 PN CA2387401-A1.  
 PD 04-SEP-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Best Local Similarity: 25.85%  
 Query Match: 6.04%  
 Mismatches: 87  
 Indels: 39  
 RESULT 1057  
 ID ADM66776 standard; cDNA; 10011 BP.  
 DE Human pericentrin-B cDNA, SEQ ID NO:3.  
 PN WO2004024887-A2.  
 PD 25-MAR-2004.  
 PA (UYMA-) UNIV MASSACHUSETTS.  
 Best Local Similarity: 23.97%  
 Query Match: 6.04%  
 Mismatches: 104  
 Indels: 52  
 RESULT 1058  
 ID AAS74106 standard; cDNA; 10438 BP.  
 DE DNA encoding novel human diagnostic protein #9910.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 23.97%  
 Query Match: 6.04%  
 Mismatches: 104  
 Indels: 52  
 RESULT 1059  
 ID ADQ24969 standard; DNA; 10725 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7789.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Best Local Similarity: 23.97%  
 Query Match: 6.04%  
 Mismatches: 104  
 Indels: 52  
 RESULT 1060  
 ID AAZ55620 standard; DNA; 10877 BP.  
 DE Human BMP-7 gene 5' upstream region.  
 PN WO9957293-A1.  
 PD 11-NOV-1999.  
 PA (HMRI) HOECHST MARION ROUSSEL LTD.  
 Best Local Similarity: 23.34%  
 Query Match: 6.04%  
 Mismatches: 110  
 Indels: 78  
 RESULT 1061  
 ID ADH50604 standard; DNA; 13000 BP.  
 DE Human IRAK-1 associated DNA sequence #1.  
 PN US2003228690-A1.  
 PD 11-DEC-2003.  
 PA (ISIS-) ISIS PHARM INC.  
 Best Local Similarity: 24.56%  
 Query Match: 6.04%  
 Mismatches: 103  
 Indels: 84  
 RESULT 1062  
 ID AAH48621 standard; DNA; 13055 BP.  
 DE Human fascin DNA fragment #1.  
 PN WO200151631-A2.  
 PD 19-JUL-2001.  
 PA (RESK/) RESKE-KUNZ A.  
 PA (ROSS/) ROSS X.  
 PA (ROSS/) ROSS R.  
 PA (BROS/) BROS M.  
 Best Local Similarity: 27.65%  
 Query Match: 6.04%  
 Mismatches: 91  
 Indels: 42  
 RESULT 1063  
 ID AAH48620 standard; DNA; 16951 BP.  
 DE Human fascin DNA fragment SEQ ID 72.  
 PN WO200151631-A2.  
 PD 19-JUL-2001.  
 PA (RESK/) RESKE-KUNZ A.  
 PA (ROSS/) ROSS X.  
 PA (ROSS/) ROSS R.  
 PA (BROS/) BROS M.  
 Best Local Similarity: 27.65%  
 Query Match: 6.04%  
 Mismatches: 91  
 Indels: 42

Query Match: 6.04% Indels: 42  
 RESULT 1064  
 ID AAH4622 standard; DNA; 16951 BP.  
 DE Human fascin DNA fragment #2.  
 PN WO200151631-A2.  
 PD 19-JUL-2001.  
 PA (RESK/) RESK-KUNZ A.  
 PA (ROSS/) ROSS X.  
 PA (ROSS/) ROSS R.  
 PA (BROS/) BROS M.  
 Best Local Similarity: 27.65% Mismatches: 91  
 Query Match: 6.04% Indels: 42  
 RESULT 1065  
 ID ADI23928 standard; DNA; 18876 BP.  
 DE Streptomyces refuineus 024A locus ORF4.  
 PN US2003198981-A1.  
 PD 23-OCT-2003.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Best Local Similarity: 23.26% Mismatches: 118  
 Query Match: 6.04% Indels: 67  
 RESULT 1066  
 ID ABZ75344 standard; DNA; 23673 BP.  
 DE Human R1128 gene cluster.  
 PN US6340774-B1.  
 PD 22-JAN-2002.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 Best Local Similarity: 26.69% Mismatches: 80  
 Query Match: 6.04% Indels: 77  
 RESULT 1067  
 ID AAA11992 standard; DNA; 37856 BP.  
 DE S. cellulosum DNA encoding polyketide and hereropolyketide enzymes.  
 PN DE19846493-A1.  
 PD 13-APR-2000.  
 PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 Best Local Similarity: 25.94% Mismatches: 92  
 Query Match: 6.04% Indels: 83  
 RESULT 1068  
 ID ADI23920 standard; DNA; 61944 BP.  
 DE Streptomyces refuineus 024A locus (NRRL 3143).  
 PN US2003198981-A1.  
 PD 23-OCT-2003.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Best Local Similarity: 23.26% Mismatches: 118  
 Query Match: 6.04% Indels: 67  
 RESULT 1069  
 ID ADQ74672 standard; DNA; 74787 BP.  
 DE Streptomyces parvulus borrelidin polyketide synthase gene cluster.  
 Best Local Similarity: 21.74% Mismatches: 87  
 Query Match: 6.04% Indels: 119  
 RESULT 1070  
 ID ADL15447 standard; DNA; 85915 BP.  
 DE Streptomyces bikiniensis NRRL 2737 chalcomycin PKS cluster DNA.  
 PN WO2004018703-A2.  
 PD 04-MAR-2004.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Best Local Similarity: 23.87% Mismatches: 101  
 Query Match: 6.04% Indels: 112  
 RESULT 1071  
 ID ADP65471 standard; DNA; 92794 BP.  
 DE Human sequence from clone RP5-1009E24 on chromosome 20 DNA.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Best Local Similarity: 22.02% Mismatches: 97  
 Query Match: 6.04% Indels: 90  
 RESULT 1072  
 ID ABD33009 standard; DNA; 99918 BP.  
 DE Human cancer-associated genomic DNA HD21-032.  
 PN WO2004074320-A2.  
 PD 02-SEP-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Best Local Similarity: 25.90% Mismatches: 73  
 Query Match: 6.04% Indels: 90

RESULT 1073  
 Best Local Similarity: 23.05% Mismatches: 86  
 Query Match: 6.04% Indels: 88  
 RESULT 1074  
 Best Local Similarity: 23.05% Mismatches: 86  
 Query Match: 6.04% Indels: 88  
 RESULT 1075  
 ID ABL68122 standard; DNA; 174424 BP.  
 DE Ovary cancer related gene sequence SEQ ID NO:6459.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Best Local Similarity: 24.56% Mismatches: 103  
 Query Match: 6.04% Indels: 84  
 RESULT 1076  
 ID ADQ19573 standard; DNA; 181343 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2392.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Best Local Similarity: 24.56% Mismatches: 103  
 Query Match: 6.04% Indels: 84  
 RESULT 1077  
 ID ABD07796 standard; DNA; 636 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6400.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 25.84% Mismatches: 59  
 Query Match: 6.01% Indels: 55  
 RESULT 1078  
 ID ACA23440 standard; DNA; 864 BP.  
 DE Prokaryotic essential gene #5097.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITPA PHARM INC.  
 Best Local Similarity: 24.80% Mismatches: 96  
 Query Match: 6.01% Indels: 59  
 RESULT 1079  
 ID ABZ38524 standard; DNA; 933 BP.  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 1637.  
 PN WO200279243-A2.  
 PD 10-OCT-2002.  
 PA (CHIR-) CHIRON SPA.  
 Best Local Similarity: 22.02% Mismatches: 67  
 Query Match: 6.01% Indels: 46  
 RESULT 1080  
 ID ABD06399 standard; DNA; 981 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5003.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 6.01% Indels: 86  
 RESULT 1081  
 ID ABD09462 standard; DNA; 993 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8066.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 19.57% Mismatches: 84  
 Query Match: 6.01% Indels: 106  
 RESULT 1082  
 ID ABD15086 standard; DNA; 1014 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13690.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 25.58% Mismatches: 108  
 Query Match: 6.01% Indels: 82  
 RESULT 1083  
 ID ABD10877 standard; DNA; 1083 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9481.

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PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 25.27%
Query Match: 6.01%
Mismatch: 64
Indel: 57
RESULT 1084
ID ABI07351 standard; cDNA; 1142 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16535.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 21.15%
Query Match: 6.01%
Mismatch: 97
Indel: 89
RESULT 1085
ID ADC32623 standard; cDNA; 1160 BP.
DE Human novel cDNA contig sequence, SEQ ID NO:2705.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 28.52%
Query Match: 6.01%
Mismatch: 85
Indel: 79
RESULT 1086
ID AAS67936 standard; cDNA; 1164 BP.
DE DNA encoding novel human diagnostic protein #3740.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 23.53%
Query Match: 6.01%
Mismatch: 113
Indel: 79
RESULT 1087
ID ABD03878 standard; DNA; 1179 BP.
DE Pseudomonas aeruginosa polynucleotide #2482.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 25.20%
Query Match: 6.01%
Mismatch: 95
Indel: 66
RESULT 1088
ID AAT18237 standard; DNA; 1233 BP.
DE Pro-urokinase gene.
PN WO9604004-A1.
PD 15-FEB-1996.
PA (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
Best Local Similarity: 24.00%
Query Match: 6.01%
Mismatch: 88
Indel: 60
RESULT 1089
ID AAT68797 standard; DNA; 1233 BP.
DE Coding sequence for pro-urokinase.
PN US5626841-A.
PD 06-MAY-1997.
PA (GURE/) GUREWICH V.
Best Local Similarity: 24.00%
Query Match: 6.01%
Mismatch: 88
Indel: 60
RESULT 1090
ID AAT61671 standard; cDNA; 1236 BP.
DE Human native prourokinase cDNA.
PN EP398361-A.
PD 22-NOV-1990.
PA (GREC) GREEN CROSS CORP.
Best Local Similarity: 24.00%
Query Match: 6.01%
Mismatch: 88
Indel: 60
RESULT 1091
ID AA041450 standard; DNA; 1236 BP.
DE Mutant human prourokinase gene.
PN EP541952-A1.
PD 19-MAY-1993.
PA (GREC) GREEN CROSS CORP.
Best Local Similarity: 24.00%
Query Match: 6.01%
Mismatch: 88
Indel: 60
RESULT 1092
ID AAQ48228 standard; DNA; 1236 BP.
DE FUK gene.
PN JP05192142-A.
PD 03-AUG-1993.
PA (GREC) GREEN CROSS CORP.
Best Local Similarity: 24.00%
Query Match: 6.01%
Mismatch: 88
Indel: 60
RESULT 1093
ID AAD27077 standard; DNA; 1236 BP.
DE Human urokinase-type plasminogen activator tcuPA and scuPA DNA.
PN WO200197752-A2.
PD 27-DEC-2001.
PA (UYPE-) UNIV PENNSYLVANIA.
Best Local Similarity: 24.00%
Query Match: 6.01%
Mismatch: 88
Indel: 60
RESULT 1094
ID ABD03749 standard; DNA; 1341 BP.
DE Pseudomonas aeruginosa polynucleotide #2353.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 25.20%
Query Match: 6.01%
Mismatch: 95
Indel: 66
RESULT 1095
ID AD747038 standard; cDNA; 1365 BP.
DE Bacterial polynucleotide #21789.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 28.17%
Query Match: 6.01%
Mismatch: 70
Indel: 84
RESULT 1096
ID ABD03960 standard; DNA; 1398 BP.
DE Pseudomonas aeruginosa polynucleotide #2564.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 25.20%
Query Match: 6.01%
Mismatch: 95
Indel: 66
RESULT 1097
ID ABD11805 standard; DNA; 1398 BP.
DE Pseudomonas aeruginosa polynucleotide #10409.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 27.84%
Query Match: 6.01%
Mismatch: 109
Indel: 51
RESULT 1098
ID ACA43969 standard; DNA; 1407 BP.
DE Prokaryotic essential gene #25626.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 22.84%
Query Match: 6.01%
Mismatch: 97
Indel: 95
RESULT 1099
ID ACA45499 standard; DNA; 1413 BP.
DE Prokaryotic essential gene #27156.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 21.15%
Query Match: 6.01%
Mismatch: 102
Indel: 82
RESULT 1100
ID ABD12148 standard; DNA; 1446 BP.
DE Pseudomonas aeruginosa polynucleotide #10752.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 27.84%
Query Match: 6.01%
Mismatch: 109
Indel: 51
RESULT 1101

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ID ACA42073 standard; DNA; 1480 BP.  
 DE Prokaryotic essential Gene #23730.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 26.27% Mismatches: 107  
 Query Match: 6.01% Indels: 43  
 RESULT 1102

ID AAC43474 standard; DNA; 1491 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 39370.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Best Local Similarity: 25.00% Mismatches: 104  
 Query Match: 6.01% Indels: 20  
 RESULT 1103

ID AB214815 standard; DNA; 1491 BP.  
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2620.  
 PN WO200216655-A2.  
 PD 28-FEB-2002.  
 PA (SCRI ) SCRIPPS RES INST.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 25.00% Mismatches: 104  
 Query Match: 6.01% Indels: 20  
 RESULT 1104

ID ADN73354 standard; cDNA; 1491 BP.  
 DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1249.  
 PN WO2004035798-A2.  
 PD 29-APR-2004.  
 PA (CROP-) CROPDISEIGN NV.  
 Best Local Similarity: 25.00% Mismatches: 104  
 Query Match: 6.01% Indels: 20  
 RESULT 1105

ID AAA09191 standard; DNA; 1500 BP.  
 DE Trametes versicolor laccase coding sequence.  
 PN WO200020615-A2.  
 PD 13-APR-2000.  
 PA (PROD-) PRODIGENE INC.  
 Best Local Similarity: 22.40% Mismatches: 117  
 Query Match: 6.01% Indels: 83  
 RESULT 1106

ID ABA92910 standard; cDNA; 1500 BP.  
 DE Trametes versicolor laccase I gene.  
 PN WO200196543-A2.  
 PD 20-DEC-2001.  
 PA (PROD-) PRODIGENE INC.  
 PA (GENV ) GENENCOR INC.  
 Best Local Similarity: 22.40% Mismatches: 117  
 Query Match: 6.01% Indels: 83  
 RESULT 1107

ID ABO94267 standard; DNA; 1728 BP.  
 DE loVF gene expression regulator At240 coding sequence.  
 PN WO200257456-A2.  
 PD 25-JUL-2002.  
 PA (MICR-) MICROBIA.  
 Best Local Similarity: 19.81% Mismatches: 101  
 Query Match: 6.01% Indels: 110  
 RESULT 1108

ID ABN79911 standard; DNA; 1728 BP.  
 DE Fungal ZBC gene sequence #148.  
 PN WO200224865-A2.  
 PD 28-MAR-2002.  
 PA (MICR-) MICROBIA INC.  
 Best Local Similarity: 19.81% Mismatches: 101  
 Query Match: 6.01% Indels: 110  
 RESULT 1109

ID ADA69634 standard; DNA; 1845 BP.  
 DE Rice gene, SEQ ID 2957.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 22.60% Mismatches: 83  
 Query Match: 6.01% Indels: 125  
 RESULT 1110

ID ABD08028 standard; DNA; 1848 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6632.  
 PN US551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 26.27% Mismatches: 107  
 Query Match: 6.01% Indels: 43  
 RESULT 1111

ID AAC49857 standard; DNA; 1883 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 62696.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Best Local Similarity: 25.00% Mismatches: 104  
 Query Match: 6.01% Indels: 20  
 RESULT 1112

ID ADG55901 standard; cDNA; 1923 BP.  
 DE Bacterial polynucleotide #7888.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 24.69% Mismatches: 86  
 Query Match: 6.01% Indels: 73  
 RESULT 1113

ID ABD08626 standard; DNA; 1932 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7230.  
 PN US551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 22.77% Mismatches: 97  
 Query Match: 6.01% Indels: 125  
 RESULT 1114

ID ABO30350 standard; DNA; 1986 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1654.  
 PN US551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 23.51% Mismatches: 98  
 Query Match: 6.01% Indels: 123  
 RESULT 1115

ID ADS14561 standard; DNA; 1995 BP.  
 DE Pseudomonas aeruginosa quorum sensing controlled gene PA1251, SEQ ID 116.  
 PN WO2004083385-A2.  
 PD 30-SEP-2004.  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 Best Local Similarity: 19.57% Mismatches: 84  
 Query Match: 6.01% Indels: 106  
 RESULT 1116

ID AQ032857 standard; DNA; 2027 BP.  
 DE Mutant bovine herpes virus type 1 - deletion in gE gene.  
 PN WO9221751-A1.  
 PD 10-DEC-1992.  
 PA (DIER-) STICHTING CENT DIERGENESKUNDIG INST.  
 Best Local Similarity: 25.93% Mismatches: 120  
 Query Match: 6.01% Indels: 49  
 RESULT 1117

ID AAQ36769 standard; DNA; 2040 BP.  
 DE Sequence of the IBR glycoprotein E gene.  
 PN WO9302104-A1.  
 PD 04-FEB-1993.  
 PA (SVTR ) SYNTRO CORP.  
 Best Local Similarity: 23.34% Mismatches: 115  
 Query Match: 6.01% Indels: 93  
 RESULT 1118

ID AAQ97671 standard; DNA; 2040 BP.  
 DE Infectious bovine rhinotracheitis virus glycoprotein E gene.  
 PN WO9521261-A1.  
 PD 10-AUG-1995.  
 PA (SVTR ) SYNTRO CORP.  
 Best Local Similarity: 23.34% Mismatches: 115  
 Query Match: 6.01% Indels: 93  
 RESULT 1119

Query Match: 6.01% Indels: 93  
RESULT 1119  
ID ABD09392 standard; DNA; 2046 BP.  
DE Pseudomonas aeruginosa polynucleotide #7996.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 25.71% Mismatches: 78  
Query Match: 6.01% Indels: 57  
RESULT 1120  
ID ABD09454 standard; DNA; 2046 BP.  
DE Pseudomonas aeruginosa polynucleotide #8058.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 25.71% Mismatches: 78  
Query Match: 6.01% Indels: 57  
RESULT 1121  
ID ABD09591 standard; DNA; 2121 BP.  
DE Pseudomonas aeruginosa polynucleotide #8195.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 25.71% Mismatches: 78  
Query Match: 6.01% Indels: 57  
RESULT 1122  
ID AAT03824 standard; DNA; 2336 BP.  
DE Bovine herpesvirus-1 FM gII glycoprotein gene.  
PN EP668356-A2.  
PD 23-AUG-1995.  
PA (HIPR-) LAB HIPRA SA.  
Best Local Similarity: 25.93% Mismatches: 120  
Query Match: 6.01% Indels: 49  
RESULT 1123  
ID AAH17671 standard; cDNA; 2348 BP.  
DE Human cDNA sequence SEQ ID NO:17236.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Best Local Similarity: 24.51% Mismatches: 86  
Query Match: 6.01% Indels: 74  
RESULT 1124  
ID ABD08027 standard; DNA; 2715 BP.  
DE Pseudomonas aeruginosa polynucleotide #6631.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 26.27% Mismatches: 107  
Query Match: 6.01% Indels: 43  
RESULT 1125  
ID ABD09507 standard; DNA; 2727 BP.  
DE Pseudomonas aeruginosa polynucleotide #8111.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 19.57% Mismatches: 84  
Query Match: 6.01% Indels: 106  
RESULT 1126  
ID ADRO7670 standard; cDNA; 2732 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 1176.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 25.89% Mismatches: 112  
Query Match: 6.01% Indels: 80  
RESULT 1127  
ID ABD08863 standard; DNA; 2898 BP.  
DE Pseudomonas aeruginosa polynucleotide #7467.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 22.77% Mismatches: 97  
Query Match: 6.01% Indels: 125

RESULT 1128  
ID ABT43728 standard; cDNA; 3181 BP.  
DE Molecule for disease detection and treatment (MDDT)-36 cDNA sequence.  
PN WO2003052049-A2.  
PD 26-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 23.16% Mismatches: 90  
Query Match: 6.01% Indels: 99  
RESULT 1129  
ID ADM87438 standard; cDNA; 3376 BP.  
DE Human EST derived nucleotide sequence SEQ ID NO:531.  
PN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Best Local Similarity: 25.40% Mismatches: 80  
Query Match: 6.01% Indels: 76  
RESULT 1130  
ID ADC59315 standard; DNA; 3399 BP.  
DE DNA encoding human polypeptide #4.  
PN JP2002360268-A.  
PD 17-DEC-2002.  
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
PA (DAUC) DAIICHI PHARM CO LTD.  
Best Local Similarity: 20.23% Mismatches: 103  
Query Match: 6.01% Indels: 58  
RESULT 1131  
ID ACA42576 standard; DNA; 3636 BP.  
DE Prokaryotic essential gene #24233.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 26.27% Mismatches: 107  
Query Match: 6.01% Indels: 43  
RESULT 1132  
ID ABD08062 standard; DNA; 3702 BP.  
DE Pseudomonas aeruginosa polynucleotide #6666.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 26.27% Mismatches: 107  
Query Match: 6.01% Indels: 43  
RESULT 1133  
ID AAQ55350 standard; DNA; 4190 BP.  
DE Sequence of the unique short (Us) region of bovine herpes virus (BHV)  
DE which forms the insertion region and comprises 3 open reading frames.  
PN WO9400586-A2.  
PD 06-JAN-1994.  
PA (INNR) RHONE MERIEUX SA.  
Best Local Similarity: 25.93% Mismatches: 120  
Query Match: 6.01% Indels: 49  
RESULT 1134  
ID AAD54622 standard; DNA; 4989 BP.  
DE Human Mastermind (Mam) homologue DNA, MAML2.  
PN WO2002102987-A2.  
PD 27-DEC-2002.  
PA (GEHO) GEN HOSPITAL CORP.  
Best Local Similarity: 20.23% Mismatches: 103  
Query Match: 6.01% Indels: 58  
RESULT 1135  
ID ABA91314 standard; DNA; 6650 BP.  
DE Human colon specific gene 203640.  
PN WO200192528-A2.  
PD 06-DEC-2001.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 22.11% Mismatches: 104  
Query Match: 6.01% Indels: 114  
RESULT 1136  
ID AAK70210 standard; DNA; 7885 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25022.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 25.48% Mismatches: 69

Query Match: 6.01% Indels: 60  
 RESULT 1137  
 ID ABT07614 standard; cDNA; 8156 BP.  
 DE Human breast cancer associated coding sequence SEQ ID NO: 93..  
 PN WO200264611-A1.  
 PD 22-AUG-2002.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 24.10% Mismatches: 65  
 Query Match: 6.01% Indels: 66  
 RESULT 1138  
 ID AAS32754 standard; DNA; 9134 BP.  
 DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 708.  
 PN WO200155319-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 26.57% Mismatches: 101  
 Query Match: 6.01% Indels: 70  
 RESULT 1139  
 ID ABZ22017 standard; cDNA; 9646 BP.  
 DE Human leukaemia associated CML nucleotide sequence SEQ ID NO:2.  
 PN CN1356390-A.  
 PD 03-JUL-2002.  
 PA (UYHO-) UNIV HOSPITAL NO 2 ATTACHED TO MEDICAL C.  
 Best Local Similarity: 26.67% Mismatches: 69  
 Query Match: 6.01% Indels: 50  
 RESULT 1140  
 ID AAL61173 standard; DNA; 9975 BP.  
 DE Actinosynnema pretiosum polyketide synthase (PKS) gene #4.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Best Local Similarity: 24.50% Mismatches: 94  
 Query Match: 6.01% Indels: 74  
 RESULT 1141  
 ID ABU50560 standard; DNA; 14071 BP.  
 DE Micromonospora carbonacea everninomicin locus nucleotide contig 6.  
 PN WO200155180-A2.  
 PD 02-AUG-2001.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Best Local Similarity: 24.92% Mismatches: 121  
 Query Match: 6.01% Indels: 69  
 RESULT 1142  
 ID ACA19579 standard; DNA; 15450 BP.  
 DE Prokaryotic essential gene #1236.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (BLIT-) ELITRA PHARM INC.  
 Best Local Similarity: 26.46% Mismatches: 89  
 Query Match: 6.01% Indels: 79  
 RESULT 1143  
 ID AAV233494 standard; DNA; 17612 BP.  
 DE Pseudomonas Xpc, OrfV, OrfX, OrfY operon.  
 PN WO9806836-A2.  
 PD 19-FEB-1998.  
 PA (GENV) GENENCOR INT INC.  
 Best Local Similarity: 24.34% Mismatches: 105  
 Query Match: 6.01% Indels: 77  
 RESULT 1144  
 ID AAA13905 standard; DNA; 17612 BP.  
 DE Pseudomonas alcaligenes nucleotide sequence SEQ ID NO:29.  
 PN US6048710-A.  
 PD 11-APR-2000.  
 PA (GENV) GENENCOR INT INC.  
 Best Local Similarity: 24.34% Mismatches: 105  
 Query Match: 6.01% Indels: 77  
 RESULT 1145  
 ID AAP30870 standard; DNA; 17612 BP.  
 DE Pseudomonas alcaligenes secretion factor gene region.  
 PN US6225106-B1.  
 PD 01-MAY-2001.  
 PA (GENV) GENENCOR INT INC.  
 Best Local Similarity: 24.34% Mismatches: 105

Query Match: 6.01% Indels: 77  
 RESULT 1146  
 ID AAD22882 standard; DNA; 17612 BP.  
 DE Pseudomonas alcaligenes 17.612 bp DNA from the insert on cosmid #600.  
 PN US6313283-B1.  
 PD 06-NOV-2001.  
 PA (GENV) GENENCOR INT INC.  
 Best Local Similarity: 24.34% Mismatches: 105  
 Query Match: 6.01% Indels: 77  
 RESULT 1147  
 ID ADA03092 standard; DNA; 29322 BP.  
 DE Human LFNG carcinoma associated gene, SEQ ID NO:1610.  
 PN WO2003057146-A2.  
 PD 17-JUL-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Best Local Similarity: 22.57% Mismatches: 104  
 Query Match: 6.01% Indels: 76  
 RESULT 1148  
 ID ADA66376 standard; DNA; 29322 BP.  
 DE Human LFNG gene genomic DNA sequence.  
 PN WO2003053224-A2.  
 PD 03-JUL-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Best Local Similarity: 22.57% Mismatches: 104  
 Query Match: 6.01% Indels: 76  
 RESULT 1149  
 ID ADB72830 standard; DNA; 29322 BP.  
 DE Human LFNG gene.  
 PN WO2003008583-A2.  
 PD 30-JAN-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Best Local Similarity: 22.57% Mismatches: 104  
 Query Match: 6.01% Indels: 76  
 RESULT 1150  
 ID ABZ66811 standard; DNA; 48221 BP.  
 DE Orthomyxovirus biosynthetic gene cluster SEQ ID NO 280.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Best Local Similarity: 24.92% Mismatches: 121  
 Query Match: 6.01% Indels: 69  
 RESULT 1151  
 ID AAD55810 standard; DNA; 60196 BP.  
 DE Micromonospora carbonacea polyketide synthase (PKS) type I gene cluster.  
 PN CA2391131-A1.  
 PD 19-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Best Local Similarity: 23.56% Mismatches: 96  
 Query Match: 6.01% Indels: 47  
 RESULT 1152  
 ID AAK83212 standard; DNA; 68356 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38024.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.19% Mismatches: 94  
 Query Match: 6.01% Indels: 87  
 RESULT 1153  
 ID AAK67283 standard; DNA; 68356 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22095.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.19% Mismatches: 94  
 Query Match: 6.01% Indels: 87  
 RESULT 1154  
 ID AAL61224 standard; DNA; 82746 BP.  
 DE Actinosynnema pretiosum aneamitocin biosynthetic gene cluster I.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Best Local Similarity: 27.95% Mismatches: 96  
 Query Match: 6.01% Indels: 43



RESULT 1155  
 Best Local Similarity: 26.98% Mismatches: 99  
 Query Match: 6.01% Indels: 76  
 RESULT 1156  
 Best Local Similarity: 29.17% Mismatches: 64  
 Query Match: 6.01% Indels: 44  
 RESULT 1157  
 Best Local Similarity: 29.17% Mismatches: 64  
 Query Match: 6.01% Indels: 44  
 RESULT 1158  
 ID ABS56565 standard; DNA; 171936 BP.  
 DE Human SULF2 genomic DNA sequence.  
 PN WO200259327-A2.  
 PD 01-AUG-2002.  
 PA (REGC ) UNIV CALIFORNIA.  
 Best Local Similarity: 23.08% Mismatches: 69  
 Query Match: 6.01% Indels: 79  
 RESULT 1159  
 ID ADN16205 standard; DNA; 171936 BP.  
 DE Mouse sulfatase SULF2 gene.  
 PN WO2004011365-A2.  
 PD 15-APR-2004.  
 PA (REGC ) UNIV CALIFORNIA.  
 Best Local Similarity: 23.08% Mismatches: 69  
 Query Match: 6.01% Indels: 79  
 RESULT 1160  
 ID AAH68534 standard; DNA; 309400 BP.  
 DE C Glutamicum coding sequence fragment SEQ ID NO: 7069.  
 PN EP108790-A2.  
 PD 20-JUN-2001.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 Best Local Similarity: 25.35% Mismatches: 91  
 Query Match: 6.01% Indels: 42  
 RESULT 1161  
 ID ABQ81842 standard; DNA; 349980 BP.  
 DE Bifidobacterium longum NCC2705 genomic sequence SEQ ID NO:1.  
 PN EP1227152-A1.  
 PD 31-JUL-2002.  
 PA (NEST ) SOC PROD NESTLE SA.  
 Best Local Similarity: 23.84% Mismatches: 105  
 Query Match: 6.01% Indels: 80  
 RESULT 1162  
 ID ADK56808 standard; DNA; 651 BP.  
 DE Plant DNA sequence which confers altered metabolic characteristic #4191.  
 PN WO2003020936-A1.  
 PD 13-MAR-2003.  
 PA (DOWC ) DOW CHEM CO.  
 Best Local Similarity: 22.03% Mismatches: 74  
 Query Match: 5.97% Indels: 37  
 RESULT 1163  
 ID ADA70766 standard; DNA; 783 BP.  
 DE Rice gene, SEQ ID 4089.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 29.45% Mismatches: 54  
 Query Match: 5.97% Indels: 48  
 RESULT 1164  
 ID ABZ11237 standard; cDNA; 866 BP.  
 DE Human polynucleotide SEQ ID NO 119.  
 PN WO200270539-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 24.76% Mismatches: 113  
 Query Match: 5.97% Indels: 90  
 RESULT 1165  
 ID ADM43755 standard; cDNA; 866 BP.  
 DE Novel human arginine-rich protein cDNA #119.  
 PN US2004053250-A1.  
 PD 18-MAR-2004.  
 PA (TANG/) TANG Y T.

PA (XUEA/) XUE A.  
 PA (DRMA/) DRMANAC R T.  
 Best Local Similarity: 24.76% Mismatches: 113  
 Query Match: 5.97% Indels: 90  
 RESULT 1166  
 ID ABL55081 standard; DNA; 1015 BP.  
 DE Human cDNA sequence #1 from clone HVARW53.  
 PN WO200222638-A1.  
 PD 21-MAR-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.26% Mismatches: 113  
 Query Match: 5.97% Indels: 84  
 RESULT 1167  
 ID ADA40227 standard; cDNA; 1015 BP.  
 DE Human secreted protein encoding cDNA.  
 PN WO2002102993-A2.  
 PD 27-DEC-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.26% Mismatches: 113  
 Query Match: 5.97% Indels: 84  
 RESULT 1168  
 ID ADC73753 standard; DNA; 1015 BP.  
 DE Human secreted protein-related DNA - SEQ ID 386.  
 PN WO2003038063-A2.  
 PD 08-MAY-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.26% Mismatches: 113  
 Query Match: 5.97% Indels: 84  
 RESULT 1169  
 ID AAS66980 standard; cDNA; 1026 BP.  
 DE DNA encoding novel human diagnostic protein #2784.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 24.87% Mismatches: 80  
 Query Match: 5.97% Indels: 41  
 RESULT 1170  
 ID AAT41786 standard; DNA; 1047 BP.  
 DE Fusion peptide #1 having G-CSF and TPO activity.  
 PN WO9634016-A1.  
 PD 31-OCT-1996.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 Best Local Similarity: 28.38% Mismatches: 97  
 Query Match: 5.97% Indels: 42  
 RESULT 1171  
 ID ABZ14593 standard; DNA; 1062 BP.  
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2398.  
 PN WO200216655-A2.  
 PD 28-FEB-2002.  
 PA (Scri ) SCRIPPS RES INST.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 20.96% Mismatches: 99  
 Query Match: 5.97% Indels: 85  
 RESULT 1172  
 ID ADG87742 standard; cDNA; 1062 BP.  
 DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #184.  
 PN WO200222675-A2.  
 PD 21-MAR-2002.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 PA (UNYC-) UNIV NORTH CAROLINA.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (WANG/) WANG X.  
 PA (DANG/) DANG J L.  
 PA (EULG/) EULGEM T.  
 PA (ZHUT/) ZHU T.  
 Best Local Similarity: 20.96% Mismatches: 99  
 Query Match: 5.97% Indels: 85  
 RESULT 1173  
 ID ADAG8341 standard; DNA; 1062 BP.  
 DE Arabidopsis thaliana gene, SEQ ID 793.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

Best Local Similarity: 20.96% Mismatches: 99  
 Query Match: 5.97% Indels: 85  
 RESULT 1174  
 ID AAS78523 standard; cDNA; 1218 BP.  
 DE DNA encoding novel human diagnostic protein #14327.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 22.83% Mismatches: 81  
 Query Match: 5.97% Indels: 90  
 RESULT 1175  
 ID ABD04990 standard; DNA; 1254 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3594.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 24.83% Mismatches: 100  
 Query Match: 5.97% Indels: 96  
 RESULT 1176  
 ID AAC47583 standard; DNA; 1267 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 54355.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Best Local Similarity: 20.96% Mismatches: 99  
 Query Match: 5.97% Indels: 85  
 RESULT 1177  
 ID ACA41158 standard; DNA; 1296 BP.  
 DE Prokaryotic essential gene #28815.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 20.54% Mismatches: 91  
 Query Match: 5.97% Indels: 113  
 RESULT 1178  
 ID ABZ39320 standard; DNA; 1302 BP.  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 3229.  
 PN WO200279243-A2.  
 PD 10-OCT-2002.  
 PA (CHIR-) CHIRON SPA.  
 Best Local Similarity: 20.54% Mismatches: 91  
 Query Match: 5.97% Indels: 113  
 RESULT 1179  
 ID AAQ13898 standard; DNA; 1307 BP.  
 DE araC gene.  
 PN WO9113978-A.  
 PD 19-SEP-1991.  
 PA (TRIN-) TRINITY COLLEGE DUB.  
 Best Local Similarity: 25.79% Mismatches: 94  
 Query Match: 5.97% Indels: 50  
 RESULT 1180  
 ID AAZ54386 standard; DNA; 1311 BP.  
 DE Neisseria gonorrhoeae ORF 904 partial DNA sequence SEQ ID NO:2721.  
 PN WO9957280-A2.  
 PD 11-NOV-1999.  
 PA (CHIR-) CHIRON CORP.  
 Best Local Similarity: 20.54% Mismatches: 91  
 Query Match: 5.97% Indels: 113  
 RESULT 1181  
 ID AAS54377 standard; DNA; 1365 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #508.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 25.35% Mismatches: 99  
 Query Match: 5.97% Indels: 86  
 RESULT 1182  
 ID ACA42795 standard; DNA; 1365 BP.  
 DE Prokaryotic essential gene #24452.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 25.35% Mismatches: 99

Query Match: 5.97% Indels: 86  
 RESULT 1183  
 ID ABD10565 standard; DNA; 1470 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9169.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 24.62% Mismatches: 118  
 Query Match: 5.97% Indels: 50  
 RESULT 1184  
 ID ADS60780 standard; cDNA; 1473 BP.  
 DE Bacterial polynucleotide #12767.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 23.63% Mismatches: 100  
 Query Match: 5.97% Indels: 57  
 RESULT 1185  
 ID AAN70356 standard; cDNA to mRNA; 1475 BP.  
 DE Human urine-derived high molecular weight type urokinase A and B-chain pre-structural gene.  
 PN EP232544-A.  
 PD 19-AUG-1987.  
 PA (GREC) GREEN CROSS CORP.  
 Best Local Similarity: 23.05% Mismatches: 96  
 Query Match: 5.97% Indels: 73  
 RESULT 1186  
 ID AD744663 standard; cDNA; 1487 BP.  
 DE Bacterial polynucleotide #19414.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 21.14% Mismatches: 86  
 Query Match: 5.97% Indels: 78  
 RESULT 1187  
 ID AAS89540 standard; cDNA; 1569 BP.  
 DE DNA encoding novel human diagnostic protein #25344.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 22.94% Mismatches: 91  
 Query Match: 5.97% Indels: 57  
 RESULT 1188  
 ID AAS77802 standard; cDNA; 1569 BP.  
 DE DNA encoding novel human diagnostic protein #13606.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 22.94% Mismatches: 91  
 Query Match: 5.97% Indels: 57  
 RESULT 1189  
 ID ADK12502 standard; DNA; 1584 BP.  
 DE Human NAC-1 coding sequence #2.  
 PN US2003100495-A1.  
 PD 29-MAY-2003.  
 PA (ZHAN/) ZHANG J.  
 Best Local Similarity: 25.33% Mismatches: 94  
 Query Match: 5.97% Indels: 44  
 RESULT 1190  
 ID ADK12501 standard; DNA; 1589 BP.  
 DE Human NAC-1 coding sequence #1.  
 PN US2003100495-A1.  
 PD 29-MAY-2003.  
 PA (ZHAN/) ZHANG J.  
 Best Local Similarity: 25.33% Mismatches: 94

Query Match:	5.97%	Indels:	44
RESULT 1191			
ID ADS60286 standard; CDNA; 1746 BP.			
DE Bacterial polynucleotide #12273.			
PD US2003233675-A1.			
PD 18-DEC-2003.			
PA (CAOY/) CAO Y.			
PA (HINK/) HINKLE G J.			
PA (SLAT/) SLATER S C.			
PA (CHEN/) CHEN X.			
PA (GOLD/) GOLDMAN B S.			
Best Local Similarity: 23.41%		Mismatches:	94
Query Match:	5.97%	Indels:	140
RESULT 1192			
ID ABD10193 standard; DNA; 1764 BP.			
DE Pseudomonas aeruginosa polynucleotide #8797.			
PD US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 24.62%		Mismatches:	118
Query Match:	5.97%	Indels:	50
RESULT 1193			
ID ABD05170 standard; DNA; 1785 BP.			
DE Pseudomonas aeruginosa polynucleotide #3774.			
PD US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 24.83%		Mismatches:	100
Query Match:	5.97%	Indels:	96
RESULT 1194			
ID ADQ83596 standard; CDNA; 1804 BP.			
DE Human tumour-associated antigenic target (TAT) CDNA sequence #410.			
PD WO2004060270-A2.			
PD 22-JUL-2004.			
PA (GETH) GENENTECH INC.			
PA (WUTD/) WU T D.			
PA (ZHOU/) ZHOU Y.			
Best Local Similarity: 25.33%		Mismatches:	94
Query Match:	5.97%	Indels:	44
RESULT 1195			
ID ABS55879 standard; CDNA; 1881 BP.			
DE Human polynucleotide #5.			
PD US2002127199-A1.			
PD 12-SEP-2002.			
PA (TANG/) TANG Y T.			
PA (ZHOU/) ZHOU P.			
PA (GOOD/) GOODRICH R.			
PA (ASUN/) ASUNDI V.			
PA (YANG/) YANG Y.			
PA (ZHAN/) ZHANG J.			
PA (WEHR/) WEHRMAN T.			
PA (DRNA/) DRMANAC R T.			
Best Local Similarity: 25.33%		Mismatches:	94
Query Match:	5.97%	Indels:	44
RESULT 1196			
ID ADJ92543 standard; DNA; 1881 BP.			
DE Human DNA #5 of the invention.			
PD US2004013657-A1.			
PD 22-JAN-2004.			
PA (TANG/) TANG Y T.			
PA (ASUN/) ASUNDI V.			
PA (WEHR/) WEHRMAN T.			
PA (YANG/) YANG Y.			
PA (ZHAN/) ZHANG J.			
PA (ZHOU/) ZHOU P.			
PA (DRNA/) DRMANAC R T.			
PA (GOOD/) GOODRICH R.			
Best Local Similarity: 25.33%		Mismatches:	94
Query Match:	5.97%	Indels:	44
RESULT 1197			
ID ADB61949 standard; CDNA; 1904 BP.			
DE Human cDNA encoding clone BRACE20061620.			
PD EP1308459-A2.			
PD 07-MAY-2003.			
PA (HELI-) HELIX RES INST.			
PA (REAS-) RES ASSOC BIOTECHNOLOGY.			
Best Local Similarity: 27.20%		Mismatches:	82
Query Match:	5.97%	Indels:	75
RESULT 1198			
ID ABO86145 standard; DNA; 2004 BP.			
DE Novel human gene. SEQ ID 16.			
PD WO200250105-A1.			
PD 27-JUN-2002.			
PA (SMIK) SMITHKLINE BEECHAM CORP.			
PA (SMIK) SMITHKLINE BEECHAM PLC.			
PA (GLAX) GLAXO GROUP LTD.			
Best Local Similarity: 24.30%		Mismatches:	93
Query Match:	5.97%	Indels:	91
RESULT 1199			
ID ADO67473 standard; CDNA; 2098 BP.			
DE Novel human cDNA sequence #2446.			
PD EP140981-A2.			
PD 28-JUL-2004.			
PA (REAS-) RES ASSOC BIOTECHNOLOGY.			
Best Local Similarity: 27.20%		Mismatches:	82
Query Match:	5.97%	Indels:	75
RESULT 1200			
ID ABX97046 standard; CDNA; 2214 BP.			
DE Human NOV22a CDNA.			
PD WO200272757-A2.			
PD 19-SEP-2002.			
PA (CURA-) CURAGEN CORP.			
Best Local Similarity: 25.33%		Mismatches:	94
Query Match:	5.97%	Indels:	44
RESULT 1201			
ID ADNG1808 standard; CDNA; 2214 BP.			
DE Human cDNA encoding NOV22a.			
PD US2004043382-A1.			
PD 04-MAR-2004.			
PA (PADI) PADIGARU M.			
PA (SPVT) SPYTEK K A.			
PA (SHEN) SHENOV S G.			
PA (TAUP) TAUPIER R J.			
PA (PENA) PENA C E A.			
PA (LILL) LI L.			
PA (ZERH) ZERHUSEN B D.			
PA (GUSE) GUSEV V Y.			
PA (JIWJ) JI W.			
PA (GORM) GORMAN L.			
PA (MILL) MILLER C E.			
PA (KEKU) KEKUDA R.			
PA (PATT) PATTURAJAN M.			
PA (GANG) GANGOLLI E A.			
PA (VERN) VERNET C A M.			
PA (GUOX) GUO X S.			
PA (TCHE) TCHERNEV V T.			
PA (FERN) FERNANDES E R.			
PA (CASM) CASMAN S J.			
PA (MALY) MALYANKAR U M.			
PA (GERL) GERLACH V.			
PA (LIUY) LIU Y.			
PA (ANDE) ANDERSON D W.			
PA (SPAD) SPADERNA S K.			
PA (CATT) CATTERTON E.			
PA (LEIT) LEITE M W.			
PA (ZHON) ZHONG H.			
PA (ALSO) ALSOBROOK J P.			
PA (LEPL) LEFLEY D M.			
PA (RIEG) RIEGER D K.			
PA (BURG) BURGESS C E.			
Best Local Similarity: 25.33%		Mismatches:	94
Query Match:	5.97%	Indels:	44
RESULT 1202			
ID ABD10306 standard; DNA; 2256 BP.			
DE Pseudomonas aeruginosa polynucleotide #8910.			
PD US6551795-B1.			

PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 24.62% Mismatches: 118  
Query Match: 5.97% Indels: 50  
RESULT 1203  
ID ADA53079 standard; cDNA; 2304 BP.  
DE Human coding sequence, SEQ ID 647.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 22.29% Mismatches: 110  
Query Match: 5.97% Indels: 104  
RESULT 1204  
ID ACA43839 standard; DNA; 2313 BP.  
DE Prokaryotic essential gene #25496.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 24.79% Mismatches: 124  
Query Match: 5.97% Indels: 94  
RESULT 1205  
ID ADG91055 standard; DNA; 2321 BP.  
DE Hepatic specific nucleic acid encoding sequence #244.  
PD 14-AUG-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 30.00% Mismatches: 58  
Query Match: 5.97% Indels: 15  
RESULT 1206  
ID ADJ39295 standard; cDNA; 2322 BP.  
DE Plant cDNA #295.  
PD 22-JAN-2004.  
PA (BUDW-) BUDWORTH P.  
PA (MOUG-) MOUGHAMER T.  
PA (BRIG-) BRIGGS S P.  
PA (COOP-) COOPER B.  
PA (GLAZ-) GLAZEBROOK J.  
PA (GOFF-) GOFF S A.  
PA (KATA-) KATAGIRI P.  
PA (KREP-) KREPS J.  
PA (PROV-) PROVANT N.  
PA (RICK-) RICK D.  
PA (ZHUT-) ZHU T.  
Best Local Similarity: 24.37% Mismatches: 95  
Query Match: 5.97% Indels: 68  
RESULT 1207  
ID AAF81369 standard; DNA; 2334 BP.  
DE Quorum sensing controlled gene qsc112 ORF.  
PD 15-MAR-2001.  
PA (IOWA-) UNIV IOWA RES FOUND.  
PA (QUOR-) QUORUM SCI INC.  
Best Local Similarity: 25.10% Mismatches: 90  
Query Match: 5.97% Indels: 58  
RESULT 1208  
ID AAC75904 standard; cDNA; 2636 BP.  
DE Human ORF1459 polynucleotide sequence SEQ ID NO:2917.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 25.31% Mismatches: 127  
Query Match: 5.97% Indels: 93  
RESULT 1209  
ID AAS66988 standard; cDNA; 2778 BP.  
DE DNA encoding novel human diagnostic protein #2792.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 24.87% Mismatches: 80  
Query Match: 5.97% Indels: 41  
RESULT 1210

ID AAC44728 standard; DNA; 2868 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 43911.  
PD 06-SEP-2000.  
Best Local Similarity: 26.04% Mismatches: 74  
Query Match: 5.97% Indels: 29  
RESULT 1211  
ID ADN73322 standard; cDNA; 3012 BP.  
DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1217.  
PD 29-APR-2004.  
PA (CROP-) CROPDISEIGN NV.  
Best Local Similarity: 26.04% Mismatches: 74  
Query Match: 5.97% Indels: 29  
RESULT 1212  
ID ABT42814 standard; DNA; 3049 BP.  
DE Human neuroblastoma-related DNA sequence, SEQ ID NO:95.  
PD 27-DEC-2002.  
PA (CHIB-) CHIBA PREFECTURE.  
PA (HISM-) HISAMITSU PHARM CO LTD.  
Best Local Similarity: 23.33% Mismatches: 79  
Query Match: 5.97% Indels: 80  
RESULT 1213  
ID ACA42098 standard; DNA; 3099 BP.  
DE Prokaryotic essential gene #23755.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 26.80% Mismatches: 95  
Query Match: 5.97% Indels: 60  
RESULT 1214  
ID ADJ27260 standard; DNA; 3174 BP.  
DE Human TRICH-44 coding sequence, SEQ ID 92.  
PD 12-FEB-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 23.91% Mismatches: 118  
Query Match: 5.97% Indels: 58  
RESULT 1215  
ID ADA70995 standard; DNA; 3189 BP.  
DE Rice gene, SEQ ID 4318.  
PD 03-JAN-2003.  
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.  
Best Local Similarity: 21.73% Mismatches: 138  
Query Match: 5.97% Indels: 87  
RESULT 1216  
ID AAS18239 standard; cDNA; 3273 BP.  
DE Human cDNA encoding hunc-2.  
PD 20-DEC-2001.  
PA (MERE-) MERCK PATENT GMBH.  
Best Local Similarity: 25.94% Mismatches: 78  
Query Match: 5.97% Indels: 63  
RESULT 1217  
ID AAC50900 standard; DNA; 3294 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 66548.  
PD 06-SEP-2000.  
Best Local Similarity: 26.04% Mismatches: 74  
Query Match: 5.97% Indels: 29  
RESULT 1218  
ID ADT45733 standard; cDNA; 3435 BP.  
DE Bacterial polynucleotide #20484.  
PD 18-DEC-2003.  
PA (CAOY-) CAO Y.  
PA (HINK-) HINKLE G J.  
PA (SLAT-) SLATER S C.  
PA (CHEN-) CHEN X.  
PA (GOLD-) GOLDMAN B S.  
Best Local Similarity: 24.65% Mismatches: 105

Query Match: 5.97% Indels: 84  
 RESULT 1219  
 ID ADR07512 standard; cDNA; 3652 BP.  
 DE Full length human cDNA useful for treating neurological disease Seq 1018.  
 PN EP1447413-A2.  
 PD 18-AUG-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Best Local Similarity: 25.59% Mismatches: 126  
 Query Match: 5.97% Indels: 69  
 RESULT 1220  
 ID ADQ81352 standard; DNA; 3711 BP.  
 DE Human Notch-like polypeptide coding sequence.  
 PN WO2004063223-A2.  
 PD 29-JUL-2004.  
 PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.  
 Best Local Similarity: 25.59% Mismatches: 126  
 Query Match: 5.97% Indels: 69  
 RESULT 1221  
 ID AAD0684 standard; DNA; 3786 BP.  
 DE Human CRUMBS (CRB) DNA #7 that modify branching morphogenesis.  
 PN US2003100005-A1.  
 PD 29-MAY-2003.  
 PA (KARI/) KARIM F D.  
 PA (KEYE/) KEYES L N.  
 PA (PLOW/) PLOWMAN G D.  
 PA (OLIM/) OLIMANN M M.  
 PA (MAXW/) MAXWELL M E.  
 PA (DIAG/) DIAGANA T T.  
 Best Local Similarity: 25.59% Mismatches: 126  
 Query Match: 5.97% Indels: 69  
 RESULT 1222  
 ID ADH22633 standard; cDNA; 3850 BP.  
 DE cDNA encoding a human transporter & ion channel (TRICH) protein SeqID131.  
 PN WO2003093444-A2.  
 PD 13-NOV-2003.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 23.91% Mismatches: 118  
 Query Match: 5.97% Indels: 58  
 RESULT 1223  
 ID ADS48637 standard; cDNA; 4135 BP.  
 DE Bacterial polynucleotide #3380.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 24.84% Mismatches: 55  
 Query Match: 5.97% Indels: 42  
 RESULT 1224  
 ID ADR08444 standard; cDNA; 4319 BP.  
 DE Full length human cDNA useful for treating neurological disease Seq 1950.  
 PN EP1447413-A2.  
 PD 18-AUG-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Best Local Similarity: 21.82% Mismatches: 101  
 Query Match: 5.97% Indels: 130  
 RESULT 1225  
 ID ACA42414 standard; DNA; 4347 BP.  
 DE Prokaryotic essential gene #24071.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 26.56% Mismatches: 102  
 Query Match: 5.97% Indels: 51  
 RESULT 1226  
 ID ADB80394 standard; DNA; 4387 BP.  
 DE Human MDDT gene Seq ID NO:81.  
 PN WO2003016497-A2.  
 PD 27-FEB-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 26.27% Mismatches: 82

Query Match: 5.97% Indels: 57  
 RESULT 1227  
 ID ADC78227 standard; cDNA; 4476 BP.  
 DE Human secreted protein encoding cDNA Seq ID NO:34.  
 PN WO2003072761-A1.  
 PD 04-SEP-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 25.36% Mismatches: 112  
 Query Match: 5.97% Indels: 72  
 RESULT 1228  
 ID ABK72242 standard; cDNA; 4483 BP.  
 DE Human NOVX polynucleotide #73.  
 PN WO200281498-A2.  
 PD 17-OCT-2002.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 25.31% Mismatches: 127  
 Query Match: 5.97% Indels: 93  
 RESULT 1229  
 ID ABK46137 standard; cDNA; 4932 BP.  
 DE cDNA encoding colon tumour protein, Seq ID No 1688.  
 PN WO200212328-A2.  
 PD 14-FEB-2002.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 23.62% Mismatches: 86  
 Query Match: 5.97% Indels: 97  
 RESULT 1230  
 ID ACC50996 standard; cDNA; 5352 BP.  
 DE Human bladder cancer associated cDNA sequence Seq ID NO:85.  
 PN WO2003003906-A2.  
 PD 16-JAN-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Best Local Similarity: 21.64% Mismatches: 106  
 Query Match: 5.97% Indels: 69  
 RESULT 1231  
 ID ABZ24581 standard; cDNA; 7564 BP.  
 DE Human cell adhesion and extracellular matrix protein 4 cDNA.  
 PN WO200288322-A2.  
 PD 07-NOV-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 25.70% Mismatches: 88  
 Query Match: 5.97% Indels: 68  
 RESULT 1232  
 ID AAK79820 standard; DNA; 8308 BP.  
 DE Human immune/haematopoietic antigen genomic sequence Seq ID NO:34632.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 25.63% Mismatches: 69  
 Query Match: 5.97% Indels: 62  
 RESULT 1233  
 ID AAX68091 standard; DNA; 8308 BP.  
 DE Human immune/haematopoietic antigen genomic sequence Seq ID NO:22903.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 25.63% Mismatches: 69  
 Query Match: 5.97% Indels: 62  
 RESULT 1234  
 ID AAS18100 standard; DNA; 10210 BP.  
 DE Human angiotensin receptor-like 1 (AGTRL1) DNA.  
 PN WO200190123-A2.  
 PD 29-NOV-2001.  
 PA (GENA-) GENAISSANCE PHARM INC.  
 Best Local Similarity: 22.14% Mismatches: 84  
 Query Match: 5.97% Indels: 95  
 RESULT 1235  
 ID AAD03809 standard; DNA; 14806 BP.  
 DE Streptomyces galilaeus gene cluster for actinomycin biosynthesis.  
 PN WO200123578-A1.  
 PD 05-APR-2001.  
 PA (GALI-) GALILAEUS OY.  
 Best Local Similarity: 23.84% Mismatches: 111  
 Query Match: 5.97% Indels: 68

RESULT 1236  
ID ABA97921 standard; DNA; 23668 BP.  
DE Human transporter protein encoding genomic DNA SEQ ID NO 2.  
PN WO200190360-A2.  
PD 29-NOV-2001.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 20.28% Mismatches: 115  
Query Match: 5.97% Indels: 124

RESULT 1237  
ID ADR86701 standard; DNA; 26000 BP.  
DE Human Ephrin B4 (EphB4) genomic DNA.  
PN WO2004080425-A2.  
PD 23-SEP-2004.  
PA (VASG-) VASGENE THERAPEUTICS INC.  
Best Local Similarity: 23.84% Mismatches: 132  
Query Match: 5.97% Indels: 59

RESULT 1238  
ID ADR82648 standard; DNA; 26000 BP.  
DE Human EphB4 gene.  
PN WO2004080418-A2.  
PD 23-SEP-2004.  
PA (VASG-) VASGENE THERAPEUTICS INC.  
Best Local Similarity: 23.84% Mismatches: 132  
Query Match: 5.97% Indels: 59

RESULT 1239  
ID AAD56075 standard; DNA; 32767 BP.  
DE Human SNL carcinoma associated (CA) gene.  
PN WO2003035837-A2.  
PD 01-MAY-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 27.48% Mismatches: 84  
Query Match: 5.97% Indels: 53

RESULT 1240  
ID ADA02437 standard; DNA; 32767 BP.  
DE Human SNL carcinoma associated gene, SEQ ID NO:956.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 27.48% Mismatches: 84  
Query Match: 5.97% Indels: 53

RESULT 1241  
ID ADB72176 standard; DNA; 32767 BP.  
DE Human SNL gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 27.48% Mismatches: 84  
Query Match: 5.97% Indels: 53

RESULT 1242  
ID ADE82920 standard; DNA; 32767 BP.  
DE Human SNL genomic DNA sequence.  
PN WO2003080808-A2.  
PD 02-OCT-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 27.48% Mismatches: 84  
Query Match: 5.97% Indels: 53

RESULT 1243  
ID ACC58251 standard; DNA; 35359 BP.  
DE Coumermycin A1 biosynthetic gene cluster.  
PN WO2003014352-A2.  
PD 20-FEB-2003.  
PA (UYTU-) UNIV TUEBINGEN.  
Best Local Similarity: 26.39% Mismatches: 106  
Query Match: 5.97% Indels: 62

RESULT 1244  
ID AAF88313 standard; DNA; 50000 BP.  
DE S. spinosa DNA fragment SEQ ID 2.  
PN DE19957268-A1.  
PD 08-MAR-2001.  
PA (FARB-) BAYER AG.  
Best Local Similarity: 19.95% Mismatches: 114  
Query Match: 5.97% Indels: 146

ID AAF88316 standard; DNA; 50000 BP.  
DE S. spinosa DNA fragment SEQ ID 5.  
PN DE19957268-A1.  
PD 08-MAR-2001.  
PA (FARB-) BAYER AG.  
Best Local Similarity: 19.95% Mismatches: 114  
Query Match: 5.97% Indels: 146

RESULT 1246  
ID ADD71050 standard; DNA; 75270 BP.  
DE Human secretory carrier membrane protein 3 gene SEQ ID NO:54.  
PN WO2003061564-A2.  
PD 31-JUL-2003.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 23.21% Mismatches: 96  
Query Match: 5.97% Indels: 50

RESULT 1247  
ID ACA63030 standard; DNA; 75270 BP.  
DE Human chromosome 1q21 region surrounding the glucocerebrosidase gene.  
PN US2003013178-A1.  
PD 16-JAN-2003.  
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.  
Best Local Similarity: 23.21% Mismatches: 96  
Query Match: 5.97% Indels: 50

RESULT 1248  
ID ADQ19735 standard; DNA; 75270 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2554.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 23.21% Mismatches: 96  
Query Match: 5.97% Indels: 50

RESULT 1249  
ID AA221501 standard; DNA; 80161 BP.  
DE DNA fragment of Saccharopolyspora spinosa containing biosynthetic genes.  
PN WO200297082-A2.  
PD 05-DEC-2002.  
PA (UYDU-) UNIV COLLEGE DUBLIN.  
Best Local Similarity: 27.71% Mismatches: 80  
Query Match: 5.97% Indels: 63

RESULT 1251  
ID AAD54480 standard; DNA; 117962 BP.  
DE Human CIP DNA #1.  
PN WO200299055-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Best Local Similarity: 23.84% Mismatches: 132  
Query Match: 5.97% Indels: 59

RESULT 1252  
ID ADQ20606 standard; DNA; 195917 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3426.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 23.62% Mismatches: 86  
Query Match: 5.97% Indels: 97

RESULT 1253  
ID ABZ72040 standard; DNA; 207433 BP.  
DE Gene 216 H194BAC1098L22 nucleotide sequence SEQ ID NO 5.  
PN WO200178894-A2.  
PD 25-OCT-2001.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 22.02% Mismatches: 97  
Query Match: 5.97% Indels: 90

RESULT 1254  
ID ABX74891 standard; DNA; 207433 BP.  
DE BAC1098L22 DNA sequence.  
PN WO200283077-A2.

PD 24-OCT-2002.  
 PA (SCHE) SCHERING CORP.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 22.02% Mismatches: 97  
 Query Match: 5.97% Indels: 90  
 RESULT 1255  
 ID ADJ36614 standard; DNA; 207433 BP.  
 DE Bacterial artificial chromosome RPCI-11.  
 PN US2004002470-A1.  
 PD 01-JAN-2004.  
 PA (KEIT/) KEITH T.  
 PA (VEER/) LITTLE R. D.  
 PA (VEER/) VAN EERDEWEGH P.  
 PA (DUPU/) DUPUIS J.  
 PA (DNAS/) DEL MASTRO R. G.  
 PA (SIMO/) SIMON J.  
 PA (ALLE/) ALLEN K.  
 PA (PAND/) PANDIT S.  
 Best Local Similarity: 22.02% Mismatches: 97  
 Query Match: 5.97% Indels: 90  
 RESULT 1256  
 ID ADL81193 standard; DNA; 207433 BP.  
 DE BAC1098L22 DNA sequence.  
 PN US2004023215-A1.  
 PD 05-FEB-2004.  
 PA (KEIT/) KEITH T.  
 PA (LITT/) LITTLE R. D.  
 PA (EERD/) EERDEWEGH P. V.  
 PA (DUPU/) DUPUIS J.  
 PA (DNAS/) DEL MASTRO R. G.  
 PA (SIMO/) SIMON J.  
 PA (ALLE/) ALLEN K.  
 PA (PAND/) PANDIT S.  
 Best Local Similarity: 22.02% Mismatches: 97  
 Query Match: 5.97% Indels: 90  
 RESULT 1257  
 ID ABR84349 standard; cDNA; 222930 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #920.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Best Local Similarity: 22.36% Mismatches: 99  
 Query Match: 5.97% Indels: 117  
 RESULT 1258  
 ID ADI73714 standard; DNA; 401 BP.  
 DE Human ovarian cancer DNA marker #6456.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Best Local Similarity: 35.96% Mismatches: 37  
 Query Match: 5.94% Indels: 10  
 RESULT 1259  
 ID ADI67317 standard; DNA; 401 BP.  
 DE Human ovarian cancer DNA marker #59.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Best Local Similarity: 35.96% Mismatches: 37  
 Query Match: 5.94% Indels: 10  
 RESULT 1260  
 ID ADK14113 standard; cDNA; 455 BP.  
 DE Human autoimmune disorder gene #17.  
 PN US2003228617-A1.  
 PD 11-DEC-2003.  
 PA (UYVA-) UNIV VANDERBILT.  
 Best Local Similarity: 25.00% Mismatches: 51  
 Query Match: 5.94% Indels: 81  
 RESULT 1261  
 ID ADL38951 standard; DNA; 458 BP.  
 DE Human ovarian cancer DNA marker #12841.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Best Local Similarity: 35.96% Mismatches: 37  
 Query Match: 5.94% Indels: 10  
 RESULT 1262  
 ID ABA57564 standard; DNA; 460 BP.  
 DE Human foetal liver single exon nucleic acid probe #5869.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 30.48% Mismatches: 37  
 Query Match: 5.94% Indels: 19  
 RESULT 1263  
 ID AAI37122 standard; DNA; 460 BP.  
 DE Probe #5808 used to measure gene expression in human placenta sample.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 30.48% Mismatches: 37  
 Query Match: 5.94% Indels: 19  
 RESULT 1264  
 ID AAK31218 standard; DNA; 460 BP.  
 DE Human bone marrow expressed single exon probe SEQ ID NO: 5775.  
 PN WO200157276-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 30.48% Mismatches: 37  
 Query Match: 5.94% Indels: 19  
 RESULT 1265  
 ID AAK05613 standard; DNA; 460 BP.  
 DE Human brain expressed single exon probe SEQ ID NO: 5604.  
 PN WO200157275-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 30.48% Mismatches: 37  
 Query Match: 5.94% Indels: 19  
 RESULT 1266  
 ID ABS30899 standard; DNA; 460 BP.  
 DE Human liver single exon probe, SEQ ID No 5889.  
 PN WO200157273-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 30.48% Mismatches: 37  
 Query Match: 5.94% Indels: 19  
 RESULT 1267  
 ID ABS05970 standard; DNA; 460 BP.  
 DE Human genome-derived single exon probe from lung SEQ ID No 5961.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 30.48% Mismatches: 37  
 Query Match: 5.94% Indels: 19  
 RESULT 1268  
 ID ACH91710 standard; DNA; 567 BP.  
 DE Human genome derived single exon probe #24905.  
 PN US2003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN/) PENN S. G.  
 PA (RANK/) RANK D. R.  
 PA (HANZ/) HANZEL D. K.  
 Best Local Similarity: 26.70% Mismatches: 69  
 Query Match: 5.94% Indels: 76  
 RESULT 1269  
 ID ADR01427 standard; DNA; 606 BP.  
 DE A. gossypii genomic DNA PAG104411.  
 PN US6239264-B1.  
 PD 29-MAY-2001.  
 PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 30.85% Mismatches: 31  
 Query Match: 5.94% Indels: 26  
 RESULT 1270  
 ID AAS78418 standard; cDNA; 645 BP.  
 DE DNA encoding novel human diagnostic protein #14222.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC. Mismatches: 78  
 Query Match: 5.94% Indels: 56  
 RESULT 1271  
 ID ABT19178 standard; DNA; 825 BP.  
 DE Aspergillus fumigatus essential gene #1536.  
 PN WO200286090-A2.  
 PD 31-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC. Mismatches: 86  
 Best Local Similarity: 24.18% Indels: 69  
 Query Match: 5.94%  
 RESULT 1272  
 ID ADK54727 standard; DNA; 855 BP.  
 DE Plant DNA sequence which confers altered metabolic characteristic #2110.  
 PN WO2003020936-A1.  
 PD 13-MAR-2003.  
 PA (DOWC) DOW CHEM CO. Mismatches: 82  
 Best Local Similarity: 22.81% Indels: 70  
 Query Match: 5.94%  
 RESULT 1273  
 ID ADK58741 standard; DNA; 879 BP.  
 DE Plant DNA sequence which confers altered metabolic characteristic #6124.  
 PN WO2003020936-A1.  
 PD 13-MAR-2003.  
 PA (DOWC) DOW CHEM CO. Mismatches: 82  
 Best Local Similarity: 22.81% Indels: 70  
 Query Match: 5.94%  
 RESULT 1274  
 ID ABD09128 standard; DNA; 996 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7732.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP. Mismatches: 109  
 Best Local Similarity: 22.68% Indels: 91  
 Query Match: 5.94%  
 RESULT 1275  
 ID ACA45839 standard; DNA; 1047 BP.  
 DE Prokaryotic essential gene #27496.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC. Mismatches: 83  
 Best Local Similarity: 26.17% Indels: 54  
 Query Match: 5.94%  
 RESULT 1276  
 ID ADA70982 standard; DNA; 1113 BP.  
 DE Rice gene, SEQ ID 4305.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG. Mismatches: 95  
 Best Local Similarity: 25.00% Indels: 91  
 Query Match: 5.94%  
 RESULT 1277  
 ID ACD27929 standard; cDNA; 1127 BP.  
 DE Human S100 protein S100P2 cDNA.  
 PN US2003096337-A1.  
 PD 22-MAY-2003.  
 PA (HILL/) HILLMAN J L. Mismatches: 82  
 PA (BAND/) BANDMAN O. Indels: 64  
 PA (CORL/) CORLEY N C.  
 PA (LALP/) LAL P.  
 PA (SHAH/) SHAH P.  
 Best Local Similarity: 22.77%  
 Query Match: 5.94%  
 RESULT 1278  
 ID AAV73499 standard; DNA; 1141 BP.  
 DE Human S100P2 DNA.  
 PN US5849528-A.  
 PD 15-DEC-1998.  
 PA (INCY-) INCYTE PHARM INC. Mismatches: 54  
 Best Local Similarity: 29.66% Indels: 30  
 Query Match: 5.94%

RESULT 1279  
 ID AA59691 standard; cDNA; 1141 BP.  
 DE cDNA encoding a human S100 polypeptide.  
 PN US6103497-A.  
 PD 15-AUG-2000.  
 PA (INCY-) INCYTE PHARM INC. Mismatches: 54  
 Best Local Similarity: 29.66% Indels: 30  
 Query Match: 5.94%  
 RESULT 1280  
 ID ACA38612 standard; DNA; 1215 BP.  
 DE Prokaryotic essential gene #20269.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC. Mismatches: 89  
 Best Local Similarity: 22.26% Indels: 103  
 Query Match: 5.94%  
 RESULT 1281  
 ID ADS80144 standard; DNA; 1215 BP.  
 DE Mycobacterium tuberculosis nutrient starvation-inducible gene #91.  
 PN WO2003004520-A2.  
 PD 16-JAN-2003.  
 PA (MICR-) MICROBIOLOGICAL RES AUTHORITY. Mismatches: 89  
 Best Local Similarity: 22.26% Indels: 103  
 Query Match: 5.94%  
 RESULT 1282  
 ID ACA40730 standard; DNA; 1218 BP.  
 DE Prokaryotic essential gene #22387.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC. Mismatches: 89  
 Best Local Similarity: 22.26% Indels: 103  
 Query Match: 5.94%  
 RESULT 1283  
 ID AAV60558 standard; DNA; 1224 BP.  
 DE GtFD gene from Amycolatopsis orientalis A82846.  
 PN US5821098-A.  
 PD 13-OCT-1998.  
 PA (ELIL) LILLY & CO ELI. Mismatches: 84  
 Best Local Similarity: 23.04% Indels: 65  
 Query Match: 5.94%  
 RESULT 1284  
 ID AAZ57050 standard; DNA; 1224 BP.  
 DE A. orientalis glycosyltransferase protein GtFD encoding DNA.  
 PN US6025174-A.  
 PD 15-FEB-2000.  
 PA (ELIL) LILLY & CO ELI. Mismatches: 84  
 Best Local Similarity: 23.04% Indels: 65  
 Query Match: 5.94%  
 RESULT 1285  
 ID AAZ57051 standard; mRNA; 1224 BP.  
 DE A. orientalis glycosyltransferase protein GtFD mRNA.  
 PN US6025174-A.  
 PD 15-FEB-2000.  
 PA (ELIL) LILLY & CO ELI. Mismatches: 84  
 Best Local Similarity: 23.04% Indels: 65  
 Query Match: 5.94%  
 RESULT 1286  
 ID ABD08963 standard; DNA; 1224 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7567.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP. Mismatches: 110  
 Best Local Similarity: 23.42% Indels: 72  
 Query Match: 5.94%  
 RESULT 1287  
 ID ABD08018 standard; DNA; 1239 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6622.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP. Mismatches: 96  
 Best Local Similarity: 27.11% Indels: 40  
 Query Match: 5.94%  
 RESULT 1288



ID ACA24586 standard; DNA; 1248 BP.  
 DE Prokaryotic essential gene #6243.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 22.50% Mismatches: 75  
 Query Match: 5.94% Indels: 49  
 RESULT 1289

ID AAS54328 standard; DNA; 1350 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #459.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 27.64% Mismatches: 109  
 Query Match: 5.94% Indels: 51  
 RESULT 1290

ID ACA42686 standard; DNA; 1350 BP.  
 DE Prokaryotic essential gene #24343.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 27.64% Mismatches: 109  
 Query Match: 5.94% Indels: 51  
 RESULT 1291

ID ADH13098 standard; DNA; 1350 BP.  
 DE P aeruginosa biotin carboxylase gene SeqID49.  
 PN WO2003084986-A2.  
 PD 16-OCT-2003.  
 PA (AFFI-) AFFINIUM PHARM INC.  
 Best Local Similarity: 27.64% Mismatches: 109  
 Query Match: 5.94% Indels: 51  
 RESULT 1292

ID ADH13100 standard; DNA; 1350 BP.  
 DE P aeruginosa biotin carboxylase gene SeqID51.  
 PN WO2003084986-A2.  
 PD 16-OCT-2003.  
 PA (AFFI-) AFFINIUM PHARM INC.  
 Best Local Similarity: 27.64% Mismatches: 109  
 Query Match: 5.94% Indels: 51  
 RESULT 1293

ID AAS54344 standard; DNA; 1425 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #475.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 31.22% Mismatches: 87  
 Query Match: 5.94% Indels: 47  
 RESULT 1294

ID ACA42715 standard; DNA; 1425 BP.  
 DE Prokaryotic essential gene #24372.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 31.22% Mismatches: 87  
 Query Match: 5.94% Indels: 47  
 RESULT 1295

ID ABD08038 standard; DNA; 1449 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6642.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 27.11% Mismatches: 96  
 Query Match: 5.94% Indels: 40  
 RESULT 1296

ID ABD15356 standard; DNA; 1467 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13960.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 25.75% Mismatches: 103  
 Query Match: 5.94% Indels: 41  
 RESULT 1297

ID AB211285 standard; cDNA; 1643 BP.

DE Human polynucleotide SEQ ID NO 167.  
 PN WO200270539-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 26.70% Mismatches: 69  
 Query Match: 5.94% Indels: 76  
 RESULT 1298

ID ADM43803 standard; cDNA; 1643 BP.  
 DE Novel human arginine-rich protein cDNA #167.  
 PN US2004053250-A1.  
 PD 18-MAR-2004.  
 PA (TANG/) TANG Y T.  
 PA (XUEA/) XUE A.  
 PA (DRMA/) DRMANAC R T.  
 Best Local Similarity: 26.70% Mismatches: 69  
 Query Match: 5.94% Indels: 76  
 RESULT 1299

ID ABD07972 standard; DNA; 1647 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6576.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 27.11% Mismatches: 96  
 Query Match: 5.94% Indels: 40  
 RESULT 1300

ID AAD5811 standard; DNA; 1683 BP.  
 DE Micromonospora carbonacea polyketide synthase (PKS) type I gene #1.  
 PN CA2391131-A1.  
 PD 19-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Best Local Similarity: 21.64% Mismatches: 120  
 Query Match: 5.94% Indels: 86  
 RESULT 1301

ID ADA47975 standard; DNA; 1770 BP.  
 DE Rice gene conferring disease resistance in plants.  
 PN WO2003000906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Best Local Similarity: 22.05% Mismatches: 103  
 Query Match: 5.94% Indels: 123  
 RESULT 1302

ID AAU51471 standard; DNA; 1916 BP.  
 DE Human epithelial cell sodium channel delta subunit coding sequence.  
 PN WO200287306-A2.  
 PD 07-NOV-2002.  
 PA (SENO-) SENOMYX INC.  
 Best Local Similarity: 23.72% Mismatches: 102  
 Query Match: 5.94% Indels: 68  
 RESULT 1303

ID ADS60101 standard; cDNA; 1917 BP.  
 DE Bacterial polynucleotide #12088.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 25.66% Mismatches: 80  
 Query Match: 5.94% Indels: 93  
 RESULT 1304

ID ABO90272 standard; DNA; 1974 BP.  
 DE M. capulatus gene #257 for DNA array.  
 PN WO200355655-A2.  
 PD 18-JUL-2002.  
 PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.  
 PA (TIGR-) TIGR.  
 Best Local Similarity: 25.73% Mismatches: 85  
 Query Match: 5.94% Indels: 67  
 RESULT 1305

ID ABD15246 standard; DNA; 2049 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13850.  
 PN US6551795-B1.

PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 25.75% Mismatches: 103  
Query Match: 5.94% Indels: 41  
RESULT 1306  
ID AAS26071 standard; cDNA; 2131 BP.  
DE Human cDNA encoding a novel secreted protein, Seq ID 250.  
PN WO200155322-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 22.07% Mismatches: 110  
Query Match: 5.94% Indels: 93  
RESULT 1307  
ID ABX73412 standard; DNA; 2131 BP.  
DE Human novel polynucleotide #240.  
PN US2002132753-A1.  
PD 19-SEP-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Best Local Similarity: 22.07% Mismatches: 110  
Query Match: 5.94% Indels: 93  
RESULT 1308  
ID AQ083852 standard; cDNA; 2166 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #666.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Best Local Similarity: 26.70% Mismatches: 69  
Query Match: 5.94% Indels: 76  
RESULT 1309  
ID AQ087301 standard; cDNA; 2166 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4178.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Best Local Similarity: 26.70% Mismatches: 69  
Query Match: 5.94% Indels: 76  
RESULT 1310  
ID ACN41498 standard; cDNA; 2198 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:373.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 23.72% Mismatches: 102  
Query Match: 5.94% Indels: 68  
RESULT 1311  
ID ADC68527 standard; cDNA; 2231 BP.  
DE S. arundinaceus fructan biosynthesis protein cDNA SEQ ID NO:19.  
PN WO2003040306-A2.  
PD 15-MAY-2003.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (WRIG-) WRIGHTSON SEEDS LTD.  
Best Local Similarity: 22.65% Mismatches: 105  
Query Match: 5.94% Indels: 122  
RESULT 1312  
ID ADA52873 standard; cDNA; 2262 BP.  
DE Human coding sequence, SEQ ID 441.  
PN EP1293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 35.96% Mismatches: 37  
Query Match: 5.94% Indels: 10  
RESULT 1313  
ID ACN41496 standard; cDNA; 2275 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:371.  
PN WO2004023973-A2.  
PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.  
Best Local Similarity: 23.72% Mismatches: 102  
Query Match: 5.94% Indels: 68  
RESULT 1314  
ID AAD24009 standard; cDNA; 2305 BP.  
DE Human drug metabolising enzyme (DME) -4 cDNA.  
PN WO200190334-A2.  
PD 29-NOV-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 19.57% Mismatches: 88  
Query Match: 5.94% Indels: 97  
RESULT 1315  
ID ADO63961 standard; cDNA; 2381 BP.  
DE Novel human cDNA sequence #1122.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 23.64% Mismatches: 106  
Query Match: 5.94% Indels: 96  
RESULT 1316  
ID AA223939 standard; DNA; 2387 BP.  
DE T. versicolor GAPDH promoter DNA.  
PN WO9951757-A1.  
PD 14-OCT-1999.  
PA (CONE) CONSORTIUM ELEKTROCHEM IND GMBH.  
Best Local Similarity: 24.69% Mismatches: 111  
Query Match: 5.94% Indels: 38  
RESULT 1317  
ID ABO77426 standard; cDNA; 2535 BP.  
DE Human CGDD cDNA 914113B1 SEQ ID 40.  
PN WO2003014322-A2.  
PD 20-FEB-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 24.80% Mismatches: 80  
Query Match: 5.94% Indels: 90  
RESULT 1318  
ID ADB63377 standard; cDNA; 2679 BP.  
DE Human cDNA encoding clone TESTI20105910.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 23.72% Mismatches: 102  
Query Match: 5.94% Indels: 68  
RESULT 1319  
ID AAD17479 standard; cDNA; 2714 BP.  
DE Human transporter and ion channel-12 (TRICH-12) cDNA.  
PN WO200162923-A2.  
PD 30-AUG-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 23.72% Mismatches: 102  
Query Match: 5.94% Indels: 68  
RESULT 1320  
ID ADJ27222 standard; DNA; 2757 BP.  
DE Human TRICH-6 coding sequence, SEQ ID 54.  
PN WO2004013293-A2.  
PD 12-FEB-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 23.87% Mismatches: 80  
Query Match: 5.94% Indels: 78  
RESULT 1321  
ID ADA53699 standard; cDNA; 2758 BP.  
DE Human coding sequence, SEQ ID 1267.  
PN EP1293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 27.39% Mismatches: 92  
Query Match: 5.94% Indels: 49  
RESULT 1322  
ID AAQ79921 standard; DNA; 2760 BP.  
DE P. aeruginosa accB and accC genes.  
PN WO9429467-A2.

PD 22-DEC-1994.  
PA (CALJ) CALGENE INC. Mismatches: 109  
Best Local Similarity: 27.64% Indels: 51  
Query Match: 5.94%  
RESULT 1323  
ID ABT07915 standard; DNA; 2848 BP.  
DE Human lung specific gene SEQ ID NO 60.  
PN WO200262945-A2.  
PD 15-AUG-2002.  
PA (DIAD-) DIADEXUS INC. Mismatches: 93  
Best Local Similarity: 25.59% Indels: 41  
Query Match: 5.94%  
RESULT 1324  
ID AA232001 standard; cDNA; 3008 BP.  
DE Human METH2 encoding cDNA.  
PN WO937660-A1.  
PD 29-JUL-1999.  
PA (IRUE/) IRUELA-ARISPE L. Mismatches: 93  
PA (HAST/) HASTINGS G A. Indels: 41  
PA (RUBE/) RUBEN S M.  
Best Local Similarity: 21.23% Mismatches: 104  
Query Match: 5.94% Indels: 147  
RESULT 1325  
ID AAC90058 standard; DNA; 3008 BP.  
DE Human METH2 coding sequence.  
PN WO200071577-A1.  
PD 30-NOV-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
PA (IRUE/) IRUELA-ARISPE L.  
PA (HAST/) HASTINGS G A.  
PA (RUBE/) RUBEN S M.  
PA (JONA/) JONAK Z L.  
PA (TRUL/) TRULLI S H.  
PA (FORN/) FORNWALD J A.  
PA (TERR/) TERRETT J A.  
Best Local Similarity: 21.23% Mismatches: 104  
Query Match: 5.94% Indels: 147  
RESULT 1326  
ID AAS78943 standard; cDNA; 3093 BP.  
DE DNA encoding novel human diagnostic protein #14747.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC. Mismatches: 69  
Best Local Similarity: 26.70% Indels: 76  
Query Match: 5.94%  
RESULT 1327  
ID AAL61181 standard; DNA; 3354 BP.  
DE Actinobryonema pretiosum transcriptional regulator gene #1.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW) UNIV WASHINGTON.  
Best Local Similarity: 24.03% Mismatches: 89  
Query Match: 5.94% Indels: 82  
RESULT 1328  
ID ADRI0432 standard; cDNA; 3370 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 3938.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 23.72% Mismatches: 102  
Query Match: 5.94% Indels: 68  
RESULT 1329  
ID ACM43323 standard; cDNA; 3443 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2198.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 22.07% Mismatches: 84  
Query Match: 5.94% Indels: 114  
RESULT 1330  
ID ADE85181 standard; DNA; 3711 BP.

DE Farnesyl transferase inhibitor modulated leukemia associated gene #400.  
PN WO2003038129-A2.  
PD 08-MAY-2003.  
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC. Mismatches: 104  
Best Local Similarity: 21.23% Indels: 147  
Query Match: 5.94%  
RESULT 1331  
ID ADR83445 standard; DNA; 3711 BP.  
DE Human METH2 DNA, target gene of miRNA.  
PN WO2004076622-A2.  
PD 10-SEP-2004.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
Best Local Similarity: 21.23% Mismatches: 104  
Query Match: 5.94% Indels: 147  
RESULT 1332  
ID ACN92835 standard; DNA; 3937 BP.  
DE Breast cancer related marker, seq id 13985.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 133  
Best Local Similarity: 24.92% Indels: 79  
Query Match: 5.94%  
RESULT 1333  
ID AAA30567 standard; DNA; 4145 BP.  
DE Genomic DNA encoding C. tropicalis cytochrome P450 oxidoreductase CPRB.  
PN WO20020566-A2.  
PD 13-APR-2000.  
PA (HENK) HENKEL CORP. Mismatches: 111  
Best Local Similarity: 19.36% Indels: 121  
Query Match: 5.94%  
RESULT 1334  
ID ABK31886 standard; DNA; 4145 BP.  
DE Candida tropicalis CPRB gene.  
PN US6331420-B1.  
PD 18-DEC-2001.  
PA (WILS) WILSON C R.  
PA (CRAF) CRAFT D L.  
PA (EIRI) EIRICH L D.  
PA (ESHO) ESHOO M.  
PA (MADD) MADDURI K M.  
PA (CORN) CORNETT C A.  
PA (BREN) BRENNER A A.  
PA (TANG) TANG M.  
PA (LOPE) LOPER J C.  
PA (GLEE) GLEESON M.  
Best Local Similarity: 19.36% Mismatches: 111  
Query Match: 5.94% Indels: 121  
RESULT 1335  
ID ABLS5695 standard; DNA; 4145 BP.  
DE Candida tropicalis cytochrome P450 reductase B gene.  
PN WO200308413-A2.  
PD 31-JAN-2002.  
PA (COGN-) COGNIS CORP. Mismatches: 111  
Best Local Similarity: 19.36% Indels: 121  
Query Match: 5.94%  
RESULT 1336  
ID ADG31765 standard; DNA; 4145 BP.  
DE Candida tropicalis CPRB DNA encoding a heterologous protein SeqID 3.  
PN WO200208412-A2.  
PD 31-JAN-2002.  
PA (COGN-) COGNIS CORP. Mismatches: 111  
Best Local Similarity: 19.36% Indels: 121  
Query Match: 5.94%  
RESULT 1337  
ID ADC45081 standard; DNA; 4145 BP.  
DE Yeast CPRB DNA.  
PN US2003049821-A1.  
PD 13-MAR-2003.  
PA (WILS) WILSON C R.  
PA (CRAF) CRAFT D L.  
PA (EIRI) EIRICH L D.  
PA (ESHO) ESHOO M.  
PA (MADD) MADDURI K M.

PA (CORN//) CORNETT C A.  
PA (BREN//) BRENNER A A.  
PA (TANG//) TANG M.  
PA (LOPE//) LOPER J C.  
PA (GLEE//) GLEESON M.  
Best Local Similarity: 19.36%  
Query Match: 5.94%  
RESULT 1338  
ID ADE45651 standard; DNA; 4145 BP.  
DE Yeast CPRB DNA.  
PN US2003049822-A1.  
PD 13-MAR-2003.  
PA (WILS//) WILSON C R.  
PA (CRAF//) CRAFT D L.  
PA (EIRI//) EIRICH L D.  
PA (ESHO//) ESHOO M.  
PA (MADD//) MADDURI K M.  
PA (CORN//) CORNETT C A.  
PA (BREN//) BRENNER A A.  
PA (TANG//) TANG M.  
PA (LOPE//) LOPER J C.  
PA (GLEE//) GLEESON M.  
Best Local Similarity: 19.36%  
Query Match: 5.94%  
RESULT 1339  
ID ADE52162 standard; DNA; 4145 BP.  
DE C. tropicalis NADPH-cytochrome P450 reductase, CPRB DNA.  
PN US2003073220-A1.  
PD 17-APR-2003.  
PA (WILS//) WILSON C R.  
PA (CRAF//) CRAFT D L.  
PA (EIRI//) EIRICH L D.  
PA (ESHO//) ESHOO M.  
PA (MADD//) MADDURI K M.  
PA (CORN//) CORNETT C A.  
PA (BREN//) BRENNER A A.  
PA (TANG//) TANG M.  
PA (LOPE//) LOPER J C.  
PA (GLEE//) GLEESON M.  
Best Local Similarity: 19.36%  
Query Match: 5.94%  
RESULT 1340  
ID ADF72469 standard; DNA; 4145 BP.  
DE NADPH cytochrome P450 oxidoreductase CPRB DNA seq id 82.  
PN US2003077795-A1.  
PD 24-APR-2003.  
PA (WILS//) WILSON C R.  
PA (CRAF//) CRAFT D L.  
PA (EIRI//) EIRICH L D.  
PA (ESHO//) ESHOO M.  
PA (MADD//) MADDURI K M.  
PA (CORN//) CORNETT C A.  
PA (BREN//) BRENNER A A.  
PA (TANG//) TANG M.  
PA (LOPE//) LOPER J C.  
PA (GLEE//) GLEESON M.  
Best Local Similarity: 19.36%  
Query Match: 5.94%  
RESULT 1341  
ID ADF11909 standard; DNA; 4145 BP.  
DE C. tropicalis CPRB DNA.  
PN US2003153060-A1.  
PD 14-AUG-2003.  
PA (WILS//) WILSON C R.  
PA (CRAF//) CRAFT D L.  
PA (EIRI//) EIRICH L D.  
PA (ESHO//) ESHOO M.  
PA (MADD//) MADDURI K M.  
PA (CORN//) CORNETT C A.  
PA (BREN//) BRENNER A A.  
PA (TANG//) TANG M.  
PA (LOPE//) LOPER J C.  
PA (GLEE//) GLEESON M.  
Best Local Similarity: 19.36%  
Query Match: 5.94%  
RESULT 1342  
ID ADF11791 standard; DNA; 4145 BP.  
DE C. tropicalis CPRB DNA.  
PN US2003148486-A1.  
PD 07-AUG-2003.  
PA (WILS//) WILSON C R.  
PA (CRAF//) CRAFT D L.  
PA (EIRI//) EIRICH L D.  
PA (ESHO//) ESHOO M.  
PA (MADD//) MADDURI K M.  
PA (CORN//) CORNETT C A.  
PA (BREN//) BRENNER A A.  
PA (TANG//) TANG M.  
PA (LOPE//) LOPER J C.  
PA (GLEE//) GLEESON M.  
Best Local Similarity: 19.36%  
Query Match: 5.94%  
RESULT 1343  
ID ADE64326 standard; DNA; 4145 BP.  
DE C. tropicalis NADPH-cytochrome P450 reductase, CPRB DNA.  
PN US2003068800-A1.  
PD 10-APR-2003.  
PA (WILS//) WILSON C R.  
PA (CRAF//) CRAFT D L.  
PA (EIRI//) EIRICH L D.  
PA (ESHO//) ESHOO M.  
PA (MADD//) MADDURI K M.  
PA (CORN//) CORNETT C A.  
PA (BREN//) BRENNER A A.  
PA (TANG//) TANG M.  
PA (LOPE//) LOPER J C.  
PA (GLEE//) GLEESON M.  
Best Local Similarity: 19.36%  
Query Match: 5.94%  
RESULT 1344  
ID ADJ26707 standard; DNA; 4145 BP.  
DE Candida tropicalis CPRB protein coding sequence.  
PN US2003186411-A1.  
PD 02-OCT-2003.  
PA (WILS//) WILSON C R.  
PA (CRAF//) CRAFT D L.  
PA (EIRI//) EIRICH L D.  
PA (ESHO//) ESHOO M.  
PA (MADD//) MADDURI K M.  
PA (CORN//) CORNETT C A.  
PA (BREN//) BRENNER A A.  
PA (TANG//) TANG M.  
PA (LOPE//) LOPER J C.  
PA (GLEE//) GLEESON M.  
Best Local Similarity: 19.36%  
Query Match: 5.94%  
RESULT 1345  
ID AA230081 standard; cDNA; 4509 BP.  
DE cDNA encoding a human MPR-related ABC transporter designated MOAT-B.  
PN WO9949735-A1.  
PD 07-OCT-1999.  
PA (FOXG-) FOX CHASE CANCER CENT.  
Best Local Similarity: 24.67%  
Query Match: 5.94%  
RESULT 1346  
ID AAD16259 standard; cDNA; 4511 BP.  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #4.  
PN WO200162977-A2.  
PD 30-AUG-2001.  
PA (PXEI-) PXE INT INC.  
PA (UYHA-) UNIV HAWAII.  
Best Local Similarity: 24.67%  
Query Match: 5.94%  
RESULT 1347  
ID AAD16262 standard; cDNA; 4512 BP.  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #7.

Best Local Similarity: 19.36%  
Query Match: 5.94%  
RESULT 1342  
ID ADF11791 standard; DNA; 4145 BP.  
DE C. tropicalis CPRB DNA.  
PN US2003148486-A1.  
PD 07-AUG-2003.  
PA (WILS//) WILSON C R.  
PA (CRAF//) CRAFT D L.  
PA (EIRI//) EIRICH L D.  
PA (ESHO//) ESHOO M.  
PA (MADD//) MADDURI K M.  
PA (CORN//) CORNETT C A.  
PA (BREN//) BRENNER A A.  
PA (TANG//) TANG M.  
PA (LOPE//) LOPER J C.  
PA (GLEE//) GLEESON M.  
Best Local Similarity: 19.36%  
Query Match: 5.94%  
RESULT 1343  
ID ADE64326 standard; DNA; 4145 BP.  
DE C. tropicalis NADPH-cytochrome P450 reductase, CPRB DNA.  
PN US2003068800-A1.  
PD 10-APR-2003.  
PA (WILS//) WILSON C R.  
PA (CRAF//) CRAFT D L.  
PA (EIRI//) EIRICH L D.  
PA (ESHO//) ESHOO M.  
PA (MADD//) MADDURI K M.  
PA (CORN//) CORNETT C A.  
PA (BREN//) BRENNER A A.  
PA (TANG//) TANG M.  
PA (LOPE//) LOPER J C.  
PA (GLEE//) GLEESON M.  
Best Local Similarity: 19.36%  
Query Match: 5.94%  
RESULT 1344  
ID ADJ26707 standard; DNA; 4145 BP.  
DE Candida tropicalis CPRB protein coding sequence.  
PN US2003186411-A1.  
PD 02-OCT-2003.  
PA (WILS//) WILSON C R.  
PA (CRAF//) CRAFT D L.  
PA (EIRI//) EIRICH L D.  
PA (ESHO//) ESHOO M.  
PA (MADD//) MADDURI K M.  
PA (CORN//) CORNETT C A.  
PA (BREN//) BRENNER A A.  
PA (TANG//) TANG M.  
PA (LOPE//) LOPER J C.  
PA (GLEE//) GLEESON M.  
Best Local Similarity: 19.36%  
Query Match: 5.94%  
RESULT 1345  
ID AA230081 standard; cDNA; 4509 BP.  
DE cDNA encoding a human MPR-related ABC transporter designated MOAT-B.  
PN WO9949735-A1.  
PD 07-OCT-1999.  
PA (FOXG-) FOX CHASE CANCER CENT.  
Best Local Similarity: 24.67%  
Query Match: 5.94%  
RESULT 1346  
ID AAD16259 standard; cDNA; 4511 BP.  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #4.  
PN WO200162977-A2.  
PD 30-AUG-2001.  
PA (PXEI-) PXE INT INC.  
PA (UYHA-) UNIV HAWAII.  
Best Local Similarity: 24.67%  
Query Match: 5.94%  
RESULT 1347  
ID AAD16262 standard; cDNA; 4512 BP.  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #7.

PN WO200162977-A2.  
PD 30-AUG-2001.  
PA (PXEI-) PXE INT INC.  
PA (UYHA-) UNIV HAWAII.  
Best Local Similarity: 24.67% Mismatches: 98  
Query Match: 5.94% Indels: 98  
RESULT 1348  
ID AAD16231 standard; cDNA; 4512 BP.  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) cDNA coding sequence.  
PN WO200162977-A2.  
PD 30-AUG-2001.  
PA (PXEI-) PXE INT INC.  
PA (UYHA-) UNIV HAWAII.  
Best Local Similarity: 24.67% Mismatches: 98  
Query Match: 5.94% Indels: 98  
RESULT 1349  
ID AAD16264 standard; cDNA; 4512 BP.  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #9.  
PN WO200162977-A2.  
PD 30-AUG-2001.  
PA (PXEI-) PXE INT INC.  
PA (UYHA-) UNIV HAWAII.  
Best Local Similarity: 24.67% Mismatches: 98  
Query Match: 5.94% Indels: 98  
RESULT 1350  
ID AAD16260 standard; cDNA; 4512 BP.  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #5.  
PN WO200162977-A2.  
PD 30-AUG-2001.  
PA (PXEI-) PXE INT INC.  
PA (UYHA-) UNIV HAWAII.  
Best Local Similarity: 24.67% Mismatches: 98  
Query Match: 5.94% Indels: 98  
RESULT 1351  
ID AAD16257 standard; cDNA; 4512 BP.  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #2.  
PN WO200162977-A2.  
PD 30-AUG-2001.  
PA (PXEI-) PXE INT INC.  
PA (UYHA-) UNIV HAWAII.  
Best Local Similarity: 24.67% Mismatches: 98  
Query Match: 5.94% Indels: 98  
RESULT 1352  
ID AAD16258 standard; cDNA; 4512 BP.  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #3.  
PN WO200162977-A2.  
PD 30-AUG-2001.  
PA (PXEI-) PXE INT INC.  
PA (UYHA-) UNIV HAWAII.  
Best Local Similarity: 24.67% Mismatches: 98  
Query Match: 5.94% Indels: 98  
RESULT 1353  
ID AAD16263 standard; cDNA; 4512 BP.  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #8.  
PN WO200162977-A2.  
PD 30-AUG-2001.  
PA (PXEI-) PXE INT INC.  
PA (UYHA-) UNIV HAWAII.  
Best Local Similarity: 24.67% Mismatches: 98  
Query Match: 5.94% Indels: 98  
RESULT 1354  
ID AAD16256 standard; cDNA; 4512 BP.  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #1.  
PN WO200162977-A2.  
PD 30-AUG-2001.  
PA (PXEI-) PXE INT INC.  
PA (UYHA-) UNIV HAWAII.  
Best Local Similarity: 24.67% Mismatches: 98  
Query Match: 5.94% Indels: 98  
RESULT 1355  
ID AAD16261 standard; cDNA; 4512 BP.  
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #6.  
PN WO200162977-A2.

PD 30-AUG-2001.  
PA (PXEI-) PXE INT INC.  
PA (UYHA-) UNIV HAWAII.  
Best Local Similarity: 24.67% Mismatches: 98  
Query Match: 5.94% Indels: 98  
RESULT 1356  
ID ADQ39092 standard; DNA; 4535 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 755.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 24.67% Mismatches: 98  
Query Match: 5.94% Indels: 98  
RESULT 1357  
ID ABN59902 standard; cDNA; 4866 BP.  
DE Novel human coding sequence SEQ ID NO: 313.  
PN WO200222660-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 23.91% Mismatches: 113  
Query Match: 5.94% Indels: 71  
RESULT 1358  
ID ACN39307 standard; cDNA; 4943 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA325546, SEQ ID NO:3367.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 23.91% Mismatches: 113  
Query Match: 5.94% Indels: 71  
RESULT 1359  
ID ADR08306 standard; cDNA; 5266 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 1812.  
PN EP4447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 23.00% Mismatches: 102  
Query Match: 5.94% Indels: 87  
RESULT 1360  
ID ADR32243 standard; cDNA; 5360 BP.  
DE Human tumour suppressor BNO208 cDNA, SEQ ID NO:13.  
PN WO200264780-A1.  
PD 22-AUG-2002.  
PA (BION-) BIONOMICS LTD.  
Best Local Similarity: 22.12% Mismatches: 123  
Query Match: 5.94% Indels: 95  
RESULT 1361  
ID ADN95876 standard; DNA; 5449 BP.  
DE Human BEC/LEC-related gene sequence SeqID800.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN-) LICENTIA LTD.  
Best Local Similarity: 23.91% Mismatches: 113  
Query Match: 5.94% Indels: 71  
RESULT 1362  
ID ADF81982 standard; DNA; 5456 BP.  
DE Leukaemia-related DNA sequence #2538.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE/) HAPERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KERN/) KERN W.  
Best Local Similarity: 24.90% Mismatches: 77  
Query Match: 5.94% Indels: 86  
RESULT 1363  
ID ADQ23094 standard; DNA; 5491 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5914.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 22.12% Mismatches: 123

Query Match: 5.94% Indels: 95  
 RESULT 1364  
 ID ADC99116 standard; cDNA; 5973 BP.  
 DE Human KPP cDNA - SEQ ID 69.  
 PN WO2003033680-A2.  
 PD 24-APR-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 23.38%  
 Query Match: 5.94% Mismatches: 64  
 Indels: 64  
 RESULT 1365  
 ID ABX34702 standard; cDNA; 5999 BP.  
 DE Human mddt cDNA SEQ ID 263.  
 PN WO200279449-A2.  
 PD 10-OCT-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 28.57%  
 Query Match: 5.94% Mismatches: 30  
 Indels: 38  
 RESULT 1366  
 ID ABX34526 standard; cDNA; 6001 BP.  
 DE Human mddt cDNA SEQ ID 87.  
 PN WO200279449-A2.  
 PD 10-OCT-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 28.57%  
 Query Match: 5.94% Mismatches: 30  
 Indels: 38  
 RESULT 1367  
 ID AAS91791 standard; cDNA; 6258 BP.  
 DE DNA encoding novel human diagnostic protein #27595.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 24.40%  
 Query Match: 5.94% Mismatches: 114  
 Indels: 114  
 RESULT 1368  
 ID AAS86371 standard; cDNA; 6306 BP.  
 DE DNA encoding novel human diagnostic protein #22175.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 24.40%  
 Query Match: 5.94% Mismatches: 114  
 Indels: 114  
 RESULT 1369  
 ID AAQ20186 standard; DNA; 7076 BP.  
 DE HlyA gene with ctxB and mer gene inserted.  
 PN WO9118979-A.  
 PD 12-DEC-1991.  
 PA (UYMA-) UNIV MARYLAND BALTI.  
 Best Local Similarity: 23.93%  
 Query Match: 5.94% Mismatches: 118  
 Indels: 96  
 RESULT 1370  
 ID ABS56664 standard; DNA; 9320 BP.  
 DE Plasmid p5-Puro-CMV-(N'-EGFP)-CMV-Red (EGFP-BJ) DNA.  
 PN WO200270740-A2.  
 PD 12-SEP-2002.  
 PA (WIES/) WIESMUELLER L.  
 Best Local Similarity: 23.88%  
 Query Match: 5.94% Mismatches: 88  
 Indels: 104  
 RESULT 1371  
 ID ADG75175 standard; DNA; 9369 BP.  
 DE Human herpesvirus 2 strain HG52 UL36 DNA - SEQ ID 247.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 22.94%  
 Query Match: 5.94% Mismatches: 115  
 Indels: 111  
 RESULT 1372  
 ID ADG75118 standard; DNA; 9369 BP.  
 DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 22.94%  
 Query Match: 5.94% Mismatches: 115  
 Indels: 111

RESULT 1373  
 ID ABR84372 standard; cDNA; 37160 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #943.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Best Local Similarity: 26.70%  
 Query Match: 5.94% Mismatches: 69  
 Indels: 76  
 RESULT 1374  
 ID AAA29349 standard; DNA; 71989 BP.  
 DE Sorangium cellulosum epothilone polyketide synthase operon genomic DNA.  
 Best Local Similarity: 21.71%  
 Query Match: 5.94% Mismatches: 100  
 Indels: 130  
 RESULT 1375  
 ID ADS73531 standard; cDNA; 73882 BP.  
 DE tcp gene cluster.  
 Best Local Similarity: 23.34%  
 Query Match: 5.94% Mismatches: 92  
 Indels: 100  
 RESULT 1376  
 ID ADQ74672 standard; DNA; 74787 BP.  
 DE Streptomyces parvulus borrelidin polyketide synthase gene cluster.  
 Best Local Similarity: 26.59%  
 Query Match: 5.94% Mismatches: 90  
 Indels: 74  
 RESULT 1377  
 ID AAL61224 standard; DNA; 82746 BP.  
 DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster I.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW ) UNIV WASHINGTON.  
 Best Local Similarity: 24.03%  
 Query Match: 5.94% Mismatches: 89  
 Indels: 82  
 RESULT 1378  
 Best Local Similarity: 26.78%  
 Query Match: 5.94% Mismatches: 97  
 Indels: 56  
 RESULT 1379  
 Best Local Similarity: 25.09%  
 Query Match: 5.94% Mismatches: 98  
 Indels: 78  
 RESULT 1380  
 Best Local Similarity: 26.78%  
 Query Match: 5.94% Mismatches: 97  
 Indels: 56  
 RESULT 1381  
 Best Local Similarity: 25.09%  
 Query Match: 5.94% Mismatches: 98  
 Indels: 78  
 RESULT 1382  
 Best Local Similarity: 24.42%  
 Query Match: 5.94% Mismatches: 113  
 Indels: 115  
 RESULT 1383  
 Best Local Similarity: 24.42%  
 Query Match: 5.94% Mismatches: 113  
 Indels: 115  
 RESULT 1384  
 Best Local Similarity: 24.42%  
 Query Match: 5.94% Mismatches: 113  
 Indels: 115  
 RESULT 1385  
 Best Local Similarity: 24.42%  
 Query Match: 5.94% Mismatches: 113  
 Indels: 115  
 RESULT 1386  
 Best Local Similarity: 24.42%  
 Query Match: 5.94% Mismatches: 113  
 Indels: 115  
 RESULT 1387  
 Best Local Similarity: 24.42%  
 Query Match: 5.94% Mismatches: 113  
 Indels: 115  
 RESULT 1388  
 ID AAD25519 standard; DNA; 154746 BP.  
 DE Human herpesvirus 2 complete DNA genome.  
 PN WO200176643-A1.  
 PD 18-OCT-2001.  
 PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
 Best Local Similarity: 22.94%  
 Query Match: 5.94% Mismatches: 115  
 Indels: 111  
 RESULT 1389  
 ID ACH72734 standard; DNA; 593 BP.  
 DE Human genome derived single exon probe #5929.  
 PN US2003194704-A1.

PD 16-OCT-2003.  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 Query Match: 5.90% Mismatches: 52  
 Indels: 33  
 RESULT 1390  
 ID AAH68388 standard; DNA; 618 BP.  
 DE C glutamicum coding sequence fragment SEQ ID NO: 3423.  
 PN EPI108790-A2.  
 PD 20-JUN-2001.  
 PA (KYOW) KYOWA HAKKO KOGYO KK.  
 Best Local Similarity: 27.84% Mismatches: 72  
 Query Match: 5.90% Indels: 35  
 RESULT 1391  
 ID AC01302 standard; DNA; 618 BP.  
 DE C. glutamicum derived ORF SEQ ID 1293.  
 PN DE10128510-A1.  
 PD 19-DEC-2002.  
 PA (DEGS) DEGUSSA AG.  
 Best Local Similarity: 27.84% Mismatches: 72  
 Query Match: 5.90% Indels: 35  
 RESULT 1392  
 ID AD054370 standard; DNA; 630 BP.  
 DE Novel canine microarray-related DNA sequence SeqID5672.  
 PN WO2004063324-A2.  
 PD 29-JUL-2004.  
 PA (GENE-) GENE LOGIC INC.  
 PA (PFIZ) PFIZER PROD INC.  
 Best Local Similarity: 28.99% Mismatches: 79  
 Query Match: 5.90% Indels: 49  
 RESULT 1393  
 ID AAL50538 standard; DNA; 873 BP.  
 DE Human B7-H1 protein open reading frame.  
 PN US2002106730-A1.  
 PD 08-AUG-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 24.49% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1394  
 ID ADC78840 standard; DNA; 873 BP.  
 DE Human PRO protein coding sequence #35.  
 PN WO2003034984-A2.  
 PD 01-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 24.49% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1395  
 ID ADH71945 standard; DNA; 873 BP.  
 DE Human gene of the invention NOV35d SEQ ID NO:841.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 24.49% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1396  
 ID AD076314 standard; cDNA; 873 BP.  
 DE Human B7-H1 cDNA open reading frame.  
 PN US2004137577-A1.  
 PD 15-JUL-2004.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 24.49% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1397  
 ID ADH71939 standard; DNA; 874 BP.  
 DE Human gene of the invention NOV35a SEQ ID NO:835.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 24.49% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1398  
 ID ADH71943 standard; DNA; 900 BP.

DE Human gene of the invention NOV35c SEQ ID NO:839.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 24.49% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1399  
 ID ADH71953 standard; DNA; 900 BP.  
 DE Human gene of the invention NOV35h SEQ ID NO:849.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 24.49% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1400  
 ID ABA03886 standard; cDNA; 967 BP.  
 DE Human POLY17 nucleotide sequence SEQ ID NO:33.  
 PN WO200179294-A2.  
 PD 25-OCT-2001.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 27.66% Mismatches: 53  
 Query Match: 5.90% Indels: 27  
 RESULT 1401  
 ID ABX56482 standard; cDNA; 967 BP.  
 DE cDNA encoding novel human prohibitin-like protein.  
 PN US2002123612-A1.  
 PD 05-SEP-2002.  
 PA (GERL) GERLACH V L.  
 PA (ELLE) ELLERMAN K.  
 PA (MACD) MACDOUGALL J R.  
 PA (SMIT) SMITHSON G.  
 Best Local Similarity: 27.66% Mismatches: 53  
 Query Match: 5.90% Indels: 27  
 RESULT 1402  
 ID ADQ87187 standard; cDNA; 1140 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #4064.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD) WU T D.  
 PA (ZHOU) ZHOU Y.  
 Best Local Similarity: 26.37% Mismatches: 93  
 Query Match: 5.90% Indels: 82  
 RESULT 1403  
 ID ADQ84909 standard; cDNA; 1140 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #1723.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD) WU T D.  
 PA (ZHOU) ZHOU Y.  
 Best Local Similarity: 26.37% Mismatches: 93  
 Query Match: 5.90% Indels: 82  
 RESULT 1404  
 ID AAN80973 standard; DNA; 1152 BP.  
 DE Sequence encoding adr type hepatitis B virus (HBV) surface antigen  
 DE (HBSAg) L protein (M protein, S protein).  
 PN EP288198-A.  
 PD 26-OCT-1988.  
 PA (TAKE) TAKEDA CHEM IND LTD.  
 Best Local Similarity: 26.57% Mismatches: 35  
 Query Match: 5.90% Indels: 60  
 RESULT 1405  
 ID ACA26577 standard; DNA; 1179 BP.  
 DE Prokaryotic essential gene #8234.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 25.56% Mismatches: 95  
 Query Match: 5.90% Indels: 44  
 RESULT 1406  
 ID ABD17700 standard; DNA; 1251 BP.  
 DE Pseudomonas aeruginosa polynucleotide #16304.

PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 31.22% Mismatches: 87  
 Query Match: 5.90% Indels: 47  
 RESULT 1407  
 ID ADC30883 standard; cDNA; 1276 BP.  
 DE Human novel cDNA sequence, SEQ ID NO:965.  
 PN WO2003029271-A2.  
 PD 10-APR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 29.48% Mismatches: 72  
 Query Match: 5.90% Indels: 89  
 RESULT 1408  
 ID ABV77054 standard; DNA; 1286 BP.  
 DE Nucleotide sequence of a modified bacterial envelope (env) L protein.  
 PN WO200286091-A2.  
 PD 31-OCT-2002.  
 PA (REGC) UNIV CALIFORNIA.  
 Best Local Similarity: 25.84% Mismatches: 41  
 Query Match: 5.90% Indels: 79  
 RESULT 1409  
 ID ABV76128 standard; cDNA; 1286 BP.  
 DE Hepatitis B virus envelope L protein gene.  
 PN WO200287594-A1.  
 PD 07-NOV-2002.  
 PA (REGC) UNIV CALIFORNIA.  
 Best Local Similarity: 25.84% Mismatches: 41  
 Query Match: 5.90% Indels: 79  
 RESULT 1410  
 ID AAH14847 standard; cDNA; 1301 BP.  
 DE Human cDNA sequence SEQ ID NO:12675.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Best Local Similarity: 24.49% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1411  
 ID ADR92566 standard; DNA; 1311 BP.  
 DE Novel S. pneumoniae DNA sequence, SEQ ID 1201.  
 PN US6800744-B1.  
 PD 05-OCT-2004.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 22.99% Mismatches: 70  
 Query Match: 5.90% Indels: 51  
 RESULT 1412  
 ID ACA42334 standard; DNA; 1314 BP.  
 DE Prokaryotic essential gene #23991.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 28.30% Mismatches: 90  
 Query Match: 5.90% Indels: 73  
 RESULT 1413  
 ID ADT46053 standard; cDNA; 1323 BP.  
 DE Bacterial polynucleotide #20804.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 22.65% Mismatches: 91  
 Query Match: 5.90% Indels: 107  
 RESULT 1414  
 ID ACH87582 standard; DNA; 1324 BP.  
 DE Human genome derived single exon probe #20777.  
 PN US2003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.

Best Local Similarity: 28.44% Mismatches: 78  
 Query Match: 5.90% Indels: 58  
 RESULT 1415  
 ID ABX56047 standard; DNA; 1347 BP.  
 DE M. echinospora calicheamicin biosynthesis gene calW.  
 PN WO200279465-A2.  
 PD 10-OCT-2002.  
 PA (SLOK) SLOAN KETTERING INST CANCER RES.  
 Best Local Similarity: 22.05% Mismatches: 83  
 Query Match: 5.90% Indels: 85  
 RESULT 1416  
 ID ABL17258 standard; DNA; 1380 BP.  
 DE Pseudomonas aeruginosa polynucleotide #15862.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 24.61% Mismatches: 93  
 Query Match: 5.90% Indels: 77  
 RESULT 1417  
 ID ADQ25304 standard; DNA; 1395 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8124.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Best Local Similarity: 29.48% Mismatches: 72  
 Query Match: 5.90% Indels: 89  
 RESULT 1418  
 ID ACC62520 standard; cDNA; 1406 BP.  
 DE Human secreted protein #46 coding sequence SEQ ID 56.  
 PN WO200299066-A2.  
 PD 12-DEC-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 29.48% Mismatches: 72  
 Query Match: 5.90% Indels: 89  
 RESULT 1419  
 ID ACC62491 standard; cDNA; 1406 BP.  
 DE Human secreted protein #17 coding sequence SEQ ID 27.  
 PN WO200299066-A2.  
 PD 12-DEC-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 29.48% Mismatches: 72  
 Query Match: 5.90% Indels: 89  
 RESULT 1420  
 ID ADT42234 standard; cDNA; 1413 BP.  
 DE Bacterial polynucleotide #16985.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 21.95% Mismatches: 83  
 Query Match: 5.90% Indels: 78  
 RESULT 1421  
 ID ADQ85209 standard; cDNA; 1528 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2023.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Best Local Similarity: 21.75% Mismatches: 107  
 Query Match: 5.90% Indels: 139  
 RESULT 1422  
 ID ADQ86369 standard; cDNA; 1528 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #3241.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Best Local Similarity: 21.75% Mismatches: 107  
 Query Match: 5.90% Indels: 139



Query Match: 5.90% Indels: 139  
 RESULT 1423  
 ID ABD02520 standard; DNA; 1533 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1124.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 23.9% Mismatches: 76  
 Query Match: 5.90% Indels: 89  
 RESULT 1424  
 ID ACA26225 standard; DNA; 1545 BP.  
 DE Prokaryotic essential gene #7882.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 25.6% Mismatches: 73  
 Query Match: 5.90% Indels: 94  
 RESULT 1425  
 ID ABD16063 standard; DNA; 1545 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14667.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 21.8% Mismatches: 82  
 Query Match: 5.90% Indels: 103  
 RESULT 1426  
 ID AAD02773 standard; cDNA; 1552 BP.  
 DE Human B7-4 membrane (B7-4M) protein DNA.  
 PN WO200114557-A1.  
 PD 01-MAR-2001.  
 PA (DAND) DANA FARBER CANCER INST INC.  
 PA (GENY) GENETICS INST INC.  
 Best Local Similarity: 24.4% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1427  
 ID AAD02708 standard; cDNA; 1553 BP.  
 DE Human B7-4 membrane (B7-4M) protein cDNA.  
 PN WO200114556-A1.  
 PD 01-MAR-2001.  
 PA (DAND) DANA FARBER CANCER INST INC.  
 Best Local Similarity: 24.4% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1428  
 ID AAD51085 standard; DNA; 1553 BP.  
 DE Human membrane B7-4 (B7-4M) DNA.  
 PN WO200279499-A1.  
 PD 10-OCT-2002.  
 PA (AMHP) WYETH.  
 PA (DAND) DANA FARBER CANCER INST INC.  
 Best Local Similarity: 24.4% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1429  
 ID ABT13989 standard; DNA; 1553 BP.  
 DE Human PD-LiM coding sequence.  
 PN WO200278731-A1.  
 PD 10-OCT-2002.  
 PA (AMHP) WYETH.  
 Best Local Similarity: 24.4% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1430  
 ID ADJ75002 standard; DNA; 1553 BP.  
 DE Marker gene SEQ ID NO:254.  
 PN EP1394274-A2.  
 PD 03-MAR-2004.  
 PA (GENO-) GENOX RES INC.  
 Best Local Similarity: 24.4% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1431  
 ID ABD05949 standard; DNA; 1572 BP.  
 DE Pseudomonas aeruginosa polynucleotide #4553.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.

Best Local Similarity: 25.73% Mismatches: 67  
 Query Match: 5.90% Indels: 68  
 RESULT 1432  
 ID ABD17809 standard; DNA; 1581 BP.  
 DE Pseudomonas aeruginosa polynucleotide #16413.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 31.22% Mismatches: 87  
 Query Match: 5.90% Indels: 47  
 RESULT 1433  
 ID ABK24010 standard; DNA; 1604 BP.  
 DE DNA encoding B7-related protein, BSL1 #1.  
 PN WO200194413-A2.  
 PD 13-DEC-2001.  
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
 Best Local Similarity: 24.49% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1434  
 ID ADA24486 standard; cDNA; 1666 BP.  
 DE Human cDNA differential expressed in adipose tissue, INCYTE209356CB1.  
 PN US2003096272-A1.  
 PD 22-MAY-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 21.75% Mismatches: 107  
 Query Match: 5.90% Indels: 139  
 RESULT 1435  
 ID ABX75849 standard; cDNA; 1674 BP.  
 DE Human NeuL cDNA #2.  
 PN US2002132293-A1.  
 PD 19-SEP-2002.  
 PA (PALM/) PALM K.  
 PA (TIMM/) TIMMUSK T.  
 Best Local Similarity: 24.80% Mismatches: 119  
 Query Match: 5.90% Indels: 52  
 RESULT 1436  
 ID AAL57526 standard; cDNA; 1674 BP.  
 DE Human neuralised-like cDNA.  
 PN WO2003061681-A2.  
 PD 31-JUN-2003.  
 PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.  
 Best Local Similarity: 24.80% Mismatches: 119  
 Query Match: 5.90% Indels: 52  
 RESULT 1437  
 ID ADS58584 standard; cDNA; 1677 BP.  
 DE Bacterial polynucleotide #10571.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 22.02% Mismatches: 116  
 Query Match: 5.90% Indels: 98  
 RESULT 1438  
 ID ABX63316 standard; cDNA; 1679 BP.  
 DE Human cDNA #316 differentially expressed in activated vascular tissue.  
 PN US2002137081-A1.  
 PD 26-SEP-2002.  
 PA (BAND/) BANDMAN O.  
 Best Local Similarity: 21.75% Mismatches: 107  
 Query Match: 5.90% Indels: 139  
 RESULT 1439  
 ID ABD05695 standard; DNA; 1686 BP.  
 DE Pseudomonas aeruginosa polynucleotide #4299.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 25.73% Mismatches: 67  
 Query Match: 5.90% Indels: 68  
 RESULT 1440  
 ID ABX75848 standard; cDNA; 1725 BP.

DE Human Neu1 cDNA #1.  
 PN US2002132293-A1.  
 PD 19-SEP-2002.  
 PA (PALM//) PALM K.  
 PA (TIMM//) TIMMUSK T.  
 Best Local Similarity: 24.80% Mismatches: 119  
 Query Match: 5.90% Indels: 52  
 RESULT 1441  
 ID ABD16181 standard; DNA; 1767 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14785.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 21.86% Mismatches: 82  
 Query Match: 5.90% Indels: 103  
 RESULT 1442  
 ID ADJ35133 standard; DNA; 1794 BP.  
 DE DNA encoding xylanase from an environmental sample seq id 349.  
 PN WO2003106654-A2.  
 PD 24-DEC-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Best Local Similarity: 25.22% Mismatches: 109  
 Query Match: 5.90% Indels: 122  
 RESULT 1443  
 ID ADU62377 standard; DNA; 1798 BP.  
 DE Human ovarian cancer DNA marker #20589.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Best Local Similarity: 21.75% Mismatches: 107  
 Query Match: 5.90% Indels: 139  
 RESULT 1444  
 ID AAS94795 standard; DNA; 1833 BP.  
 DE Human DNA sequence #50 expressed during foam cell differentiation.  
 PN WO200177389-A2.  
 PD 18-OCT-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 21.75% Mismatches: 107  
 Query Match: 5.90% Indels: 139  
 RESULT 1445  
 ID ADB47391 standard; cDNA; 1833 BP.  
 DE Human cDNA upregulated in dendritic cells SEQ ID NO 91.  
 PN US2003134283-A1.  
 PD 17-JUL-2003.  
 PA (PETE//) PETERSON D P.  
 PA (PEAR//) PEARSON C I.  
 PA (COCK//) COCKS B G.  
 Best Local Similarity: 21.75% Mismatches: 107  
 Query Match: 5.90% Indels: 139  
 RESULT 1446  
 ID ADS62794 standard; cDNA; 1860 BP.  
 DE Bacterial polynucleotide #14781.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY//) CAO Y.  
 PA (HINK//) HINKLE G J.  
 PA (SLAT//) SLATER S C.  
 PA (CHEN//) CHEN X.  
 PA (GOLD//) GOLDMAN B S.  
 Best Local Similarity: 22.65% Mismatches: 109  
 Query Match: 5.90% Indels: 94  
 RESULT 1447  
 ID ADS62948 standard; cDNA; 1869 BP.  
 DE Bacterial polynucleotide #14935.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY//) CAO Y.  
 PA (HINK//) HINKLE G J.  
 PA (SLAT//) SLATER S C.  
 PA (CHEN//) CHEN X.  
 PA (GOLD//) GOLDMAN B S.  
 Best Local Similarity: 22.65% Mismatches: 109  
 Query Match: 5.90% Indels: 94

RESULT 1448  
 ID ADS59386 standard; cDNA; 1949 BP.  
 DE Bacterial polynucleotide #11373.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY//) CAO Y.  
 PA (HINK//) HINKLE G J.  
 PA (SLAT//) SLATER S C.  
 PA (CHEN//) CHEN X.  
 PA (GOLD//) GOLDMAN B S.  
 Best Local Similarity: 22.65% Mismatches: 109  
 Query Match: 5.90% Indels: 94  
 RESULT 1449  
 ID AAZ28095 standard; cDNA; 1976 BP.  
 DE Human FREAC3 protein encoding cDNA.  
 PN WO9954493-A2.  
 PD 28-OCT-1999.  
 PA (UYAL-) UNIV ALBERTA.  
 Best Local Similarity: 25.91% Mismatches: 81  
 Query Match: 5.90% Indels: 77  
 RESULT 1450  
 ID ABD09538 standard; DNA; 2031 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8142.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 22.38% Mismatches: 88  
 Query Match: 5.90% Indels: 99  
 RESULT 1451  
 ID ABL17287 standard; DNA; 2106 BP.  
 DE Pseudomonas aeruginosa polynucleotide #15891.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 24.61% Mismatches: 93  
 Query Match: 5.90% Indels: 77  
 RESULT 1452  
 ID ACA26420 standard; DNA; 2184 BP.  
 DE Prokaryotic essential gene #8077.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 24.00% Mismatches: 105  
 Query Match: 5.90% Indels: 49  
 RESULT 1453  
 ID AAX77135 standard; DNA; 2207 BP.  
 DE Human nerve mutation factor protein encoding DNA.  
 PN WO9925827-A1.  
 PD 27-MAY-1999.  
 PA (SUME-) SUMITOMO ELECTRIC IND CO.  
 Best Local Similarity: 24.80% Mismatches: 119  
 Query Match: 5.90% Indels: 52  
 RESULT 1454  
 ID AAH1621 standard; cDNA; 2314 BP.  
 DE Human cDNA sequence SEQ ID NO:17145.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Best Local Similarity: 21.05% Mismatches: 86  
 Query Match: 5.90% Indels: 95  
 RESULT 1455  
 ID ABQ90266 standard; DNA; 2343 BP.  
 DE M. capulatus gene #251 for DNA array.  
 PN WO200255655-A2.  
 PD 18-JUL-2002.  
 PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.  
 PA (TIGR-) TIGR.  
 Best Local Similarity: 25.09% Mismatches: 82  
 Query Match: 5.90% Indels: 98  
 RESULT 1456  
 ID AAD07571 standard; cDNA; 2382 BP.  
 DE Human secreted protein-encoding gene 1 cDNA clone HCE3T57, SEQ ID NO:11.  
 PN WO200132676-A1.

PD 10-MAY-2001.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 22.64% Mismatches: 66  
Query Match: 5.90% Indels: 71  
RESULT 1457  
ID AAO63477 standard; DNA; 2386 BP.  
DE Micrococcal putrescine oxidase gene.  
PN JP06098778-A.  
PD 12-APR-1994.  
PA (BEPF/) BEPPU T.  
Best Local Similarity: 24.91% Mismatches: 116  
Query Match: 5.90% Indels: 62  
RESULT 1458  
ID AAK94224 standard; cDNA; 2472 BP.  
DE Human full-length cDNA, SEQ ID NO: 2806.  
PN EP1130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Best Local Similarity: 22.64% Mismatches: 66  
Query Match: 5.90% Indels: 71  
RESULT 1459  
ID AD130773 standard; cDNA; 2472 BP.  
DE Full length human cDNA clone SeqID 2806.  
PN EP1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 22.64% Mismatches: 66  
Query Match: 5.90% Indels: 71  
RESULT 1460  
ID AB033315 standard; cDNA; 2478 BP.  
DE Human cancer-associated (CA) cDNA HR07-056.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Best Local Similarity: 26.64% Mismatches: 82  
Query Match: 5.90% Indels: 76  
RESULT 1461  
ID ABX05463 standard; cDNA; 2484 BP.  
DE Human novel polynucleotide #478.  
PN WO200274961-A1.  
PD 26-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 26.64% Mismatches: 82  
Query Match: 5.90% Indels: 76  
RESULT 1462  
ID AAD33659 standard; cDNA; 2917 BP.  
DE Human TRICH-14 cDNA.  
PN WO200212340-A2.  
PD 14-FEB-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 22.64% Mismatches: 66  
Query Match: 5.90% Indels: 71  
RESULT 1463  
ID ACN42900 standard; cDNA; 2965 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1775.  
PN WO2004023373-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 25.36% Mismatches: 112  
Query Match: 5.90% Indels: 72  
RESULT 1464  
ID ADD24552 standard; DNA; 3096 BP.  
DE DNA polymerase III subunit protein encoding DNA, dnaE #2, SEQ ID NO 71.  
PN WO200292769-A2.  
PD 21-NOV-2002.  
PA (REPL-) REPLIDYNE INC.  
Best Local Similarity: 25.00% Mismatches: 77  
Query Match: 5.90% Indels: 49  
RESULT 1465  
ID ADD24551 standard; DNA; 3096 BP.  
DE DNA polymerase III subunit protein encoding DNA, dnaE #2, SEQ ID NO 70.  
PN WO200292769-A2.  
PD 21-NOV-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 22.64% Mismatches: 66  
Query Match: 5.90% Indels: 71  
RESULT 1466  
ID AD09490 standard; DNA; 3162 BP.  
DE Pseudomonas aeruginosa polynucleotide #8094.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 22.38% Mismatches: 88  
Query Match: 5.90% Indels: 99  
RESULT 1467  
ID ACN43533 standard; cDNA; 3208 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2408.  
PN WO2004023373-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 22.64% Mismatches: 66  
Query Match: 5.90% Indels: 71  
RESULT 1468  
ID ADQ18548 standard; DNA; 3291 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1367.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 23.49% Mismatches: 129  
Query Match: 5.90% Indels: 93  
RESULT 1469  
ID ADI21763 standard; cDNA; 3323 BP.  
DE Novel human protein cDNA #22.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 22.64% Mismatches: 66  
Query Match: 5.90% Indels: 71  
RESULT 1470  
ID ADQ97093 standard; DNA; 3331 BP.  
DE Human cancer associated sequence HR1-10-005, SEQ ID 69.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Best Local Similarity: 22.64% Mismatches: 66  
Query Match: 5.90% Indels: 71  
RESULT 1471  
ID AAD21996 standard; cDNA; 3343 BP.  
DE Human transporters and ion channels (TRICH)-4 cDNA.  
PN WO200177174-A2.  
PD 18-OCT-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 22.64% Mismatches: 66  
Query Match: 5.90% Indels: 71  
RESULT 1472  
ID ADL12773 standard; cDNA; 3343 BP.  
DE Human steroid-induced C3A liver cell cDNA #502.  
PN US6673549-B1.  
PD 06-JAN-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 22.64% Mismatches: 66  
Query Match: 5.90% Indels: 71  
RESULT 1473  
ID ACN43532 standard; cDNA; 3374 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2407.  
PN WO2004023373-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 22.64% Mismatches: 66  
Query Match: 5.90% Indels: 71  
RESULT 1474  
ID AAH75190 standard; cDNA; 3408 BP.  
DE Nucleotide sequence of a human 33894 transporter polypeptide.  
PN WO200164875-A2.  
PD 07-SEP-2001.  
PA (MILL-) MILLENNIUM PHARM INC.

Best Local Similarity: 22.64% Mismatches: 66  
 Query Match: 5.90% Indels: 71  
 RESULT 1475  
 ID AAX09012 standard; DNA; 3411 BP.  
 DE Human axin gene.  
 PN WO9902179-A1.  
 PD 21-JAN-1999.  
 PA (UYCO-) UNIV COLUMBIA NEW YORK.  
 Best Local Similarity: 22.22% Mismatches: 124  
 Query Match: 5.90% Indels: 113  
 RESULT 1476  
 ID ABA82681 standard; DNA; 3411 BP.  
 DE Wnt signaling gene (AXIN) SEQ ID NO:67.  
 PN WO200177327-A1.  
 PD 18-OCT-2001.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 22.22% Mismatches: 124  
 Query Match: 5.90% Indels: 113  
 RESULT 1477  
 ID ACC46001 standard; DNA; 3411 BP.  
 DE Human Wnt signalling gene AXIN.  
 PN WO200292764-A2.  
 PD 21-NOV-2002.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 PA (AMHP-) WYETH.  
 Best Local Similarity: 22.22% Mismatches: 124  
 Query Match: 5.90% Indels: 113  
 RESULT 1478  
 ID ADB98695 standard; DNA; 3411 BP.  
 DE Human axin (AXIN) DNA.  
 PN WO200292000-A2.  
 PD 21-NOV-2002.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 PA (AMHP-) WYETH.  
 Best Local Similarity: 22.22% Mismatches: 124  
 Query Match: 5.90% Indels: 113  
 RESULT 1479  
 ID ADD14620 standard; cDNA; 3411 BP.  
 DE Human src biomarker polynucleotide SEQ ID NO:14.  
 PN WO2003062395-A2.  
 PD 31-JUL-2003.  
 PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
 Best Local Similarity: 22.22% Mismatches: 124  
 Query Match: 5.90% Indels: 113  
 RESULT 1480  
 ID ADE82491 standard; DNA; 3411 BP.  
 DE Human DNA sequence related to the invention #35.  
 PN WO200292015-A2.  
 PD 21-NOV-2002.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 PA (AMHP-) WYETH.  
 Best Local Similarity: 22.22% Mismatches: 124  
 Query Match: 5.90% Indels: 113  
 RESULT 1481  
 ID ABT07557 standard; cDNA; 3414 BP.  
 DE Human breast cancer associated coding sequence SEQ ID NO: 36.  
 PN WO200264611-A1.  
 PD 22-AUG-2002.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 19.54% Mismatches: 96  
 Query Match: 5.90% Indels: 65  
 RESULT 1482  
 ID ADD71208 standard; cDNA; 3489 BP.  
 DE Human intracellular signalling molecule INTS1G-45 cDNA SEQ ID NO:97.  
 PN WO2003039348-A2.  
 PD 15-MAY-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 26.56% Mismatches: 101  
 Query Match: 5.90% Indels: 60  
 RESULT 1483  
 ID ADQ97095 standard; DNA; 3503 BP.  
 DE Human cancer associated sequence HR2-10-005, SEQ ID 71.  
 PN WO2004060304-A2.

PD 22-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Best Local Similarity: 22.64% Mismatches: 66  
 Query Match: 5.90% Indels: 71  
 RESULT 1484  
 ID ACM43530 standard; cDNA; 3503 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2405.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 22.64% Mismatches: 66  
 Query Match: 5.90% Indels: 71  
 RESULT 1485  
 ID ABV74348 standard; DNA; 3512 BP.  
 DE Human ABC transporter ABCB9 encoding polynucleotide SEQ ID NO 1.  
 PN WO200264781-A2.  
 PD 22-AUG-2002.  
 PA (ACTI-) ACTIVE PASS PHARM INC.  
 Best Local Similarity: 22.64% Mismatches: 66  
 Query Match: 5.90% Indels: 71  
 RESULT 1486  
 ID AAD06381 standard; cDNA; 3536 BP.  
 DE Human ATP binding cassette, ABCB9 transporter cDNA.  
 PN WO200140305-A1.  
 PD 07-JUN-2001.  
 PA (ACTI-) ACTIVE PASS PHARM INC.  
 Best Local Similarity: 22.64% Mismatches: 66  
 Query Match: 5.90% Indels: 71  
 RESULT 1487  
 ID AAD05053 standard; cDNA; 3568 BP.  
 DE Human secreted protein-encoding gene 1 cDNA clone HDPAP35, SEQ ID NO:11.  
 PN WO200134768-A2.  
 PD 17-MAY-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 24.49% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1488  
 ID AAS02121 standard; cDNA; 3575 BP.  
 DE Human TANGO 509, variant cDNA sequence #4.  
 PN WO200121631-A2.  
 PD 29-MAR-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 24.49% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1489  
 ID AAS02119 standard; cDNA; 3575 BP.  
 DE Human TANGO 509, alternative cDNA sequence #2.  
 PN WO200121631-A2.  
 PD 29-MAR-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 24.49% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1490  
 ID AAS02118 standard; cDNA; 3575 BP.  
 DE Human TANGO 509, alternative cDNA sequence #1.  
 PN WO200121631-A2.  
 PD 29-MAR-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 24.49% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1491  
 ID AAS02120 standard; cDNA; 3575 BP.  
 DE Human TANGO 509, alternative cDNA sequence #3.  
 PN WO200121631-A2.  
 PD 29-MAR-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 24.49% Mismatches: 73  
 Query Match: 5.90% Indels: 53  
 RESULT 1492  
 ID AAS02076 standard; cDNA; 3575 BP.  
 DE Human TANGO 509 cDNA sequence.  
 PN WO200121631-A2.  
 PD 29-MAR-2001.

PA (MILL-) MILLENNIUM PHARM INC.			
Best Local Similarity: 24.49%	Mismatches: 73		
Query Match: 5.90%	Indels: 53		
RESULT 1493			
ID AAD44205 standard; cDNA; 3575 BP.			
DE Human TANGO 509 cDNA.			
PN US200205139-A1.			
PD 09-MAY-2002.			
PA (HOLT/) HOLTZMAN D A.			
PA (SHAR/) SHARP J D.			
PA (LEIB/) LEIBY K R.			
PA (BOSS/) BOSSONE S.			
PA (PANY/) PAN Y.			
PA (BARN/) BARNES T M.			
PA (FRAS/) FRASER C C.			
PA (WRIG/) WRIGHTON N.			
PA (MYER/) MYERS P S.			
PA (KING/) KINGSBURY G.			
Best Local Similarity: 24.49%	Mismatches: 73		
Query Match: 5.90%	Indels: 53		
RESULT 1494			
ID AAS06592 standard; cDNA; 3616 BP.			
DE Human immunoregulatory protein B7-H1 cDNA sequence.			
PN WO200139722-A2.			
PD 07-JUN-2001.			
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.			
Best Local Similarity: 24.49%	Mismatches: 73		
Query Match: 5.90%	Indels: 53		
RESULT 1495			
ID ABK24011 standard; DNA; 3621 BP.			
DE DNA encoding B7-related protein, BSL1 #2.			
PN WO200194413-A2.			
PD 13-DEC-2001.			
PA (BRIM) BRISTOL-MYERS SQUIBB CO.			
Best Local Similarity: 24.49%	Mismatches: 73		
Query Match: 5.90%	Indels: 53		
RESULT 1496			
ID ADN05336 standard; cDNA; 3639 BP.			
DE Antipsoriatic cDNA sequence #890.			
PN WO2004028479-A2.			
PD 08-APR-2004.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 24.49%	Mismatches: 73		
Query Match: 5.90%	Indels: 53		
RESULT 1497			
ID ADP55776 standard; cDNA; 3639 BP.			
DE Human PRO cDNA sequence SEQ ID NO:1752.			
PN WO2004039956-A2.			
PD 13-MAY-2004.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 24.49%	Mismatches: 73		
Query Match: 5.90%	Indels: 53		
RESULT 1498			
ID ADL45714 standard; DNA; 3660 BP.			
DE Human ovarian cancer DNA marker #19604.			
PN WO200170979-A2.			
PD 27-SEP-2001.			
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.			
Best Local Similarity: 24.49%	Mismatches: 73		
Query Match: 5.90%	Indels: 53		
RESULT 1499			
ID AAH42339 standard; DNA; 3726 BP.			
DE Nucleotide sequence of a human xylosyltransferase (XT) isoform XT-I.			
PN WO200149831-A2.			
PD 12-JUL-2001.			
PA (KLEE/) KLEESIEK K.			
Best Local Similarity: 26.64%	Mismatches: 82		
Query Match: 5.90%	Indels: 76		
RESULT 1500			
ID ADO31179 standard; DNA; 3728 BP.			
DE Human XT-I gene for glucosaminoglycan reduction in glial scars.			
PN WO2004041197-A2.			
PD 21-MAY-2004.			

PA (UYCA-) UNIV CASE WESTERN RESERVE.  
 Best Local Similarity: 26.64% Mismatches: 82  
 Query Match: 5.90% Indels: 76

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 29, 2005, 08:04:14 ; Search time 182 Seconds

(without alignments)

2517.349 Million cell updates/sec

Title: US-10-015-388A-54

Perfect score: 1432

Sequence: 1 MCFNLKLLALLVGLWLFQIP.....LRAQPEPARGERRGCSRA 280

Scoring table:

BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO spool\_p/US10015388/runat\_28032005\_130453\_6155/app.query.fasta\_1.455

-DB=Issued Patents\_NA -QWTF=fastcap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPEXT=0

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-LIST=1500 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

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-USER=US10015388 @CGN 1 1 105 @runat\_28032005\_130453\_6155 -NCPUS=6 -ICPU=3

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-DEV\_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*

2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*

3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*

4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	1265	88.3	2240	4	US-09-799-451-571	Sequence 571, Appl
C 2	111.5	7.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 3	111.5	7.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 4	109	7.6	1712	1	US-08-171-299B-1	Sequence 1, Appli
C 5	106.5	7.4	12445	4	US-09-949-016-14632	Sequence 14632, A
C 6	106.5	7.4	21691	4	US-09-949-016-15748	Sequence 15748, A
C 7	104.5	7.3	1350	4	US-09-252-991A-690	Sequence 690, App
C 8	104.5	7.3	3054	4	US-09-252-991A-720	Sequence 720, App
C 9	104.5	7.3	6885	4	US-09-252-991A-660	Sequence 660, App
C 10	104	7.3	6063	4	US-09-902-540-807	Sequence 807, App
C 11	103.5	7.2	1131	4	US-09-252-991A-1675	Sequence 1675, Ap
C 12	103.5	7.2	2745	4	US-09-902-540-4835	Sequence 4835, Ap

86	94	6.6	4287	4	US-09-252-991A-14160	Sequence 14160, A	159	90	6.3	18031	4	US-09-902-540-1180	Sequence 1180, Ap
87	93.5	6.5	1230	4	US-09-252-991A-12810	Sequence 12810, A	c 160	90	6.3	536165	4	US-09-214-808-1	Sequence 1, Appli
c 88	93.5	6.5	3542	4	US-09-620-312D-233	Sequence 233, App	c 161	89.5	6.2	1227	3	US-09-385-028-23	Sequence 23, Appl
89	93.5	6.5	5630	2	US-08-937-931-1	Sequence 1, Appli	c 162	89.5	6.2	1227	4	US-09-726-614-23	Sequence 23, Appl
90	93.5	6.5	5630	3	US-09-285-502-1	Sequence 1, Appli	c 163	89.5	6.2	1227	4	US-09-385-040-23	Sequence 23, Appl
91	93.5	6.5	5630	3	US-09-709-126-1	Sequence 1, Appli	c 164	89.5	6.2	1227	4	US-09-252-991A-8312	Sequence 8312, Ap
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c 93	93.5	6.5	18265	4	US-09-949-016-14118	Sequence 14118, A	c 166	89.5	6.2	1227	4	US-08-961-527-184	Sequence 184, App
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98	93	6.5	1320	4	US-09-252-991A-6860	Sequence 6860, Ap	c 171	89.5	6.2	1227	4	US-09-820-155-1	Sequence 1, Appli
c 99	93	6.5	1359	4	US-09-252-991A-6765	Sequence 6765, Ap	c 172	89.5	6.2	1227	4	US-09-902-540-674	Sequence 674, App
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C 388	86	6.0	3109	4	US-09-902-540-413	Sequence 413, Appl	C 461	85	5.9	4512	4	US-09-902-540-763	Sequence 763, Appl
C 389	86	6.0	3399	4	US-09-902-540-3731	Sequence 3731, Ap	C 462	85	5.9	6196	4	US-09-902-540-788	Sequence 788, Appl
C 390	86	6.0	3702	4	US-09-252-991A-6666	Sequence 6666, Ap	C 463	85	5.9	8237	4	US-09-949-016-12067	Sequence 12067, A
C 391	86	6.0	4190	3	US-08-924-345-1	Sequence 1, Appl	C 464	85	5.9	8237	4	US-09-949-016-13888	Sequence 13888, A
C 392	86	6.0	17612	3	US-08-911-853-29	Sequence 29, Appl	C 465	85	5.9	9369	4	US-10-237-551-190	Sequence 190, Appl
C 393	86	6.0	17612	3	US-09-479-409-29	Sequence 29, Appl	C 466	85	5.9	9369	4	US-10-237-551-247	Sequence 247, Appl
C 394	86	6.0	17612	3	US-09-479-453-29	Sequence 29, Appl	C 467	85	5.9	23368	4	US-09-949-016-15418	Sequence 15418, A
C 395	86	6.0	17897	4	US-09-902-540-1182	Sequence 1182, Ap	C 468	85	5.9	33655	4	US-09-949-016-13947	Sequence 13947, A
C 396	86	6.0	19112	4	US-09-902-540-1181	Sequence 1181, Ap	C 469	85	5.9	34316	4	US-09-902-540-1257	Sequence 1257, Ap
C 397	86	6.0	20093	4	US-09-949-016-15207	Sequence 15207, A	C 470	85	5.9	71989	3	US-09-443-501A-2	Sequence 2, Appl
C 398	86	6.0	26640	4	US-09-949-016-17431	Sequence 17431, A	C 471	85	5.9	92334	4	US-09-949-016-13920	Sequence 13920, A
C 399	86	6.0	26420	4	US-09-949-016-12052	Sequence 12052, A	C 472	85	5.9	92363	4	US-09-827-688-8	Sequence 12146, A
C 400	86	6.0	77772	4	US-09-949-016-17417	Sequence 17417, A	C 473	85	5.9	154746	4	US-09-949-016-12146	Sequence 12146, A
C 401	86	6.0	77997	4	US-09-949-016-12249	Sequence 12249, A	C 474	85	5.9	181429	4	US-09-949-016-12372	Sequence 12372, A
C 402	86	6.0	128470	4	US-09-949-016-13765	Sequence 13765, A	C 475	85	5.9	181430	4	US-09-949-016-15772	Sequence 15772, A
C 403	85.5	6.0	866	4	US-09-799-451-119	Sequence 119, Appl	C 476	84.5	5.9	870	4	US-09-451-291-2	Sequence 2, Appl
C 404	85.5	6.0	1254	4	US-09-252-991A-3594	Sequence 3594, Ap	C 477	84.5	5.9	873	4	US-09-910-174B-22	Sequence 22, Appl
C 405	85.5	6.0	1293	4	US-09-902-540-5995	Sequence 5995, Ap	C 478	84.5	5.9	873	4	US-09-620-461-22	Sequence 22, Appl
C 406	85.5	6.0	1470	4	US-09-902-540-5919	Sequence 5919, Ap	C 479	84.5	5.9	1251	4	US-09-252-991A-16304	Sequence 16304, A
C 407	85.5	6.0	1521	4	US-09-902-540-6676	Sequence 6676, Ap	C 480	84.5	5.9	1286	4	US-10-133-907-3	Sequence 3, Appl
C 408	85.5	6.0	1545	4	US-09-902-540-5163	Sequence 5163, Ap	C 481	84.5	5.9	1311	4	US-09-107-433-1201	Sequence 1201, Ap
C 409	85.5	6.0	1764	4	US-09-252-991A-8797	Sequence 8797, Ap	C 482	84.5	5.9	1347	4	US-09-724-797-43	Sequence 43, Appl
C 410	85.5	6.0	1785	4	US-09-252-991A-3774	Sequence 3774, Ap	C 483	84.5	5.9	1380	4	US-09-252-991A-15862	Sequence 15862, A
C 411	85.5	6.0	2256	4	US-09-252-991A-8910	Sequence 8910, Ap	C 484	84.5	5.9	1433	4	US-09-252-991A-4011	Sequence 4011, Ap
C 412	85.5	6.0	2637	4	US-09-902-540-3252	Sequence 3252, Ap	C 485	84.5	5.9	1533	4	US-09-252-991A-1124	Sequence 1124, Ap
C 413	85.5	6.0	5114	4	US-09-949-016-14195	Sequence 14195, A	C 486	84.5	5.9	1545	4	US-09-252-991A-14667	Sequence 14667, A
C 414	85.5	6.0	5421	4	US-09-949-016-11832	Sequence 11832, A	C 487	84.5	5.9	1553	4	US-09-645-069-3	Sequence 3, Appl
C 415	85.5	6.0	7301	4	US-09-949-016-14229	Sequence 14229, A	C 488	84.5	5.9	1572	4	US-09-252-991A-4553	Sequence 4553, Ap
C 416	85.5	6.0	8090	4	US-09-902-540-855	Sequence 855, Appl	C 489	84.5	5.9	1581	4	US-09-252-991A-16413	Sequence 16413, A
C 417	85.5	6.0	9165	4	US-09-902-540-1050	Sequence 1050, Ap	C 490	84.5	5.9	1614	4	US-09-949-016-2542	Sequence 2542, Ap
C 418	85.5	6.0	9401	5	PCT-US91-02225-9	Sequence 9, Appl	C 491	84.5	5.9	1686	4	US-09-252-991A-4299	Sequence 4299, Ap
C 419	85.5	6.0	10505	4	US-09-902-540-1044	Sequence 1044, Ap	C 492	84.5	5.9	1688	4	US-09-949-016-2187	Sequence 2187, Ap
C 420	85.5	6.0	11805	4	US-09-902-540-1016	Sequence 1016, Ap	C 493	84.5	5.9	1767	4	US-09-252-991A-14785	Sequence 14785, A
C 421	85.5	6.0	12225	4	US-09-949-016-17360	Sequence 17360, Ap	C 494	84.5	5.9	2031	4	US-09-252-991A-8142	Sequence 8142, Ap
C 422	85.5	6.0	15789	4	US-09-902-540-1139	Sequence 1139, Ap	C 495	84.5	5.9	2106	4	US-09-252-991A-15891	Sequence 15891, A
C 423	85.5	6.0	20441	4	US-09-949-016-13052	Sequence 13052, A	C 496	84.5	5.9	3162	4	US-09-252-991A-8094	Sequence 8094, Ap
C 424	85.5	6.0	28555	4	US-09-949-016-13106	Sequence 13106, A	C 497	84.5	5.9	3343	4	US-09-976-594-502	Sequence 502, Appl
C 425	85.5	6.0	29559	4	US-09-902-540-1254	Sequence 1254, Ap	C 498	84.5	5.9	3411	3	US-08-890-865A-3	Sequence 3, Appl
C 426	85.5	6.0	80161	3	US-09-036-987A-1	Sequence 1, Appl	C 499	84.5	5.9	3422	4	US-09-949-016-1919	Sequence 1919, Ap
C 427	85.5	6.0	80161	3	US-09-370-700-1	Sequence 1, Appl	C 500	84.5	5.9	3536	4	US-09-724-653-1	Sequence 1, Appl
C 428	85.5	6.0	80161	3	US-09-603-207-1	Sequence 1, Appl	C 501	84.5	5.9	3616	4	US-09-451-291-5	Sequence 5, Appl
C 429	85	5.9	606	3	US-08-998-416-119	Sequence 119, Appl	C 502	84.5	5.9	4236	4	US-09-252-991A-11837	Sequence 11837, A
C 430	85	5.9	850	4	US-09-270-767-6468	Sequence 6468, Ap	C 503	84.5	5.9	4432	4	US-09-774-328-148	Sequence 148, Appl
C 431	85	5.9	850	4	US-09-270-767-21750	Sequence 21750, A	C 504	84.5	5.9	4459	4	US-09-949-016-5641	Sequence 5641, Ap
C 432	85	5.9	996	4	US-09-252-991A-7732	Sequence 7732, Ap	C 505	84.5	5.9	6891	3	US-09-038-219B-5	Sequence 5, Appl
C 433	85	5.9	1141	2	US-08-918-727-4	Sequence 4, Appl	C 506	84.5	5.9	10846	3	US-09-038-219B-5	Sequence 5, Appl
C 434	85	5.9	1141	3	US-09-205-680A-4	Sequence 4, Appl	C 507	84.5	5.9	10846	4	US-10-164-204-5	Sequence 5, Appl
C 435	85	5.9	1224	1	US-08-924-847A-1	Sequence 1, Appl	C 508	84.5	5.9	10846	4	US-09-923-109-5	Sequence 5, Appl
C 436	85	5.9	1224	1	US-08-924-847A-3	Sequence 3, Appl	C 509	84.5	5.9	10900	3	US-09-038-219B-6	Sequence 6, Appl
C 437	85	5.9	1224	3	US-09-120-052-3	Sequence 3, Appl	C 510	84.5	5.9	10900	4	US-10-164-204-6	Sequence 6, Appl
C 438	85	5.9	1224	3	US-09-120-052-3	Sequence 3, Appl	C 511	84.5	5.9	10900	4	US-09-923-109-6	Sequence 6, Appl
C 439	85	5.9	1224	4	US-09-252-991A-7567	Sequence 7567, Ap	C 512	84.5	5.9	11199	4	US-09-902-540-1017	Sequence 1017, Ap
C 440	85	5.9	1239	4	US-09-252-991A-6622	Sequence 6622, Ap	C 513	84.5	5.9	16350	4	US-09-902-540-1144	Sequence 1144, Ap
C 441	85	5.9	1415	4	US-09-902-540-3734	Sequence 3734, Ap	C 514	84.5	5.9	19954	4	US-09-902-540-1150	Sequence 1150, Ap
C 442	85	5.9	1449	4	US-09-252-991A-6642	Sequence 6642, Ap	C 515	84.5	5.9	26533	4	US-09-902-540-1199	Sequence 1199, Ap
C 443	85	5.9	1467	4	US-09-252-991A-13960	Sequence 13960, A	C 516	84.5	5.9	26831	4	US-09-949-016-16250	Sequence 16250, A
C 444	85	5.9	1643	4	US-09-799-451-167	Sequence 167, Appl	C 517	84.5	5.9	34266	4	US-09-949-016-13250	Sequence 13250, A
C 445	85	5.9	1647	4	US-09-252-991A-6576	Sequence 6576, Ap	C 518	84.5	5.9	36611	4	US-09-949-016-17287	Sequence 17287, A
C 446	85	5.9	2049	4	US-09-252-991A-13850	Sequence 13850, A	C 519	84.5	5.9	60917	4	US-09-949-016-12638	Sequence 12638, A
C 447	85	5.9	2387	4	US-09-647-492A-3	Sequence 3, Appl	C 520	84.5	5.9	60917	4	US-09-949-016-16057	Sequence 16057, A
C 448	85	5.9	3231	5	PCT-US94-06447-4	Sequence 4, Appl	C 521	84	5.9	780	4	US-09-252-991A-3741	Sequence 3741, Ap
C 449	85	5.9	4145	3	PCT-US94-06447-4	Sequence 4, Appl	C 522	84	5.9	960	4	US-09-252-991A-3730	Sequence 3730, Ap
C 450	85	5.9	4145	3	US-09-302-620B-82	Sequence 82, Appl	C 523	84	5.9	1089	4	US-09-252-991A-3785	Sequence 3785, Ap

524	84	5.9	1107	4	US-09-252-991A-456	Sequence 456, App	597	83	5.8	1038	4	US-09-902-540-5171	Sequence 5171, Ap
c 525	84	5.9	1227	4	US-09-489-039A-1526	Sequence 1526, App	c 598	83	5.8	1116	4	US-09-252-991A-2102	Sequence 2102, Ap
c 526	84	5.9	1326	4	US-09-252-991A-409	Sequence 409, App	c 599	83	5.8	1173	4	US-09-902-540-6402	Sequence 6402, Ap
527	84	5.9	1731	4	US-09-489-039A-1730	Sequence 1730, App	c 600	83	5.8	1194	4	US-09-902-540-7565	Sequence 7565, Ap
528	84	5.9	1767	4	US-09-252-991A-16401	Sequence 16401, A	c 601	83	5.8	1209	4	US-09-826-509-556	Sequence 556, App
c 529	84	5.9	1950	3	US-08-685-466C-1	Sequence 1, Appli	c 602	83	5.8	1224	4	US-09-252-991A-1793	Sequence 1793, Ap
c 530	84	5.9	2031	4	US-09-902-540-3637	Sequence 3637, Ap	c 603	83	5.8	1278	4	US-09-252-991A-11277	Sequence 11277, A
c 531	84	5.9	2125	4	US-09-949-016-3562	Sequence 3562, Ap	c 604	83	5.8	1335	4	US-09-252-991A-973	Sequence 973, App
c 532	84	5.9	2388	4	US-09-902-540-3283	Sequence 3283, Ap	c 605	83	5.8	1376	4	US-09-016-434-1361	Sequence 1361, Ap
c 533	84	5.9	2475	4	US-09-252-991A-15758	Sequence 15758, A	c 606	83	5.8	1394	2	US-08-068-729-3	Sequence 3, Appli
534	84	5.9	2781	4	US-09-344-624-20	Sequence 20, Appl	c 607	83	5.8	1394	3	US-09-255-671-3	Sequence 3, Appli
535	84	5.9	2785	4	US-09-949-016-1161	Sequence 1161, Ap	c 608	83	5.8	1394	3	US-09-395-366-3	Sequence 3, Appli
c 536	84	5.9	3489	4	US-09-252-991A-16193	Sequence 16193, A	c 608	83	5.8	1394	3	US-09-902-540-9658	Sequence 9658, Ap
c 537	84	5.9	4563	4	US-09-252-991A-930	Sequence 930, App	c 610	83	5.8	1610	4	US-09-616-289-45	Sequence 45, Appl
c 538	84	5.9	8230	4	US-09-949-016-15445	Sequence 15445, A	c 611	83	5.8	1650	4	US-09-252-991A-10150	Sequence 10150, A
539	84	5.9	10182	4	US-09-902-540-1049	Sequence 1049, Ap	c 612	83	5.8	1659	1	US-08-333-358-7	Sequence 7, Appli
c 540	84	5.9	12359	4	US-09-949-016-17004	Sequence 17004, A	c 613	83	5.8	1659	1	US-08-463-694-7	Sequence 7, Appli
c 541	84	5.9	19269	4	US-09-902-540-1175	Sequence 1175, Ap	c 614	83	5.8	1659	1	US-08-694-501-7	Sequence 7, Appli
c 542	84	5.9	27903	4	US-09-902-540-1235	Sequence 1235, Ap	c 615	83	5.8	1725	4	US-09-252-991A-9926	Sequence 9926, Ap
c 543	84	5.9	43550	4	US-09-949-016-12400	Sequence 12400, A	c 616	83	5.8	1806	4	US-09-252-991A-11213	Sequence 11213, A
c 544	84	5.9	43555	4	US-09-949-016-13993	Sequence 13993, A	c 617	83	5.8	2091	4	US-09-252-991A-12312	Sequence 12312, A
545	84	5.9	60990	4	US-09-949-016-14080	Sequence 14080, A	c 618	83	5.8	2529	4	US-09-902-540-7018	Sequence 7018, Ap
c 546	84	5.9	88758	4	US-09-949-016-13502	Sequence 13502, A	c 619	83	5.8	2802	4	US-09-417-197-134	Sequence 134, App
c 547	84	5.9	139952	4	US-09-949-016-11782	Sequence 11782, A	c 620	83	5.8	3650	4	US-09-949-016-5637	Sequence 5637, Ap
548	84	5.9	329524	4	US-09-949-016-13280	Sequence 13280, A	c 621	83	5.8	4003	4	US-09-902-540-618	Sequence 618, App
c 549	84	5.9	385034	4	US-09-949-016-14957	Sequence 14957, A	c 622	83	5.8	4761	4	US-09-902-540-739	Sequence 739, App
c 550	84	5.9	329504	4	US-09-949-016-11774	Sequence 11774, A	c 623	83	5.8	4826	4	US-09-772-304A-1	Sequence 1, Appli
c 551	83.5	5.8	601	4	US-09-949-016-24153	Sequence 24153, A	c 624	83	5.8	5455	1	US-08-342-930-1	Sequence 1, Appli
c 552	83.5	5.8	601	4	US-09-949-016-69020	Sequence 69020, A	c 625	83	5.8	6492	4	US-09-902-540-853	Sequence 853, App
c 553	83.5	5.8	831	4	US-09-252-991A-5118	Sequence 5118, Ap	c 626	83	5.8	9198	4	US-09-902-540-366	Sequence 966, App
c 554	83.5	5.8	863	4	US-09-902-540-144	Sequence 144, App	c 627	83	5.8	12865	4	US-09-902-540-1048	Sequence 1048, Ap
555	83.5	5.8	993	4	US-09-876-216-1	Sequence 1, Appli	c 628	83	5.8	14462	4	US-09-902-540-9597	Sequence 9597, Ap
c 556	83.5	5.8	1035	4	US-09-252-991A-15890	Sequence 15890, A	c 629	83	5.8	14462	4	US-09-902-540-1048	Sequence 1048, Ap
c 557	83.5	5.8	1086	4	US-09-252-991A-15921	Sequence 15921, A	c 630	83	5.8	15125	4	US-09-949-016-14647	Sequence 14647, A
558	83.5	5.8	1265	4	US-09-252-991A-15921	Sequence 15921, A	c 631	83	5.8	18417	4	US-09-949-016-13389	Sequence 13389, A
c 559	83.5	5.8	1422	4	US-09-620-312D-892	Sequence 892, App	c 632	83	5.8	23091	4	US-09-902-540-1204	Sequence 1204, Ap
c 560	83.5	5.8	1422	4	US-09-252-991A-14835	Sequence 14835, A	c 633	83	5.8	23417	4	US-09-902-540-1204	Sequence 1204, Ap
c 561	83.5	5.8	1446	4	US-09-252-991A-15091	Sequence 15091, A	c 634	83	5.8	28058	4	US-09-902-540-1252	Sequence 1252, Ap
c 562	83.5	5.8	1649	2	US-08-466-120-1	Sequence 1, Appli	c 635	83	5.8	34199	4	US-09-902-540-1255	Sequence 1255, Ap
c 563	83.5	5.8	1649	5	PCT-US94-07266-1	Sequence 1, Appli	c 636	83	5.8	111509	4	US-09-949-016-17379	Sequence 17379, A
564	83.5	5.8	1782	4	US-09-252-991A-1412	Sequence 1412, Ap	c 637	83	5.8	139577	4	US-09-949-016-17398	Sequence 17398, A
c 565	83.5	5.8	1956	4	US-09-602-777A-53	Sequence 53, Appl	c 638	83	5.8	139577	4	US-09-949-016-12879	Sequence 12879, A
c 566	83.5	5.8	2194	4	US-09-949-016-2036	Sequence 2036, Ap	c 639	83	5.8	536165	4	US-09-214-808-1	Sequence 1, Appli
c 567	83.5	5.8	2376	4	US-09-252-991A-6630	Sequence 6630, Ap	c 640	83	5.8	1230025	4	US-09-198-452A-1	Sequence 1, Appli
c 568	83.5	5.8	2898	4	US-09-602-777A-49	Sequence 49, Appl	c 641	82.5	5.8	900	4	US-09-902-540-9504	Sequence 9504, Ap
569	83.5	5.8	3144	4	US-09-774-528-112	Sequence 112, App	c 642	82.5	5.8	921	4	US-09-489-039A-5065	Sequence 5065, Ap
c 570	83.5	5.8	3144	4	US-09-614-069-2	Sequence 2, Appli	c 643	82.5	5.8	1161	4	US-09-252-991A-10489	Sequence 10489, A
571	83.5	5.8	3144	4	US-09-855-323-8	Sequence 8, Appli	c 644	82.5	5.8	1305	4	US-09-252-991A-10664	Sequence 10664, A
572	83.5	5.8	3540	4	US-09-252-991A-1324	Sequence 1324, Ap	c 645	82.5	5.8	1347	4	US-09-489-039A-5620	Sequence 5620, Ap
573	83.5	5.8	4955	4	US-09-902-540-553	Sequence 553, App	c 646	82.5	5.8	1386	4	US-09-016-434-1339	Sequence 1339, Ap
574	83.5	5.8	5153	5	PCT-US95-04910-8	Sequence 8, Appli	c 647	82.5	5.8	1476	4	US-09-585-174-99	Sequence 99, Appl
c 575	83.5	5.8	6351	4	US-09-902-540-757	Sequence 757, App	c 648	82.5	5.8	1509	4	US-09-252-991A-7072	Sequence 7072, Ap
c 576	83.5	5.8	7515	4	US-09-902-540-888	Sequence 888, App	c 649	82.5	5.8	1521	4	US-09-902-540-6676	Sequence 6676, Ap
c 577	83.5	5.8	8604	4	US-09-902-540-5331	Sequence 5331, Ap	c 650	82.5	5.8	1524	4	US-09-252-991A-7027	Sequence 7027, Ap
c 578	83.5	5.8	9843	4	US-09-949-016-13133	Sequence 50, Appl	c 651	82.5	5.8	1527	4	US-09-902-540-3237	Sequence 3237, Ap
c 579	83.5	5.8	12425	4	US-09-616-289-50	Sequence 50, Appl	c 652	82.5	5.8	1554	1	US-08-469-486-1	Sequence 1, Appli
c 580	83.5	5.8	16047	4	US-09-902-540-1136	Sequence 1136, Ap	c 653	82.5	5.8	1554	2	US-08-469-658-1	Sequence 1, Appli
c 581	83.5	5.8	16047	4	US-09-902-540-1136	Sequence 1136, Ap	c 654	82.5	5.8	1575	4	US-09-252-991A-1139	Sequence 1139, Ap
c 582	83.5	5.8	20662	4	US-09-949-016-16717	Sequence 16717, A	c 655	82.5	5.8	1599	4	US-09-949-016-5029	Sequence 5029, Ap
c 583	83.5	5.8	27883	4	US-09-902-540-1242	Sequence 1242, Ap	c 656	82.5	5.8	1608	4	US-09-252-991A-9498	Sequence 9498, Ap
c 584	83.5	5.8	35100	2	US-08-770-379-19	Sequence 19, Appl	c 657	82.5	5.8	1616	4	US-09-949-016-330	Sequence 330, App
c 585	83.5	5.8	35100	3	US-08-757-669A-19	Sequence 19, Appl	c 658	82.5	5.8	1653	4	US-09-252-991A-1111	Sequence 1111, Ap
c 586	83.5	5.8	35100	3	US-09-230-371A-19	Sequence 19, Appl	c 659	82.5	5.8	1659	3	US-09-083-351-3	Sequence 3, Appli
c 587	83.5	5.8	35399	4	US-09-902-540-1260	Sequence 1260, Ap	c 660	82.5	5.8	1659	3	US-09-083-352-3	Sequence 3, Appli
588	83.5	5.8	38155	3	US-09-453-702B-79	Sequence 79, Appl	c 661	82.5	5.8	1662	4	US-09-612-809B-3	Sequence 3, Appli
c 589	83.5	5.8	42755	4	US-09-949-016-12533	Sequence 12533, A	c 662	82.5	5.8	1917	4	US-09-252-991A-10497	Sequence 10497, A
c 590	83.5	5.8	77626	4	US-09-949-016-12608	Sequence 12608, A	c 663	82.5	5.8	2013	4	US-09-252-991A-10296	Sequence 10296, A
c 591	83.5	5.8	160759	4	US-09-949-016-16514	Sequence 16514, A	c 664	82.5	5.8	2073	4	US-09-252-991A-10279	Sequence 10279, A
c 592	83	5.8	645	4	US-09-252-991A-2836	Sequence 2836, Ap	c 665	82.5	5.8	2112	4	US-09-270-767-13414	Sequence 13414, A
c 593	83	5.8	714	4	US-09-252-991A-11042	Sequence 11042, Ap	c 666	82.5	5.8	2266	4	US-09-799-451-917	Sequence 917, App
c 594	83	5.8	984	4	US-09-252-991A-3477	Sequence 3477, Ap	c 667	82.5	5.8	2290	4	US-09-799-451-864	Sequence 864, App
595	83	5.8	996	4	US-09-252-991A-4469	Sequence 4469, Ap	c 668	82.5	5.8	2379	4	US-09-252-991A-9252	Sequence 9252, Ap
596	83	5.8	1014	4	US-09-252-991A-3031	Sequence 3031, Ap	c 669	82.5	5.8	2511	4	US-09-252-991A-10560	Sequence 10560, A

c 670	82.5	5.8	2592	4	US-09-902-540-3407	Sequence 3407, Ap	c 743	82	5.7	2078	4	US-09-799-451-486	Sequence 486, App
c 671	82.5	5.8	2772	4	US-09-252-991A-10577	Sequence 10577, A	c 744	82	5.7	2265	4	US-09-252-991A-5738	Sequence 5738, Ap
c 672	82.5	5.8	2859	4	US-09-252-991A-944	Sequence 944, App	c 745	82	5.7	2625	4	US-09-902-540-8554	Sequence 8554, Ap
c 673	82.5	5.8	2865	4	US-09-252-991A-4675	Sequence 4675, Ap	c 746	82	5.7	3889	4	US-09-902-540-492	Sequence 492, App
c 674	82.5	5.8	3168	4	US-09-902-540-8270	Sequence 8270, Ap	c 747	82	5.7	4683	4	US-09-902-540-9346	Sequence 9346, Ap
c 675	82.5	5.8	3828	4	US-08-426-630-48	Sequence 48, App	c 748	82	5.7	4824	4	US-09-902-540-9627	Sequence 9627, Ap
c 676	82.5	5.8	3931	1	US-08-144-121-1	Sequence 1, Appli	c 749	82	5.7	6858	4	US-09-252-991A-1219	Sequence 1219, Ap
c 677	82.5	5.8	3931	2	US-08-735-893-1	Sequence 1, Appli	c 750	82	5.7	7562	4	US-09-902-540-902	Sequence 902, App
c 678	82.5	5.8	3946	3	US-09-083-351-1	Sequence 1, Appli	c 751	82	5.7	7881	2	US-08-751-189-1	Sequence 1, Appli
c 679	82.5	5.8	3946	3	US-09-083-351-1	Sequence 1, Appli	c 752	82	5.7	7881	3	US-09-060-836-1	Sequence 1, Appli
c 680	82.5	5.8	4563	4	US-09-252-991A-4765	Sequence 4765, Ap	c 753	82	5.7	7881	3	US-09-184-445-1	Sequence 1, Appli
c 681	82.5	5.8	4825	4	US-09-949-016-15912	Sequence 15912, A	c 754	82	5.7	9399	4	US-09-949-016-13206	Sequence 13206, A
c 682	82.5	5.8	5661	4	US-09-555-166-3	Sequence 3, Appli	c 755	82	5.7	9905	4	US-09-902-540-998	Sequence 998, App
c 683	82.5	5.8	6114	4	US-09-914-272A-4	Sequence 4, Appli	c 756	82	5.7	11612	4	US-09-902-540-981	Sequence 981, App
c 684	82.5	5.8	6114	4	US-10-638-333-4	Sequence 4, Appli	c 757	82	5.7	16187	4	US-09-902-540-1093	Sequence 1093, Ap
c 685	82.5	5.8	6269	4	US-09-902-540-726	Sequence 726, App	c 758	82	5.7	19019	4	US-09-902-540-1171	Sequence 1171, Ap
c 686	82.5	5.8	6388	4	US-09-949-016-15137	Sequence 15137, A	c 759	82	5.7	19990	4	US-09-949-016-14967	Sequence 14967, A
c 687	82.5	5.8	6491	4	US-09-585-174-1	Sequence 1, Appli	c 760	82	5.7	21964	4	US-09-902-540-1190	Sequence 1190, Ap
c 688	82.5	5.8	6855	4	US-09-252-991A-6976	Sequence 6976, Ap	c 761	82	5.7	25048	4	US-09-902-540-1239	Sequence 1239, Ap
c 689	82.5	5.8	6930	4	US-09-902-540-856	Sequence 856, App	c 762	82	5.7	26289	4	US-09-902-540-1210	Sequence 1210, Ap
c 690	82.5	5.8	9036	4	US-09-949-016-16866	Sequence 16866, A	c 763	82	5.7	28493	4	US-09-902-540-1241	Sequence 1241, Ap
c 691	82.5	5.8	9165	4	US-09-902-540-1050	Sequence 1050, Ap	c 764	82	5.7	44377	2	US-08-804-227C-7	Sequence 7, Appli
c 692	82.5	5.8	13144	4	US-08-426-630-41	Sequence 41, Appli	c 765	82	5.7	44377	2	US-08-804-198-1	Sequence 1, Appli
c 693	82.5	5.8	14431	4	US-09-902-540-1149	Sequence 1149, Ap	c 766	82	5.7	51354	4	US-09-902-540-1270	Sequence 1270, Ap
c 694	82.5	5.8	16423	4	US-09-902-540-1120	Sequence 1120, Ap	c 767	82	5.7	51807	4	US-09-949-016-15333	Sequence 15333, A
c 695	82.5	5.8	17654	4	US-09-902-540-1161	Sequence 1161, Ap	c 768	82	5.7	68750	3	US-09-335-409-1	Sequence 1, Appli
c 696	82.5	5.8	21490	4	US-09-949-016-14168	Sequence 14168, A	c 769	82	5.7	68750	3	US-09-568-102-1	Sequence 1, Appli
c 697	82.5	5.8	25709	4	US-09-949-016-13338	Sequence 13338, A	c 770	82	5.7	68750	3	US-09-567-969-1	Sequence 1, Appli
c 698	82.5	5.8	25778	4	US-09-949-016-12167	Sequence 12167, A	c 771	82	5.7	68750	3	US-09-568-480-1	Sequence 1, Appli
c 699	82.5	5.8	27579	4	US-09-949-016-15005	Sequence 15005, A	c 772	82	5.7	68750	3	US-09-568-480-1	Sequence 1, Appli
c 700	82.5	5.8	33498	4	US-09-949-016-11982	Sequence 11982, A	c 773	82	5.7	68750	3	US-09-568-472-1	Sequence 1, Appli
c 701	82.5	5.8	33551	4	US-09-949-016-16666	Sequence 16666, A	c 774	82	5.7	68750	3	US-09-567-899-1	Sequence 1, Appli
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c 705	82.5	5.8	50725	4	US-09-902-540-1271	Sequence 1271, Ap	c 778	81.5	5.7	601	4	US-09-949-016-92631	Sequence 92631, A
c 706	82.5	5.8	54484	4	US-09-902-540-1272	Sequence 1272, Ap	c 779	81.5	5.7	774	4	US-09-252-991A-9665	Sequence 9665, Ap
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c 709	82.5	5.8	131724	4	US-09-949-016-12893	Sequence 12893, A	c 782	81.5	5.7	1008	4	US-09-252-991A-3831	Sequence 3831, Ap
c 710	82	5.7	601	4	US-09-949-016-72838	Sequence 72838, A	c 783	81.5	5.7	1104	1	US-09-252-991A-15592	Sequence 15592, A
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c 712	82	5.7	836	4	US-09-077-674-11	Sequence 11, Appli	c 785	81.5	5.7	1131	4	US-09-252-991A-76	Sequence 76, Appli
c 713	82	5.7	885	4	US-09-252-991A-7021	Sequence 7021, Ap	c 786	81.5	5.7	1173	4	US-09-902-540-5559	Sequence 5559, Ap
c 714	82	5.7	900	4	US-09-902-540-6576	Sequence 6576, Ap	c 787	81.5	5.7	1213	4	US-09-902-540-3750	Sequence 3750, Ap
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c 716	82	5.7	1068	4	US-09-252-991A-9933	Sequence 9933, Ap	c 789	81.5	5.7	1278	4	US-09-252-991A-8517	Sequence 8517, Ap
c 717	82	5.7	1088	3	US-09-077-675A-6	Sequence 6, Appli	c 790	81.5	5.7	1392	4	US-09-252-991A-3486	Sequence 3486, Ap
c 718	82	5.7	1095	4	US-09-077-674-6	Sequence 6, Appli	c 791	81.5	5.7	1467	4	US-09-252-991A-8763	Sequence 8763, Ap
c 719	82	5.7	1101	4	US-09-252-991A-3352	Sequence 3352, Ap	c 792	81.5	5.7	1528	4	US-09-016-434-1448	Sequence 1448, Ap
c 720	82	5.7	1101	4	US-09-016-434-1148	Sequence 1148, Ap	c 793	81.5	5.7	1528	4	US-10-329-668-1	Sequence 1, Appli
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c 723	82	5.7	1119	3	US-09-434-288-9	Sequence 9, Appli	c 796	81.5	5.7	1758	4	US-09-252-991A-7085	Sequence 7085, Ap
c 724	82	5.7	1172	4	US-09-252-991A-1172	Sequence 1172, Ap	c 797	81.5	5.7	1848	4	US-09-252-991A-6632	Sequence 6632, Ap
c 725	82	5.7	1185	4	US-09-252-991A-10495	Sequence 10495, A	c 798	81.5	5.7	1911	4	US-09-252-991A-6716	Sequence 6716, Ap
c 726	82	5.7	1212	4	US-09-880-503-15	Sequence 15, Appli	c 799	81.5	5.7	1951	3	US-08-910-973-16	Sequence 16, Appli
c 727	82	5.7	1221	4	US-09-252-991A-2160	Sequence 2160, Ap	c 800	81.5	5.7	1951	3	US-09-499-227-16	Sequence 16, Appli
c 728	82	5.7	1236	4	US-09-023-655-927	Sequence 927, App	c 801	81.5	5.7	2082	4	US-09-902-540-7754	Sequence 7754, Ap
c 729	82	5.7	1251	4	US-09-252-991A-10142	Sequence 10142, A	c 802	81.5	5.7	2136	4	US-09-252-991A-11628	Sequence 11628, A
c 730	82	5.7	1281	4	US-09-489-039A-2650	Sequence 2650, Ap	c 803	81.5	5.7	2478	3	US-08-485-355B-47	Sequence 47, Appli
c 731	82	5.7	1293	4	US-09-252-991A-12207	Sequence 12207, A	c 804	81.5	5.7	2478	3	US-08-485-355B-49	Sequence 49, Appli
c 732	82	5.7	1299	4	US-09-252-991A-14682	Sequence 14682, A	c 805	81.5	5.7	2478	3	US-09-194-613-1	Sequence 1, Appli
c 733	82	5.7	1338	4	US-09-252-991A-12135	Sequence 12135, A	c 806	81.5	5.7	2479	3	US-08-485-355B-51	Sequence 51, Appli
c 734	82	5.7	1482	4	US-09-252-991A-1723	Sequence 1723, Ap	c 807	81.5	5.7	2484	4	US-09-252-991A-1388	Sequence 1388, Ap
c 735	82	5.7	1494	3	US-08-724-466B-5	Sequence 5, Appli	c 808	81.5	5.7	2499	4	US-09-252-991A-2681	Sequence 2681, Ap
c 736	82	5.7	1494	3	US-08-724-466B-5	Sequence 5, Appli	c 809	81.5	5.7	2544	4	US-09-252-991A-2775	Sequence 2775, Ap
c 737	82	5.7	1542	4	US-09-252-991A-16087	Sequence 16087, A	c 810	81.5	5.7	2544	4	US-09-949-016-1140	Sequence 1140, Ap
c 738	82	5.7	1542	4	US-09-252-991A-5713	Sequence 5713, Ap	c 811	81.5	5.7	2671	6	5168051-9	Patent No. 5168051
c 739	82	5.7	1659	4	US-09-252-991A-12388	Sequence 12388, A	c 812	81.5	5.7	2671	6	5168051-9	Patent No. 5168051
c 740	82	5.7	1659	4	US-09-252-991A-12388	Sequence 12388, A	c 813	81.5	5.7	2676	4	US-09-252-991A-9024	Sequence 9024, Ap
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c 742	82	5.7	1869	4	US-09-252-991A-11876	Sequence 11876, A	c 815	81.5	5.7	2730	2	US-08-811-897A-39	Sequence 39, Appli

C 816	81.5	5.7	2730	2	US-08-855-213-39	Sequence 39, Appl	C 889	81	5.7	4377	4	US-09-902-540-676	Sequence 676, App
C 817	81.5	5.7	2730	3	US-09-201-474-39	Sequence 39, Appl	C 890	81	5.7	4561	4	US-09-902-540-700	Sequence 700, App
C 818	81.5	5.7	2814	2	US-08-811-897A-38	Sequence 38, Appl	C 891	81	5.7	4591	4	US-09-902-540-3369	Sequence 3369, App
C 819	81.5	5.7	2814	3	US-08-855-213-38	Sequence 38, Appl	C 892	81	5.7	4743	3	US-09-339-964-1	Sequence 1, Appl
C 820	81.5	5.7	2814	3	US-09-201-474-38	Sequence 38, Appl	C 893	81	5.7	4760	3	US-09-907-843-3	Sequence 3, Appl
C 821	81.5	5.7	3402	4	US-09-252-991A-15560	Sequence 15560, A	C 894	81	5.7	5267	3	US-08-976-255-2	Sequence 2, Appl
C 822	81.5	5.7	3597	4	US-09-902-540-5402	Sequence 5402, A	C 895	81	5.7	5337	4	US-09-902-540-810	Sequence 810, App
C 823	81.5	5.7	3606	4	US-09-252-991A-15688	Sequence 15688, A	C 896	81	5.7	5567	4	US-09-902-540-732	Sequence 732, App
C 824	81.5	5.7	3684	4	US-09-252-991A-65	Sequence 65, Appl	C 897	81	5.7	6645	4	US-09-902-540-8819	Sequence 8819, App
C 825	81.5	5.7	4194	4	US-09-902-540-2099	Sequence 2099, Appl	C 898	81	5.7	6776	4	US-09-902-540-884	Sequence 884, App
C 826	81.5	5.7	4698	3	US-09-439-261-33	Sequence 33, Appl	C 899	81	5.7	7000	4	US-09-902-540-833	Sequence 833, App
C 827	81.5	5.7	4698	3	US-09-227-613-33	Sequence 33, Appl	C 900	81	5.7	7704	4	US-09-902-540-743	Sequence 743, App
C 828	81.5	5.7	4902	4	US-09-902-540-5635	Sequence 5635, App	C 901	81	5.7	7858	4	US-09-902-540-943	Sequence 943, App
C 829	81.5	5.7	5280	4	US-09-902-540-770	Sequence 770, App	C 902	81	5.7	7956	4	US-09-902-540-915	Sequence 915, App
C 830	81.5	5.7	6308	4	US-09-949-016-12496	Sequence 12496, A	C 903	81	5.7	8514	4	US-09-902-540-982	Sequence 982, App
C 831	81.5	5.7	6429	4	US-09-902-540-804	Sequence 804, App	C 904	81	5.7	9937	4	US-09-902-540-946	Sequence 946, App
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C 833	81.5	5.7	7527	4	US-09-252-991A-71	Sequence 71, Appl	C 906	81	5.7	11706	4	US-09-902-540-1038	Sequence 1038, App
C 834	81.5	5.7	8144	4	US-09-902-540-820	Sequence 820, App	C 907	81	5.7	11744	4	US-08-426-630-41	Sequence 41, Appl
C 835	81.5	5.7	8544	4	US-09-902-540-917	Sequence 917, App	C 908	81	5.7	17125	4	US-09-902-540-1158	Sequence 1158, App
C 836	81.5	5.7	8544	4	US-09-902-540-917	Sequence 917, App	C 909	81	5.7	17262	4	US-09-902-540-1146	Sequence 1146, App
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C 838	81.5	5.7	25431	4	US-09-949-016-13234	Sequence 13234, A	C 911	81	5.7	28762	4	US-09-902-540-1232	Sequence 1232, App
C 839	81.5	5.7	27632	4	US-09-949-016-12903	Sequence 12903, A	C 912	81	5.7	28958	1	US-08-258-261B-6	Sequence 6, Appl
C 840	81.5	5.7	34552	4	US-09-902-540-1262	Sequence 1262, App	C 913	81	5.7	28958	1	US-08-456-837-6	Sequence 6, Appl
C 841	81.5	5.7	41170	4	US-09-902-540-1267	Sequence 1267, App	C 914	81	5.7	28958	1	US-08-457-342-6	Sequence 6, Appl
C 842	81.5	5.7	49225	4	US-09-902-540-1269	Sequence 1269, App	C 915	81	5.7	28958	1	US-08-457-646A-6	Sequence 6, Appl
C 843	81.5	5.7	58593	4	US-09-949-016-12232	Sequence 12232, A	C 916	81	5.7	28958	1	US-08-458-076A-6	Sequence 6, Appl
C 844	81.5	5.7	62311	4	US-09-949-016-14582	Sequence 14582, A	C 917	81	5.7	28958	1	US-08-764-233A-4	Sequence 4, Appl
C 845	81.5	5.7	70563	4	US-09-949-016-16743	Sequence 16743, A	C 918	81	5.7	28958	1	US-08-457-335A-6	Sequence 6, Appl
C 846	81.5	5.7	72704	4	US-09-902-540-1273	Sequence 1273, App	C 919	81	5.7	28958	1	US-08-729-214-6	Sequence 6, Appl
C 847	81.5	5.7	168971	4	US-09-949-016-13807	Sequence 13807, A	C 920	81	5.7	28958	3	US-09-928-934-6	Sequence 6, Appl
C 848	81	5.7	601	4	US-09-949-016-124099	Sequence 124099, A	C 921	81	5.7	30001	2	US-08-125-468-1	Sequence 1, Appl
C 849	81	5.7	729	4	US-09-489-039A-6006	Sequence 6006, App	C 922	81	5.7	30783	4	US-09-902-540-1258	Sequence 1258, App
C 850	81	5.7	752	4	US-09-799-451-202	Sequence 202, App	C 923	81	5.7	31199	4	US-09-949-016-15515	Sequence 15515, A
C 851	81	5.7	768	4	US-09-252-991A-5834	Sequence 5834, App	C 924	81	5.7	43507	4	US-09-949-016-13297	Sequence 13297, A
C 852	81	5.7	906	3	US-08-957-351-6	Sequence 6, Appl	C 925	81	5.7	43507	4	US-09-949-016-13297	Sequence 13297, A
C 853	81	5.7	978	4	US-09-902-540-3161	Sequence 3161, App	C 926	81	5.7	50397	4	US-08-764-233A-1	Sequence 1, Appl
C 854	81	5.7	984	4	US-09-252-991A-12144	Sequence 12144, A	C 927	81	5.7	50397	4	US-09-949-016-14469	Sequence 14469, A
C 855	81	5.7	984	4	US-09-252-991A-12872	Sequence 12872, A	C 928	81	5.7	50397	4	US-09-949-016-15097	Sequence 15097, A
C 856	81	5.7	984	4	US-09-252-991A-14326	Sequence 14326, A	C 929	81	5.7	71989	3	US-09-443-501A-2	Sequence 2, Appl
C 857	81	5.7	999	4	US-09-252-991A-1387	Sequence 1387, App	C 930	81	5.7	14644	4	US-09-949-016-15238	Sequence 15238, A
C 858	81	5.7	1014	4	US-09-252-991A-13159	Sequence 13159, A	C 931	81	5.7	14644	4	US-09-949-016-13032	Sequence 13032, A
C 859	81	5.7	1014	4	US-09-252-991A-13159	Sequence 13159, A	C 932	81	5.7	187848	4	US-09-949-016-12111	Sequence 12111, A
C 860	81	5.7	1053	4	US-09-270-767-14065	Sequence 14065, A	C 933	80.5	5.6	617	4	US-09-949-016-3825	Sequence 3825, App
C 861	81	5.7	1083	4	US-09-252-991A-6452	Sequence 6452, App	C 934	80.5	5.6	771	2	US-08-972-008-3	Sequence 3, Appl
C 862	81	5.7	1185	4	US-09-902-540-8648	Sequence 8648, App	C 935	80.5	5.6	771	3	US-09-267-409-3	Sequence 3, Appl
C 863	81	5.7	1251	4	US-09-252-991A-14352	Sequence 14352, A	C 936	80.5	5.6	771	4	US-09-252-991A-3257	Sequence 3257, App
C 864	81	5.7	1299	4	US-09-252-991A-8119	Sequence 8119, App	C 937	80.5	5.6	771	4	US-09-252-991A-15324	Sequence 15324, A
C 865	81	5.7	1335	4	US-09-252-991A-3925	Sequence 3925, App	C 938	80.5	5.6	921	4	US-09-252-991A-3438	Sequence 3438, App
C 866	81	5.7	1392	4	US-09-252-991A-8186	Sequence 8186, App	C 939	80.5	5.6	933	4	US-09-252-991A-6813	Sequence 6813, App
C 867	81	5.7	1458	4	US-08-426-630-42	Sequence 42, Appl	C 940	80.5	5.6	945	4	US-09-252-991A-3427	Sequence 3427, App
C 868	81	5.7	1593	4	US-09-252-991A-14376	Sequence 14376, A	C 941	80.5	5.6	981	4	US-09-902-540-6237	Sequence 6237, App
C 869	81	5.7	1680	4	US-09-252-991A-8121	Sequence 8121, App	C 942	80.5	5.6	990	4	US-09-252-991A-16419	Sequence 16419, A
C 870	81	5.7	1737	4	US-09-252-991A-8542	Sequence 8542, App	C 943	80.5	5.6	1011	4	US-09-252-991A-12242	Sequence 12242, A
C 871	81	5.7	1831	4	US-09-799-451-646	Sequence 646, App	C 944	80.5	5.6	1032	4	US-09-252-991A-8059	Sequence 8059, App
C 872	81	5.7	1956	3	US-08-313-553-6	Sequence 6, Appl	C 945	80.5	5.6	1075	2	US-09-252-991A-13599	Sequence 13599, A
C 873	81	5.7	1956	3	US-08-767-993-6	Sequence 6, Appl	C 946	80.5	5.6	1095	2	US-08-851-088-3	Sequence 3, Appl
C 874	81	5.7	1959	3	US-08-743-1688-39	Sequence 39, Appl	C 947	80.5	5.6	1257	4	US-09-252-991A-15464	Sequence 15464, A
C 875	81	5.7	2019	4	US-09-902-540-9185	Sequence 9185, App	C 948	80.5	5.6	1263	4	US-09-252-991A-3462	Sequence 3462, App
C 876	81	5.7	2028	4	US-09-902-540-7226	Sequence 7226, App	C 949	80.5	5.6	1308	4	US-09-252-991A-13991	Sequence 13991, A
C 877	81	5.7	2223	4	US-09-252-991A-4015	Sequence 4015, App	C 950	80.5	5.6	1317	4	US-09-252-991A-12317	Sequence 12317, A
C 878	81	5.7	2319	4	US-09-252-991A-13550	Sequence 13550, A	C 951	80.5	5.6	1332	4	US-09-902-540-9124	Sequence 9124, App
C 879	81	5.7	2461	4	US-08-282-141-1	Sequence 1, Appl	C 952	80.5	5.6	1335	4	US-09-252-991A-9561	Sequence 9561, App
C 880	81	5.7	2461	4	US-09-814-918A-6	Sequence 6, Appl	C 953	80.5	5.6	1338	4	US-09-252-991A-14144	Sequence 14144, A
C 881	81	5.7	2640	4	US-09-857-447-3	Sequence 3, Appl	C 954	80.5	5.6	1349	4	US-09-949-016-1391	Sequence 1391, App
C 882	81	5.7	2640	4	US-09-857-447-3	Sequence 3, Appl	C 955	80.5	5.6	1398	4	US-09-252-991A-14375	Sequence 14375, App
C 883	81	5.7	2695	4	US-09-620-312D-473	Sequence 473, App	C 956	80.5	5.6	1416	4	US-09-252-991A-14328	Sequence 14328, A
C 884	81	5.7	2844	4	US-09-252-991A-12788	Sequence 12788, A	C 957	80.5	5.6	1461	4	US-09-252-991A-5911	Sequence 5911, App
C 885	81	5.7	2866	4	US-09-902-540-499	Sequence 499, App	C 958	80.5	5.6	1500	3	US-09-593-711A-10	Sequence 10, Appl
C 886	81	5.7	2992	4	US-09-252-991A-13891	Sequence 13891, A	C 959	80.5	5.6	1524	4	US-09-252-991A-6861	Sequence 6861, App
C 887	81	5.7	3342	4	US-09-252-991A-12644	Sequence 12644, A	C 960	80.5	5.6	1707	4	US-09-489-039A-819	Sequence 819, App
C 888	81	5.7	3342	4	US-09-252-991A-12644	Sequence 12644, A	C 961	80.5	5.6	1707	4	US-09-489-039A-819	Sequence 819, App

962	80.5	5.6	1725	4	US-09-252-991A-14297	Sequence 14297, A	c1035	80	5.6	1122	4	US-09-252-991A-2855	Sequence 2855, Ap
c 963	80.5	5.6	1746	4	US-09-252-991A-8948	Sequence 8948, Ap	1036	80	5.6	1134	4	US-09-949-016-90	Sequence 90, Appl
c 964	80.5	5.6	1746	4	US-09-485-529-57	Sequence 57, Appl	c1037	80	5.6	1194	4	US-09-724-737-25	Sequence 25, Appl
965	80.5	5.6	1776	4	US-09-902-540-7046	Sequence 7046, Ap	c1038	80	5.6	1221	4	US-09-252-991A-7990	Sequence 7990, Ap
c 966	80.5	5.6	1833	4	US-09-252-991A-3525	Sequence 3525, Ap	1039	80	5.6	1230	4	US-09-252-991A-8268	Sequence 8268, Ap
c 967	80.5	5.6	1845	4	US-09-902-540-7042	Sequence 7042, Ap	1040	80	5.6	1263	4	US-09-252-991A-928	Sequence 928, App
c 968	80.5	5.6	1893	4	US-09-252-991A-9055	Sequence 9055, Ap	c1041	80	5.6	1320	4	US-09-902-540-8133	Sequence 8133, Ap
c 969	80.5	5.6	2052	4	US-09-252-991A-12103	Sequence 12103, A	1042	80	5.6	1341	3	US-09-199-637A-133	Sequence 133, App
c 970	80.5	5.6	2184	4	US-09-902-540-5116	Sequence 5116, Ap	1043	80	5.6	1368	4	US-09-252-991A-971	Sequence 971, App
c 971	80.5	5.6	2256	4	US-09-252-991A-6199	Sequence 6199, Ap	1044	80	5.6	1440	4	US-09-252-991A-10395	Sequence 10395, A
c 972	80.5	5.6	2271	4	US-09-902-540-6006	Sequence 6006, Ap	c1045	80	5.6	1555	4	US-09-902-540-267	Sequence 267, App
c 973	80.5	5.6	2304	4	US-09-252-991A-8731	Sequence 8731, Ap	c1046	80	5.6	1557	4	US-09-252-991A-7033	Sequence 7033, Ap
c 974	80.5	5.6	2389	4	US-09-902-540-4764	Sequence 4764, Ap	c1047	80	5.6	1758	4	US-09-252-991A-1644	Sequence 1644, Ap
c 975	80.5	5.6	2407	4	US-09-949-016-2650	Sequence 2650, Ap	c1048	80	5.6	1785	4	US-09-252-991A-10764	Sequence 10764, A
c 976	80.5	5.6	2445	4	US-09-252-991A-6352	Sequence 6352, Ap	c1049	80	5.6	1795	4	US-09-620-312D-864	Sequence 864, App
977	80.5	5.6	2495	3	US-09-141-027-1	Sequence 1, Appl	c1050	80	5.6	2049	4	US-09-252-991A-15326	Sequence 15326, A
978	80.5	5.6	2495	4	US-09-617-804-1	Sequence 1, Appl	c1051	80	5.6	2098	1	US-08-153-848-41	Sequence 41, Appl
979	80.5	5.6	2500	4	US-09-949-016-791	Sequence 791, App	c1052	80	5.6	2098	3	US-09-299-843A-41	Sequence 41, Appl
980	80.5	5.6	2525	2	US-08-973-008-1	Sequence 1, Appl	c1053	80	5.6	2098	3	US-09-088-337B-41	Sequence 41, Appl
981	80.5	5.6	2525	3	US-09-267-409-1	Sequence 1, Appl	c1054	80	5.6	2098	5	PCT-US93-11153-41	Sequence 41, Appl
c 982	80.5	5.6	2709	4	US-09-485-529-3	Sequence 3, Appl	1055	80	5.6	2127	4	US-09-252-991A-15511	Sequence 15511, A
c 983	80.5	5.6	2796	4	US-09-252-991A-9979	Sequence 477, App	c1056	80	5.6	2132	4	US-09-270-767-12419	Sequence 12419, A
984	80.5	5.6	2988	4	US-09-902-540-477	Sequence 477, App	c1057	80	5.6	2200	1	US-08-592-126-102	Sequence 102, App
c 985	80.5	5.6	3102	4	US-09-949-016-2460	Sequence 2460, Ap	c1058	80	5.6	2200	4	US-09-168-595-102	Sequence 102, App
c 986	80.5	5.6	3346	4	US-09-252-991A-4429	Sequence 4429, Ap	c1059	80	5.6	2232	4	US-09-489-039A-4139	Sequence 4139, Ap
987	80.5	5.6	3739	4	US-09-684-405-5	Sequence 5, Appl	c1060	80	5.6	2325	4	US-09-252-991A-8052	Sequence 8052, Ap
c 988	80.5	5.6	3924	4	US-09-902-540-680	Sequence 680, App	1061	80	5.6	2448	4	US-09-252-991A-10680	Sequence 10680, A
c 989	80.5	5.6	4087	4	US-09-902-540-625	Sequence 625, App	c1062	80	5.6	2751	4	US-09-252-991A-7066	Sequence 7066, Ap
c 990	80.5	5.6	4167	4	US-09-169-768-12	Sequence 12, Appl	1063	80	5.6	3024	4	US-09-902-540-1868	Sequence 1868, Ap
c 991	80.5	5.6	4176	4	US-09-902-540-872	Sequence 872, App	c1064	80	5.6	3186	4	US-09-489-039A-5569	Sequence 5569, Ap
992	80.5	5.6	4237	1	US-07-844-298B-1	Sequence 1, Appl	c1065	80	5.6	3618	4	US-09-902-540-9652	Sequence 9652, Ap
c 993	80.5	5.6	4329	4	US-09-902-540-2431	Sequence 2431, Ap	1066	80	5.6	3968	4	US-09-949-016-1601	Sequence 1601, Ap
c 994	80.5	5.6	4465	4	US-09-949-016-2042	Sequence 2042, Ap	c1067	80	5.6	4895	3	US-09-053-866-1	Sequence 1, Appl
c 995	80.5	5.6	4532	4	US-09-902-540-626	Sequence 626, App	c1068	80	5.6	4895	3	US-09-479-130-1	Sequence 1, Appl
c 996	80.5	5.6	4604	4	US-09-902-540-602	Sequence 602, App	c1069	80	5.6	4895	4	US-09-472-130A-1	Sequence 1, Appl
997	80.5	5.6	5535	1	US-08-089-755A-1	Sequence 1, Appl	c1070	80	5.6	5656	4	US-09-902-540-694	Sequence 694, App
998	80.5	5.6	5535	1	US-08-089-755A-4	Sequence 4, Appl	1071	80	5.6	6404	4	US-09-902-540-760	Sequence 760, App
999	80.5	5.6	5535	1	US-08-421-754-1	Sequence 1, Appl	c1072	80	5.6	6436	4	US-09-600-099-1	Sequence 1, Appl
1000	80.5	5.6	5535	2	US-08-421-754-4	Sequence 4, Appl	1073	80	5.6	7152	4	US-09-492-709A-142	Sequence 142, App
1001	80.5	5.6	5535	2	US-08-421-791-1	Sequence 1, Appl	c1074	80	5.6	8773	4	US-09-902-540-965	Sequence 965, App
1002	80.5	5.6	5535	2	US-08-421-791-1	Sequence 1, Appl	c1075	80	5.6	8983	4	US-09-949-016-15437	Sequence 15437, A
c1004	80.5	5.6	7490	4	US-09-949-016-17606	Sequence 17606, A	1076	80	5.6	9164	4	US-09-814-915A-80	Sequence 80, Appl
c1005	80.5	5.6	9365	4	US-09-827-688-7	Sequence 7, Appl	c1077	80	5.6	18632	4	US-09-949-016-16574	Sequence 16574, A
1005	80.5	5.6	10276	4	US-09-902-540-975	Sequence 975, App	c1078	80	5.6	21330	4	US-09-902-540-1209	Sequence 1209, Ap
c1006	80.5	5.6	10317	4	US-09-902-540-1027	Sequence 1027, Ap	1079	80	5.6	21511	4	US-09-902-540-1201	Sequence 1201, Ap
1007	80.5	5.6	10505	4	US-09-902-540-1044	Sequence 1044, Ap	c1080	80	5.6	23417	4	US-09-902-540-1207	Sequence 1207, Ap
1008	80.5	5.6	10644	4	US-09-902-540-1028	Sequence 1028, Ap	1081	80	5.6	30780	4	US-09-902-540-1243	Sequence 1243, Ap
1009	80.5	5.6	11662	4	US-09-949-016-16978	Sequence 16978, A	c1082	80	5.6	31035	4	US-09-949-016-12272	Sequence 12272, A
1010	80.5	5.6	12317	4	US-09-949-016-14782	Sequence 14782, A	c1083	80	5.6	31035	4	US-09-949-016-17266	Sequence 17266, A
1011	80.5	5.6	13332	4	US-09-902-540-1047	Sequence 1047, Ap	c1084	80	5.6	34662	4	US-09-902-540-1261	Sequence 1261, Ap
c1012	80.5	5.6	13871	4	US-09-949-016-12037	Sequence 12037, A	1085	80	5.6	57280	4	US-09-949-016-11796	Sequence 11796, A
c1013	80.5	5.6	13871	4	US-09-949-016-15363	Sequence 15363, A	1086	80	5.6	57280	4	US-09-949-016-12843	Sequence 12843, A
1014	80.5	5.6	14809	4	US-09-902-540-1032	Sequence 1032, Ap	1087	80	5.6	57280	4	US-09-949-016-12844	Sequence 12844, A
1015	80.5	5.6	14899	4	US-09-902-540-1107	Sequence 1107, Ap	1088	80	5.6	57280	4	US-09-949-016-12846	Sequence 12846, A
c1016	80.5	5.6	17415	3	US-08-486-343A-1	Sequence 1, Appl	1089	80	5.6	57280	4	US-09-949-016-13542	Sequence 13542, A
c1017	80.5	5.6	17415	4	US-09-423-821B-1	Sequence 1, Appl	1090	80	5.6	57280	4	US-09-949-016-13543	Sequence 13543, A
c1018	80.5	5.6	17415	5	PCT-US95-07349-1	Sequence 1, Appl	1091	80	5.6	57280	4	US-09-949-016-13544	Sequence 13544, A
c1019	80.5	5.6	28509	4	US-09-902-540-1240	Sequence 1240, Ap	1092	80	5.6	57280	4	US-09-949-016-13545	Sequence 13545, A
1020	80.5	5.6	34094	4	US-09-292-034-1	Sequence 1, Appl	1093	80	5.6	57280	4	US-09-949-016-14633	Sequence 14633, A
c1021	80.5	5.6	41768	4	US-09-902-540-1266	Sequence 1266, Ap	1094	80	5.6	57280	4	US-09-949-016-14635	Sequence 14635, A
c1022	80.5	5.6	5216	4	US-09-716-865-23	Sequence 23, Appl	1095	80	5.6	57280	4	US-09-949-016-14636	Sequence 14636, A
1023	80.5	5.6	70000	3	US-09-851-896-3	Sequence 3, Appl	1096	80	5.6	57280	4	US-09-949-016-14637	Sequence 14637, A
1024	80.5	5.6	76399	4	US-09-949-016-16819	Sequence 16819, A	1097	80	5.6	57280	4	US-09-949-016-14638	Sequence 14638, A
1025	80.5	5.6	251769	4	US-09-949-016-13185	Sequence 13185, A	1098	80	5.6	57280	4	US-09-949-016-14639	Sequence 14639, A
1026	80.5	5.6	251769	4	US-09-949-016-13186	Sequence 13186, A	1099	80	5.6	57280	4	US-09-949-016-14640	Sequence 14640, A
1027	80.5	5.6	266748	4	US-09-949-016-13187	Sequence 13187, A	1100	80	5.6	57280	4	US-09-949-016-14640	Sequence 14640, A
1028	80.5	5.6	266748	4	US-09-949-016-13188	Sequence 13188, A	c1101	80	5.6	60990	4	US-09-949-016-14080	Sequence 14080, A
c1029	80	5.6	601	4	US-09-949-016-46365	Sequence 46365, A	c1102	80	5.6	77535	4	US-09-410-551B-1	Sequence 1, Appl
c1030	80	5.6	601	4	US-09-949-016-53376	Sequence 53376, A	c1103	80	5.6	77535	4	US-09-940-316B-1	Sequence 1, Appl
1031	80	5.6	601	4	US-09-949-016-132487	Sequence 132487, A	1104	80	5.6	450395	4	US-09-949-016-15473	Sequence 15473, A
c1032	80	5.6	828	4	US-09-252-991A-2146	Sequence 2146, Ap	c1105	79.5	5.6	484	3	US-09-643-597-198	Sequence 198, App
c1033	80	5.6	954	4	US-09-252-991A-13130	Sequence 13130, A	c1106	79.5	5.6	484	4	US-09-480-884A-198	Sequence 198, App
1034	80	5.6	1035	4	US-09-902-540-5365	Sequence 5365, Ap	c1107	79.5	5.6	484	4	US-09-542-615A-198	Sequence 198, App

c1108	79.5	5.6	484	4	US-09-606-421B-198	Sequence 199, App	1181	79.5	5.6	14158	4	US-09-902-540-1069	Sequence 1069, Ap
c1109	79.5	5.6	484	4	US-09-466-396A-198	Sequence 199, App	c1182	79.5	5.6	17247	4	US-09-902-540-1185	Sequence 1185, Ap
c1110	79.5	5.6	484	4	US-09-476-496A-198	Sequence 199, App	c1183	79.5	5.6	18324	4	US-09-902-540-1196	Sequence 1196, Ap
c1111	79.5	5.6	484	4	US-09-630-940B-198	Sequence 198, App	c1184	79.5	5.6	18848	4	US-09-902-540-1174	Sequence 1174, Ap
c1112	79.5	5.6	507	4	US-09-270-767-5332	Sequence 5332, App	c1185	79.5	5.6	21964	4	US-09-902-540-1190	Sequence 1190, Ap
c1113	79.5	5.6	507	4	US-09-270-767-70614	Sequence 20614, A	c1186	79.5	5.6	26103	4	US-09-949-016-15685	Sequence 15685, A
c1114	79.5	5.6	601	4	US-09-949-016-71124	Sequence 71124, A	c1187	79.5	5.6	26103	4	US-09-949-016-11879	Sequence 11879, A
c1115	79.5	5.6	714	4	US-09-328-352-4055	Sequence 4055, App	c1188	79.5	5.6	29433	4	US-09-949-016-15740	Sequence 15740, A
c1116	79.5	5.6	738	4	US-09-252-991A-9456	Sequence 9456, App	c1189	79.5	5.6	33529	3	US-09-144-085-3	Sequence 3, Appli
c1117	79.5	5.6	750	4	US-09-902-540-7791	Sequence 7791, App	1189:	79.5	5.6	36519	3	US-08-923-137-2	Sequence 2, Appli
c1118	79.5	5.6	816	4	US-09-252-991A-9480	Sequence 9480, App	1191	79.5	5.6	38078	4	US-09-949-016-12429	Sequence 12429, A
c1119	79.5	5.6	843	4	US-09-252-991A-2829	Sequence 2829, App	1192	79.5	5.6	38084	4	US-09-949-016-16459	Sequence 16459, A
c1120	79.5	5.6	846	4	US-09-252-991A-3196	Sequence 3196, App	c1193	79.5	5.6	41927	4	US-09-902-540-1268	Sequence 1268, Ap
c1121	79.5	5.6	995	3	US-09-540-014-10	Sequence 10, Appl	c1194	79.5	5.6	58821	4	US-09-949-016-15897	Sequence 15897, A
c1122	79.5	5.6	995	3	US-09-540-014-23	Sequence 23, Appl	1194	79.5	5.6	58821	4	US-09-949-016-12615	Sequence 12615, A
c1123	79.5	5.6	995	4	US-10-091-841A-10	Sequence 10, Appl	c1196	79.5	5.6	76264	4	US-09-949-016-15773	Sequence 15773, A
c1124	79.5	5.6	995	4	US-10-091-841A-23	Sequence 23, Appl	c1197	79.5	5.6	83617	4	US-09-949-016-12254	Sequence 12254, A
c1125	79.5	5.6	1014	4	US-09-252-991A-12024	Sequence 12024, A	1198	79.5	5.6	86380	4	US-09-949-016-14837	Sequence 14837, A
c1126	79.5	5.6	1071	4	US-09-252-991A-15521	Sequence 15521, A	c1199	79.5	5.6	86956	4	US-09-949-016-12994	Sequence 12994, A
c1127	79.5	5.6	1107	4	US-09-252-991A-3087	Sequence 3087, App	c1200	79.5	5.6	90150	4	US-09-949-016-17383	Sequence 17383, A
c1128	79.5	5.6	1107	4	US-09-902-540-6053	Sequence 6053, App	c1201	79.5	5.6	99748	4	US-09-949-016-11990	Sequence 11990, A
c1129	79.5	5.6	1108	4	US-09-949-016-355	Sequence 355, App	c1202	79.5	5.6	99749	4	US-09-949-016-16518	Sequence 16518, A
c1130	79.5	5.6	1108	4	US-09-902-540-249	Sequence 249, App	1203	79.5	5.6	325034	4	US-09-949-016-14957	Sequence 14957, A
c1131	79.5	5.6	1119	4	US-09-252-991A-11990	Sequence 11990, A	1204	79.5	5.6	389504	4	US-09-949-016-11774	Sequence 11774, A
c1132	79.5	5.6	1122	4	US-09-252-991A-3335	Sequence 3335, App	c1205	79.5	5.6	525	4	US-09-902-540-8594	Sequence 8594, Ap
c1133	79.5	5.6	1122	4	US-09-949-016-3915	Sequence 3915, App	c1206	79.5	5.6	601	4	US-09-949-016-46366	Sequence 46366, A
c1134	79.5	5.6	1134	4	US-09-622-439-21	Sequence 21, Appl	c1207	79.5	5.6	651	4	US-09-252-991A-7997	Sequence 7997, Ap
c1135	79.5	5.6	1134	4	US-10-318-142-21	Sequence 21, Appl	c1208	79.5	5.6	741	4	US-09-252-991A-16102	Sequence 16102, A
c1136	79.5	5.6	1140	4	US-09-252-991A-11857	Sequence 11857, A	c1209	79.5	5.6	906	4	US-09-252-991A-2239	Sequence 2239, Ap
c1137	79.5	5.6	1173	4	US-09-252-991A-3233	Sequence 3233, App	c1210	79.5	5.6	963	4	US-09-252-991A-16178	Sequence 16178, A
c1138	79.5	5.6	1177	4	US-09-270-767-11017	Sequence 11017, A	c1211	79.5	5.6	963	4	US-09-949-016-4316	Sequence 4316, Ap
c1139	79.5	5.6	1215	4	US-09-252-991A-1312	Sequence 1312, App	c1212	79.5	5.6	972	4	US-09-902-540-8031	Sequence 8031, Ap
c1140	79.5	5.6	1240	4	US-09-252-991A-6985	Sequence 6985, App	c1213	79.5	5.6	1004	4	US-09-252-991A-9420	Sequence 9420, Ap
c1141	79.5	5.6	1240	4	US-09-252-991A-6985	Sequence 6985, App	1214	79.5	5.6	1012	4	US-09-252-991A-15280	Sequence 15280, A
c1142	79.5	5.6	1371	4	US-09-252-991A-15313	Sequence 15313, A	1215	79.5	5.6	1014	4	US-09-902-540-1879	Sequence 1879, Ap
c1143	79.5	5.6	1398	4	US-09-252-991A-91	Sequence 91, Appl	c1216	79.5	5.6	1032	4	US-09-252-991A-6591	Sequence 6591, Ap
c1144	79.5	5.6	1432	4	US-09-902-540-264	Sequence 264, App	c1217	79.5	5.6	1047	4	US-09-902-540-7125	Sequence 7125, Ap
c1145	79.5	5.6	1432	4	US-09-902-540-6080	Sequence 6080, App	c1218	79.5	5.6	1058	4	US-09-634-137-39	Sequence 29, Appl
c1146	79.5	5.6	1452	4	US-09-252-991A-3933	Sequence 3933, App	1219	79.5	5.6	1089	4	US-09-252-991A-3785	Sequence 3785, Ap
c1147	79.5	5.6	1506	4	US-09-902-540-9624	Sequence 9624, App	c1220	79.5	5.6	1125	4	US-09-252-991A-6994	Sequence 6994, Ap
c1148	79.5	5.6	1554	4	US-09-252-991A-9350	Sequence 9350, App	c1221	79.5	5.6	1179	4	US-09-252-991A-3430	Sequence 3430, Ap
c1149	79.5	5.6	1590	4	US-09-489-039A-1653	Sequence 1653, App	c1222	79.5	5.6	1197	4	US-09-902-540-3968	Sequence 3968, Ap
c1150	79.5	5.6	1617	4	US-09-902-540-4903	Sequence 1553, App	c1223	79.5	5.6	1218	4	US-09-252-991A-7912	Sequence 7912, Ap
c1151	79.5	5.6	1752	4	US-09-252-991A-4682	Sequence 4682, App	c1224	79.5	5.6	1257	4	US-09-252-991A-1027	Sequence 1027, Ap
c1152	79.5	5.6	1878	4	US-09-252-991A-3300	Sequence 3300, App	c1225	79.5	5.6	1290	4	US-09-902-540-8370	Sequence 8370, Ap
c1153	79.5	5.6	1917	4	US-09-252-991A-3039	Sequence 3039, App	c1226	79.5	5.6	1302	3	US-09-199-637A-348	Sequence 348, App
c1154	79.5	5.6	2013	4	US-09-902-540-5920	Sequence 5920, App	1227:	79.5	5.6	1329	4	US-09-252-991A-6714	Sequence 6714, Ap
c1155	79.5	5.6	2039	4	US-09-902-540-179	Sequence 179, App	c1228	79.5	5.6	1332	4	US-09-252-991A-4685	Sequence 4685, Ap
c1156	79.5	5.6	2404	4	US-09-902-540-3817	Sequence 3817, App	c1229	79.5	5.6	1344	3	US-09-199-637A-350	Sequence 350, App
c1157	79.5	5.6	2412	4	US-09-252-991A-2921	Sequence 2921, App	c1230	79.5	5.6	1344	4	US-09-252-991A-16526	Sequence 16526, A
c1158	79.5	5.6	2449	4	US-09-949-016-4067	Sequence 4067, App	c1231	79.5	5.6	1413	4	US-09-252-991A-9741	Sequence 9741, A
c1159	79.5	5.6	2754	4	US-09-902-540-5587	Sequence 5587, App	1232	79.5	5.6	1428	4	US-09-252-991A-9266	Sequence 9266, Ap
c1160	79.5	5.6	2823	4	US-09-252-991A-2840	Sequence 2840, App	1233	79.5	5.6	1439	3	US-09-056-556-167	Sequence 167, App
c1161	79.5	5.6	2934	4	US-09-252-991A-84	Sequence 84, Appl	1234	79.5	5.6	1439	3	US-09-072-596-162	Sequence 162, App
c1162	79.5	5.6	3204	4	US-09-252-991A-3126	Sequence 3126, App	c1235	79.5	5.6	1439	4	US-09-072-967-167	Sequence 167, App
c1163	79.5	5.6	3225	4	US-09-252-991A-4622	Sequence 4622, App	c1236	79.5	5.6	1440	4	US-09-902-540-8640	Sequence 8640, App
c1164	79.5	5.6	3435	1	US-08-366-577-1	Sequence 1, Appli	c1237	79.5	5.6	1476	4	US-09-252-991A-4812	Sequence 4812, Ap
c1165	79.5	5.6	3435	5	PCT-US96-00005-1	Sequence 1, Appli	1238	79.5	5.6	1476	4	US-09-252-991A-2443	Sequence 2443, Ap
c1166	79.5	5.6	3519	1	US-08-035-558-1	Sequence 1, Appli	c1239	79.5	5.6	1509	4	US-09-252-991A-6819	Sequence 6819, Ap
c1167	79.5	5.6	3981	4	US-09-252-991A-1361	Sequence 1361, App	1240	79.5	5.6	1545	4	US-09-252-991A-9274	Sequence 9274, Ap
c1168	79.5	5.6	4179	4	US-09-252-991A-1244	Sequence 1244, App	c1241	79.5	5.6	1551	4	US-09-252-991A-4758	Sequence 4758, Ap
c1169	79.5	5.6	4261	4	US-09-949-016-3867	Sequence 3867, App	1242	79.5	5.6	1560	4	US-09-252-991A-8114	Sequence 8114, Ap
c1170	79.5	5.6	4284	4	US-09-252-991A-4006	Sequence 4006, App	1243	79.5	5.6	1566	4	US-09-252-991A-14361	Sequence 14361, A
c1171	79.5	5.6	5001	4	US-09-902-540-8618	Sequence 8618, App	1244	79.5	5.6	1642	4	US-09-799-451-873	Sequence 873, App
c1172	79.5	5.6	5561	2	US-08-400-159-1	Sequence 1, Appli	1245	79.5	5.6	1674	4	US-09-252-991A-12046	Sequence 12046, A
c1173	79.5	5.6	5561	3	US-08-611-729A-1	Sequence 1, Appli	1246	79.5	5.6	1692	4	US-09-252-991A-978	Sequence 978, App
c1174	79.5	5.6	5561	4	US-09-195-524-1	Sequence 1, Appli	1247	79.5	5.6	1695	4	US-09-252-991A-9380	Sequence 9380, Ap
c1175	79.5	5.6	8154	4	US-09-949-016-15657	Sequence 15657, A	c1248	79.5	5.6	1770	4	US-09-902-540-7790	Sequence 7790, Ap
c1176	79.5	5.6	1032	4	US-09-949-016-13070	Sequence 13070, A	c1249	79.5	5.6	1835	3	US-08-923-454A-7	Sequence 7, Appli
c1177	79.5	5.6	1692	4	US-09-902-540-960	Sequence 960, App	c1250	79.5	5.6	1842	4	US-09-252-991A-15508	Sequence 15508, A
c1178	79.5	5.6	12194	4	US-09-902-540-1091	Sequence 1091, App	1251	79.5	5.6	1869	4	US-09-252-991A-3231	Sequence 3231, Ap
c1179	79.5	5.6	12253	4	US-09-902-540-1060	Sequence 1060, App	c1252	79.5	5.6	1878	4	US-09-252-991A-11966	Sequence 11966, A
c1180	79.5	5.6	13631	4	US-09-902-540-1092	Sequence 1092, App	c1253	79.5	5.6	1929	4	US-09-252-991A-7017	Sequence 7017, Ap



1254	79	5.5	1932	4	US-09-252-991A-1911	Sequence 1911, Ap	c1327	79	5.5	30360	4	US-09-949-016-15716	Sequence 15716, A
c1255	79	5.5	1939	4	US-09-949-016-715	Sequence 715, App	c1328	79	5.5	33318	4	US-09-949-016-12495	Sequence 12495, A
1256	79	5.5	1947	4	US-09-252-991A-7111	Sequence 711, Ap	c1329	79	5.5	33319	4	US-09-949-016-15963	Sequence 15963, A
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c1258	79	5.5	1950	3	US-09-479-409-14	Sequence 14, Appl	c1331	79	5.5	42235	3	US-09-199-637A-1	Sequence 1, Appl
c1259	79	5.5	1950	3	US-09-479-453-14	Sequence 14, Appl	1332	79	5.5	44952	4	US-09-949-016-12197	Sequence 12197, A
1260	79	5.5	2082	4	US-09-252-991A-9500	Sequence 9500, Ap	1333	79	5.5	44960	4	US-09-949-016-17583	Sequence 17583, A
c1261	79	5.5	2166	3	US-09-232-200-101	Sequence 101, App	1334	79	5.5	54552	4	US-08-733-234A-30	Sequence 30, Appl
c1262	79	5.5	2166	3	US-09-232-197-101	Sequence 101, App	c1335	79	5.5	57559	4	US-09-949-016-13077	Sequence 13077, A
c1263	79	5.5	2166	3	US-09-232-201-101	Sequence 101, App	c1336	79	5.5	57560	4	US-09-949-016-12536	Sequence 12536, A
c1264	79	5.5	2166	3	US-09-232-195-101	Sequence 101, App	c1337	79	5.5	58014	4	US-09-949-016-17448	Sequence 17448, A
c1265	79	5.5	2187	3	US-08-923-454A-23	Sequence 23, Appl	1338	79	5.5	67930	4	US-09-949-016-12270	Sequence 12270, A
c1266	79	5.5	2220	4	US-09-252-991A-16207	Sequence 16207, A	c1339	79	5.5	67745	4	US-09-949-016-17251	Sequence 17251, A
c1267	79	5.5	2256	4	US-09-252-991A-10853	Sequence 10853, A	1340	79	5.5	89916	4	US-08-816-095-3	Sequence 3, Appl
c1268	79	5.5	2415	4	US-09-252-991A-5105	Sequence 5105, Ap	1341	79	5.5	108690	4	US-09-949-016-13525	Sequence 13525, A
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1270	79	5.5	2505	4	US-09-252-991A-1830	Sequence 1830, Ap	c1343	79	5.5	132438	4	US-09-949-016-14349	Sequence 14349, A
c1271	79	5.5	2571	4	US-09-252-991A-8190	Sequence 8190, Ap	c1344	79	5.5	132438	4	US-09-949-016-14350	Sequence 14350, A
1272	79	5.5	2766	4	US-09-252-991A-3756	Sequence 3756, Ap	c1345	79	5.5	194889	4	US-09-949-016-15654	Sequence 15654, A
1273	79	5.5	2874	4	US-09-252-991A-3837	Sequence 3837, Ap	1346	79	5.5	197131	4	US-09-949-016-12675	Sequence 12675, A
1274	79	5.5	2910	4	US-09-252-991A-9547	Sequence 9547, Ap	1347	79	5.5	197132	4	US-09-949-016-17170	Sequence 17170, A
c1275	79	5.5	3033	4	US-09-724-797-81	Sequence 81, Appl	c1348	79	5.5	529885	4	US-09-949-016-14340	Sequence 14340, A
c1276	79	5.5	3225	4	US-09-902-540-3099	Sequence 3099, Ap	c1349	79	5.5	529885	4	US-09-949-016-14341	Sequence 14341, A
1277	79	5.5	3783	4	US-09-902-540-4846	Sequence 4846, Ap	c1350	79	5.5	529885	4	US-09-949-016-14342	Sequence 14342, A
1278	79	5.5	3813	2	US-08-650-000-3	Sequence 3, Appl	c1351	79	5.5	529885	4	US-09-949-016-14343	Sequence 14343, A
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c1280	79	5.5	3813	4	US-09-902-540-7085	Sequence 7085, Ap	c1353	79	5.5	529885	4	US-09-949-016-14345	Sequence 14345, A
1281	79	5.5	3813	6	5395760-3	Patent No. 5395760	c1354	79	5.5	529885	4	US-09-949-016-14346	Sequence 14346, A
1282	79	5.5	3813	6	5395760-3	Patent No. 5395760	c1355	79	5.5	529885	4	US-09-949-016-14347	Sequence 14347, A
1283	79	5.5	3815	4	US-09-902-540-634	Sequence 634, App	1356	79	5.5	1230230	4	US-09-438-185A-1	Sequence 1, Appl
1284	79	5.5	3861	4	US-09-252-991A-8018	Sequence 8018, Ap	1357	78.5	5.5	582	4	US-09-874-923-114	Sequence 114, App
c1285	79	5.5	3946	4	US-09-949-016-2607	Sequence 2607, Ap	c1358	78.5	5.5	601	4	US-09-252-991A-3659	Sequence 3659, Ap
c1286	79	5.5	3946	4	US-09-949-016-2608	Sequence 2608, Ap	c1359	78.5	5.5	601	4	US-09-949-016-49806	Sequence 49806, A
1287	79	5.5	4200	4	US-08-912-951-6	Sequence 6, Appl	c1360	78.5	5.5	601	4	US-09-949-016-145812	Sequence 145812, A
c1288	79	5.5	4284	4	US-09-252-991A-4006	Sequence 4006, Ap	c1361	78.5	5.5	601	4	US-09-949-016-146080	Sequence 146080, A
1289	79	5.5	4321	3	US-08-402-181B-6	Sequence 6, Appl	c1362	78.5	5.5	611	4	US-09-949-016-146348	Sequence 146348, A
1290	79	5.5	4335	3	US-08-974-549A-6	Sequence 6, Appl	c1363	78.5	5.5	701	3	US-09-655-270A-18	Sequence 18, Appl
c1291	79	5.5	4430	4	US-09-721-456-6	Sequence 6, Appl	c1364	78.5	5.5	711	3	US-09-651-941-22	Sequence 22, Appl
1292	79	5.5	4430	4	US-09-902-540-491	Sequence 491, App	c1365	78.5	5.5	711	3	US-09-955-597-22	Sequence 22, Appl
1293	79	5.5	4704	4	US-09-252-991A-3906	Sequence 3906, Ap	c1366	78.5	5.5	882	4	US-09-252-991A-5870	Sequence 5870, Ap
c1294	79	5.5	4928	4	US-09-578-063-67	Sequence 67, Appl	c1367	78.5	5.5	894	4	US-09-902-540-6139	Sequence 6139, Ap
c1295	79	5.5	4978	4	US-09-902-540-775	Sequence 775, App	c1368	78.5	5.5	1032	4	US-09-252-991A-14504	Sequence 14504, A
c1296	79	5.5	5117	4	US-09-949-016-2598	Sequence 2598, Ap	c1369	78.5	5.5	1137	4	US-09-252-991A-5529	Sequence 5529, Ap
c1297	79	5.5	5117	4	US-09-949-016-2599	Sequence 2599, Ap	c1370	78.5	5.5	1155	4	US-09-252-991A-412	Sequence 412, App
c1298	79	5.5	5117	4	US-09-949-016-2600	Sequence 2600, Ap	1371	78.5	5.5	1173	4	US-09-894-844-60	Sequence 60, Appl
c1299	79	5.5	5177	4	US-09-949-016-2601	Sequence 2601, Ap	1372	78.5	5.5	1200	3	US-08-854-531-5	Sequence 5, Appl
c1300	79	5.5	5303	4	US-09-949-016-2602	Sequence 2602, Ap	1373	78.5	5.5	1200	5	PCT-US95-13552-5	Sequence 5, Appl
c1301	79	5.5	5303	4	US-09-949-016-2603	Sequence 2603, Ap	1374	78.5	5.5	1212	4	US-09-489-039A-4706	Sequence 4706, Ap
c1302	79	5.5	5303	4	US-09-949-016-2604	Sequence 2604, Ap	c1375	78.5	5.5	1212	4	US-09-902-540-3501	Sequence 3501, Ap
c1303	79	5.5	5303	4	US-09-949-016-2605	Sequence 2605, Ap	c1376	78.5	5.5	1233	4	US-09-489-039A-4691	Sequence 4691, Ap
c1304	79	5.5	5497	4	US-09-902-540-652	Sequence 652, App	c1377	78.5	5.5	1299	4	US-09-252-991A-14606	Sequence 14606, A
c1305	79	5.5	6655	4	US-09-902-540-777	Sequence 777, App	c1378	78.5	5.5	1396	4	US-09-902-540-2306	Sequence 2306, Ap
c1306	79	5.5	6715	4	US-09-902-540-818	Sequence 818, App	1379	78.5	5.5	1404	4	US-09-252-991A-14856	Sequence 14856, A
1307	79	5.5	7225	4	US-09-902-540-876	Sequence 876, App	c1380	78.5	5.5	1476	4	US-09-902-540-6774	Sequence 6774, Ap
1308	79	5.5	7261	4	US-09-902-540-845	Sequence 845, App	c1381	78.5	5.5	1503	4	US-09-687-360-1	Sequence 1, Appl
c1309	79	5.5	8241	4	US-09-902-540-798	Sequence 798, App	c1382	78.5	5.5	1509	4	US-09-252-991A-3614	Sequence 3614, Ap
c1310	79	5.5	9996	4	US-09-902-540-999	Sequence 999, App	c1383	78.5	5.5	1545	4	US-09-252-991A-5553	Sequence 5553, Ap
1311	79	5.5	12739	4	US-09-902-540-1011	Sequence 1011, Ap	c1384	78.5	5.5	1560	4	US-09-252-991A-15809	Sequence 15809, A
c1312	79	5.5	14467	4	US-09-902-540-1058	Sequence 1058, Ap	c1385	78.5	5.5	1584	4	US-09-252-991A-15886	Sequence 15886, A
1313	79	5.5	15418	4	US-09-783-203-1	Sequence 1, Appl	c1386	78.5	5.5	1662	4	US-09-252-991A-1413	Sequence 1413, Ap
1314	79	5.5	15418	4	US-09-994-427A-1	Sequence 1, Appl	1387	78.5	5.5	1671	4	US-09-252-991A-9711	Sequence 9711, Ap
1315	79	5.5	15418	4	US-09-244-438-1	Sequence 1, Appl	c1388	78.5	5.5	1680	4	US-09-252-991A-15645	Sequence 15645, A
c1316	79	5.5	15499	4	US-09-902-540-1140	Sequence 1140, Ap	1389	78.5	5.5	1690	4	US-09-620-312D-69	Sequence 69, Appl
c1317	79	5.5	15782	4	US-09-949-016-13762	Sequence 13762, A	1390	78.5	5.5	1702	4	US-09-902-540-292	Sequence 292, App
1318	79	5.5	17612	3	US-08-911-853-29	Sequence 1094, Ap	c1391	78.5	5.5	1716	4	US-09-252-991A-9577	Sequence 9577, Ap
1319	79	5.5	17612	3	US-09-479-409-29	Sequence 29, Appl	c1392	78.5	5.5	1734	4	US-09-711-164-179	Sequence 179, App
1320	79	5.5	17612	3	US-09-479-453-29	Sequence 29, Appl	1393	78.5	5.5	1758	4	US-09-252-991A-15835	Sequence 15835, A
1321	79	5.5	18324	4	US-09-902-540-1196	Sequence 1196, Ap	c1394	78.5	5.5	1824	4	US-09-252-991A-16072	Sequence 16072, A
1322	79	5.5	19455	4	US-09-902-540-1147	Sequence 1147, Ap	1395	78.5	5.5	1842	4	US-09-543-681A-1840	Sequence 1840, Ap
1323	79	5.5	21758	4	US-09-902-540-1238	Sequence 1238, Ap	1396	78.5	5.5	1899	4	US-09-252-991A-15709	Sequence 15709, A
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c1410	78.5	5.5	2526	4	US-09-758-282B-213	Sequence 213, App	c1483	78.5	5.5	86414	4	US-09-949-016-15758	Sequence 15758, A
c1411	78.5	5.5	2526	4	US-09-577-304A-213	Sequence 213, App	c1484	78.5	5.5	128470	4	US-09-949-016-13765	Sequence 13765, A
c1412	78.5	5.5	2610	4	US-09-252-991A-1107	Sequence 1107, Ap	c1485	78.5	5.5	125254	4	US-09-949-016-13194	Sequence 13194, A
c1413	78.5	5.5	2754	4	US-09-252-991A-1147	Sequence 1147, Ap	c1486	78.5	5.5	152524	4	US-09-949-016-11851	Sequence 11851, A
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c1416	78.5	5.5	3046	1	US-08-276-099A-1	Sequence 1, Appli	c1489	78.5	5.5	229354	4	US-09-705-400-64	Sequence 64, Appl
c1417	78.5	5.5	3046	1	US-08-781-890-1	Sequence 1, Appli	c1490	78.5	5.5	321022	4	US-09-949-016-11852	Sequence 11852, A
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c1439	78.5	5.5	5275	4	US-09-902-540-771	Sequence 771, App							
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c1441	78.5	5.5	5515	3	US-09-125-642C-8	Sequence 8, Appli							
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c1457	78.5	5.5	8756	4	US-09-949-016-1438	Sequence 1438, Ap							
c1458	78.5	5.5	9710	4	US-09-902-540-978	Sequence 978, App							
c1459	78.5	5.5	12356	4	US-09-902-540-1006	Sequence 1006, Ap							
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c1463	78.5	5.5	17245	4	US-09-902-540-1073	Sequence 1073, Ap							
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## ALIGNMENTS

RESULT 1  
US-09-799-451-571  
; Sequence 571, Application US/09799451  
; Patent No. 6783969  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wang, Jiong-Rui  
; APPLICANT: Ma, Yungqing  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Ghosh, Reena  
; APPLICANT: Drmanac, Radjoje T.  
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 803  
; CURRENT APPLICATION NUMBER: US/09/799, 451  
; CURRENT FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 948  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 571  
; LENGTH: 2240  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1779)  
US-09-799-451-571  
Alignment Scores: 2.33e-132 Length: 2240  
Pred. No.:



Score: 1265.00 Matches: 246  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 88.34% Indels: 0  
DB: 4 Gaps: 0

US-10-015-388A-54 (1-280) x US-09-799-451-571 (1-2240)

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QY 1 MetCysPheLeuAsnLysLeuLeuLeuAlaValLeuGlyThrPheGlnIlePro 20
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QY 21 ThrValProGluAspLeuPheLeuGluGluGlyProSerTyrAlaPheGluValAsp 40
DB 412 ACAGTCCCTGAGGACTTGTCTTCTGGAAGAGGTCCCTCATATGCTTTGAGGTGAC 471
QY 41 ThrValAlaProGluHisGlyLeuAspAsnAlaProValValAspGlnLeuLeuTyr 60
DB 472 ACAGTAGCCCAAGAGCATGGCTTGACCAATGCGCTGTGGTGGACAGCAGCTGCTCTAC 531
QY 61 ThrCysCysProTyrIleGlyGluLeuArgLysLeuLeuAlaSerTrpValSerGlySer 80
DB 532 ACTGCTGCCCTACATCGAGAGCTCCGAAACTGCTCGCTTCGTGGTGTGAGGCAGT 591
QY 81 SerGlyArgSerGlyPheMetArgLysIleThrProThrThrThrSerLeuGly 100
DB 592 AGTGACGAGTGGGGCTTCATGAGGAAATCACCCCACTACCAACAGCCTGGGA 651
QY 101 AlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAlaGlnAlaPhePheHis 120
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QY 241 LeuSerAlaAsnIleThr 246
DB 1072 CTGTGACCAACATCACA 1089
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## RESULT 2

US-09-103-840A-2/c  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Alignment Scores:  
Pred. No.: 5.55e+03 Length: 4403765  
Score: 111.50 Matches: 61  
Percent Similarity: 37.92% Conservatives: 30  
Best Local Similarity: 25.42% Mismatches: 89  
Query Match: 7.79% Indels: 60  
DB: 3 Gaps: 11

US-10-015-388A-54 (1-280) x US-09-103-840A-2 (1-4403765)  
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QY 82 GlyArgSerGlyGlyPheMetArgLysIleThrProThrThrThrSerLeuGlyAla 101  
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QY 102 GlnPro---SerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAlaGlnAlaPhePheHis 120  
DB 2472739 CGGCTGCGCCCAATACCGTTACTGTTGATCGCTCGCGCGCGGTGCGTACTTCAAG 2472680  
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QY 139 SerAsnCysValLysHisIleLysAlaThrLeuValAlaAspLeuValArgGlnAlaGlu 158  
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QY 159 SerLeuLeuGlnGlnLeuValThrGlnGlyGluGlyGlyAspProAlaGlnLeu 178  
DB 2472559 GCC-----GCCGAGAACGATGCGACCCAGGTGGTGTGG 2472527  
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QY 199 GluPheCysGlnArgLys-----SerProGlyAla 208  
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QY 229 AlaValGlyLeuAlaThrGlu-LysAlaCysAlaTrpLeu-----Se 242  
DB 2472412 CTGCCCCGGGATCACACGGGATTCGTTGTGAGTTGGTATGATGCGGATTCGCGGTC 2472353  
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DB 2472352 GAGGAACGCGAGGTGATATCGACAGTGGCGAAGAAGAGCCCGCGCGGAGATCAC 2472293  
QY 258 rArgThrLeuArgAlaGlnGlyProGluProAlaAlaArgGlyGluArgGlyCys 277  
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RESULT 3  
US-09-103-840A-1/c





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Qy 243 AlaAsnIleThrAlaLeuIleArgGluValLysAlaAlaValSerArgThrLeuArg 262
Db 9938 -----GAGTCCCTCGCTCGCGGTGCGGCTCGCCCTCGGGGGGCCA 9906
Qy 263 AlaGlnGlyProGlu-----ProAlaAlaArgGlyGluArgArgGlyCys 277
Db 9905 GCAACAGGCGCTGAGACCACTCCACGAGGCGCGCTCAGCCTGTGTGCGAGGAGGACTTGT 9846

RESULT 6
US-09-949-016-15748/c
; Sequence 15748, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15748
; LENGTH: 21691
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(21691)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15748

Alignment Scores:
Pred. No.: 4.45 Length: 21691
Score: 106.50 Matches: 79
Percent Similarity: 34.29% Conservative: 17
Best Local Similarity: 28.21% Mismatches: 102
Query Match: 7.44% Indels: 83
DB: 4 Gaps: 14

US-10-015-388A-54 (1-280) x US-09-949-016-15748 (1-21691)

Qy 56 GlnGlnLeuLeuThrCysCysProTyrIleGlyGluLeuArgLysLeuLeuAlaSer 75
Db 10595 CAGCACCACCTTTACTACGCTGTCTCTGCATT-----CAACTCTGC 10554
Qy 76 TrpValSerGlySerSerGly-----ArgSerGlyGlyPheMetArgLysIle----- 91
Db 10553 TGGGCCCCAGGGTCTCGGGAGGCCCCACCCAGGTGGGAGGGAGGAGAGCTGGAGGAG 10494
Qy 92 -----ThrProThrThrThrSerLeuGlyAlaGlnProSerGln 105
Db 10493 CCCCAGCGCTGGATGGCTGCTCCCTGTGCCACAGCCAGCGGTGGTGCCACCAGCAGCAG 10434
Qy 106 ---ThrSerGlnGlyLeuGlnAlaGlnLeuAlaGlnAlaPheHisAsnGlnProPro 124
Db 10433 TTCTCTCTACTTGGGTCTCAGGCTGGACACGGACAGGCC-----AGACCAGGACCGGG 10380
Qy 125 SerLeuArgArgThrValGlnPheValAla-----GluArgIleGlySerAsn 140
Db 10379 TCGGTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 10323
Qy 141 CysValLysHisIleLysAlaThrLeuValAlaAspLeuValArgGlnAlaGluSer--- 159

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Db 10322 -----GTGGTGGGGGCACCTCGGCGCTCTCTAGCAGGCTTGTGAGCCAGGG 10275
Qy 160 -----LeuLeuGlnGlnLeuValThrGlnGlyGluGluGly----- 172
Db 10274 GGCTCTCTGCATCTCTTCTGCAGGAGTAAACAGTAGGAGGAGGAGGAGGAGGAGGAGGAG 10215
Qy 173 -----GlyAspProAlaGlnLeuLeuGluLeuLeuCys----- 183
Db 10214 GGCCCGTGGCAGCGCGCGCTGTGTTC-CTAAGATGTTTCGGGCGCGCGGCTCTCTGCG 10156
Qy 184 -----SerGlnLeuCysProHisGlyAlaGlnAlaLeuAla 195
Db 10155 GGCCCCCGCGGCGCACCTCGGCGCAGCGCGCTCTTTCGAGCGGCGACCTTCCCTGGGG 10096
Qy 196 LeuGlyArgGluPheCysGlnArgLysSerPro-----GlyAlaVal 209
Db 10095 GATGGCGCTCAACAGCGGCTCTGTAGAGCCCTCTCGGCTGCATCATCCGCGGCTTCT 10036
Qy 210 ArgAlaLeuLeuProGluThrProAlaAlaValLeuSerSerAlaGluAsnIleAla 229
Db 10035 CCAGCCACACCTCCGGAACAGTGCCTGCAGGCTGCCAGCGGGGCTGGCCATTGACCG 9976
Qy 230 ValGlyLeuAla-----ThrGluLysAlaCysAlaTyrLeuSer 242
Db 9975 GTGGGCTGGGCTGTGGCGCAGGTGGGCGCGCACCTGTCTGGCTGTGTGG----- 9922
Qy 243 AlaAsnIleThrAlaLeuIleArgArgGluValLysAlaAlaValSerArgThrLeuArg 262
Db 9921 -----GAGTCCCTCGCTCGCGCTGCCCTCGCGGGCGCA 9889
Qy 263 AlaGlnGlyProGlu-----ProAlaAlaArgGlyGluArgArgGlyCys 277
Db 9888 GCAACAGGCGCTGAGACCACTCCACGAAGGCCCGCTCAGCCTGTGTGAGGAGGAGGAG 9829

RESULT 7
US-09-252-991A-690/c
; Sequence 690, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 690
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-690

Alignment Scores:
Pred. No.: 0.0913 Length: 1350
Score: 104.50 Matches: 83
Percent Similarity: 31.91% Conservative: 22
Best Local Similarity: 25.23% Mismatches: 98
Query Match: 7.30% Indels: 127
DB: 4 Gaps: 14

US-10-015-388A-54 (1-280) x US-09-252-991A-690 (1-1350)

Qy 25 AspLeuPhePheLeuGluGluGlyProSerTyrAlaPheGluValAspThrValAlaPro 44
Db 1119 GACCTTGGCTGTCTCGGAGAGTCCCGCGCAGGCTCTCGCGGGGAGCTCGGGCGG--- 1063
Qy 45 GluHisGlyLeuAspAsnAlaProValValAspGln----- 56

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Db 1062 ---CACCACCAGGACGAAGCTGGCGTTGTTCGATCAGGCTGGCTGCGTGCATCGCGAC 1006  
Qy 56 ----- 56  
Db 1005 GTGCGACCGCTAGCGCTTCTCGACGATCGGATGCGGATCGCTTTGGCTGCGTGCATCACCCT 946  
Qy 57 ---GlnLeuLeuTyThrCysCysProTyrIleGlyGluLeu----- 69  
Db 945 CGCCAGCGCTGGCGAGCGGCGAGCATCACCGGGGGAAGTGGCGGCGAGTCTGCTGTG 886  
Qy 70 -----ArgLyLeuLeuLeuSerTrpValSerGlySerSerGlyArgSerGlyGly 86  
Db 885 GTTGTACACCGGTACTCTCGGACCGCGCTGGCTGGCTGGCGTGAAGT----- 838  
Qy 87 PheMetArgLyLeuLeuThrProThrThrThrSerLeuGlyAlaGlnProSerGln--- 105  
Db 837 -----ACAGAACTCGCGGCGAGCCAGGCGCCAGGTTTC 808  
Qy 106 -----ThrSerGlnGlyLeu 110  
Db 807 GCGGTACAGCTCTCGGGGTGCGCGGCGGCGGCGGAGCGTGCAGTGCAGTGGGCGCTC 748  
Qy 111 GlnAla-----GlnLeuAlaGln-----AlaPhePheHisAsnGlnProProSer 125  
Db 747 GCGCGGCTTACAGTTCGAGCAGCAGGAAGTGGCGGATTTCCGAGGCGGCGCC 694  
Qy 126 LeuArgArgThrValGluPheValAlaGluArgIleGlySerAsnCysVallyHisIle 145  
Db 693 -----GGCGCTGGATGC---CACCACCG 673  
Qy 146 LysAlaThrLeuValAlaAspLeuValArgGlnAlaGluSerLeuGlnGlnLeu 165  
Db 672 CCGCGCAGGCGCTCGCGCGCTGTGTGAGCAGGCGCCAGCAGCTCTTGGCGAGGA--- 616  
Qy 166 ValThrGlnGlyGluGluGlyClyAspProAlaGlnLeuLeuGluLeuLeuCysSerGln 185  
Db 615 ---CCGCCAGGCGCGCGCGCGGCAATGTCGAGCACCGCGCGCAGTAGTCTCTGTCAG 559  
Qy 186 LeuCysProHisGlyAlaGlnAlaLeuAlaLeuGlyArgGluPheCysGlnArgLysSer 205  
Db 558 -----GCT 556  
Qy 206 ProGlyAlaValArgAlaLeuLeuProGluThrProAlaAlaValLeuSerSerAla 225  
Db 555 CAGGCGCTGTGTCGCGCGCTTCTCGCGACCGCGCGACCGCCAGCGCGGTATTGCGC 496  
Qy 226 GluAlaLeuAlaValGlyLeuAlaThrGluLysAlaCysAlaTrpLeuSerAlaAsnIle 245  
Db 495 GAGCGCGTGGCTCGGTGAGCAGCGGGAAGCTGTGCTGCC---CAGGGCCACCGGGGC 439  
Qy 246 ThrAlaLeuIleArgArgGluValLysAlaAlaValSer-----ArgThrLeu 261  
Db 438 GCGGCTCTCGA-AGCGGCATTGTGTCGCGCACTTCTGCACTTGCACCTGGCTGAGTAGCGG 380  
Qy 262 ArgAlaGlnGlyProGluPro-----AlaAlaArg 271  
Db 379 CGCGCGCAGGCGCTCGCGCTCTACCGTGTGCGGGTGCAGCCCGCTTTCAGCGGCA 320  
Qy 272 GlyGluArgArgGlyCysSerArgAla 280  
Db 319 GCGCGAGGTAGCATGCTCGCGCA 293

## RESULT 8

US-09-252-991A-720  
; Sequence 720, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 720  
; LENGTH: 3054  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-720

Alignment Scores:  
Pred. No.: 0.333 Length: 3054  
Score: 104.50 Matches: 83  
Percent Similarity: 31.91% Conservative: 22  
Best Local Similarity: 25.23% Mismatches: 98  
Query Match: 7.30% Indels: 127  
DB: 4 Gaps: 14

US-10-015-388A-54 (1-280) x US-09-252-991A-720 (1-3054)

Qy 25 AspLeuPhePheLeuGluGluGlyProSerTyrAlaPheGluValAspThrValAlaPro 44  
Db 1390 GACCTTGCCCTGCTGCGGAAGTCCCGCGCAGGCTCTCGCCGCGGACGTCGCGCG 1446  
Qy 45 GluHisGlyLeuAspAsnAlaProValValAspGln----- 56  
Db 1447 ---CACCACAGGACGAAGCTGGCGTTGTTCGATCAGGCTGGCGTGCATCGCGAC 1503  
Qy 56 ----- 56  
Db 1504 GTGCACCGCTAGGCTTCTCGACGATCGGATCGGATCGCTTGGCGTGCATCACCCT 1563  
Qy 57 ---GlnLeuLeuTyThrCysCysProTyrIleGlyGluLeu----- 69  
Db 1564 CGCCAGCGCTTGGCGCGAGGCGAGCATCACCGGCGGAAGTGGCGGCGCAGTCTGCTG 1623  
Qy 70 -----ArgLysLeuLeuAlaSerTrpValSerGlySerSerGlyArgSerGlyGly 86  
Db 1624 GTGTACACCGGTACTCTCGGACCGCGCTGGCTGGCGTGAAGT----- 1671  
Qy 87 PheMetArgLysIleThrProThrThrThrSerLeuGlyAlaGlnProSerGln--- 105  
Db 1672 -----ACAGAACTCGCGCGCCAGGCGCCAGGTTCC 1701  
Qy 106 -----ThrSerGlnGlyLeu 110  
Db 1702 GCGGTACAGCTCTCGCGGTGCGAGCGGCGCACGCGGACAGGTGACCGAGTGGCGCTC 1761  
Qy 111 GlnAla-----GlnLeuAlaGln-----AlaPhePheHisAsnGlnProProSer 125  
Db 1762 GCGCGGTTGACCAAGTTGACGAGCAGCAAGTCCGCGATTTCCGAGGCGGCCCC 1815  
Qy 126 LeuArgArgThrValGluPheValAlaGluArgIleGlySerAsnCysValLysHisIle 145  
Db 1816 -----GGCGTGGATGC---CACCACCG 1836  
Qy 146 LysAlaThrLeuValAlaAspLeuValArgGlnAlaGluSerLeuGlnGlnLeu 165  
Db 1837 CCGGCGAGGCGTTCGCGCGCTGGTGGAGCAGGCCAGCAGCTCTTGGCGAAGGA--- 1893  
Qy 166 ValThrGlnGlyGluGluGlyGlyAspProAlaGlnLeuLeuLeuLeuLeuCysSerGln 185  
Db 1894 ---CGCCAGGCGGCGCGCGCGCAATGTGAGCAGCCGCGGCGAGGTAGTCTCGTCCAG 1950  
Qy 186 LeuCysProHisGlyAlaGlnAlaLeuAlaLeuGlyArgGluPheCysGlnArgLysSer 205  
Db 1951 -----GCT 1953  
Qy 206 ProGlyAlaValArgAlaLeuLeuProGluThrProAlaAlaValLeuSerSerAla 225  
Db 1954 CAGGCGCTGTTCGCGCGCTTCTCGCGGACCGCGGAGCCGCCAGCGCGGTATTGCGC 2013







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Qy 193 aleuAlaLeuGlyArgGluPheCysGlnArgLysSer-----Pr 206
Db 792 ACAGCGCTTGGCGCGAGGAGCGATCGACGGCGCGAGCTGGGGAAACATGCGCAACC 851
Qy 206 oGlyAlaValArgAlaLeuLeuProGluThrProAlaAlaValLeuSerSerAlaG1 226
Db 852 AGGCGCGCTTCCCGGC-----CGGCGCTTCTCCGTGGCCAGCA 890
Qy 226 uAsnIleAlaValGlyLeuAlaThrGluLysAlaCysAlaTrpLeuSerAlaAsnIleTh 246
Db 891 GCGGGCGCGCGCCCACTCGCGCGCGAGCGCGAGCGCTTGGCGAAGCGCA-----942
Qy 246 rAlaLeuIleArgGluValLysAlaAlaValSerArgThrLeuArgAlaGlnGly-- 265
Db 943 -----GCAGCGAGCAGCAACGCGCGCCAGTAGCGGATGCTGTCTGAACCGGGAGG 995
Qy 266 -----ProGluProAlaAlaArgGlyGluArgGlyCy 277
Db 996 AGCGGATCAGGGTGGTGACACCCCATCAGCAGCAGGCGGACCGAGGTTGACTTG 1055
Qy 277 sSerArg 279
Db 1056 CGCCCGA 1062

RESULT 12
US-09-902-540-4835
; Sequence 4835, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4835
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4835

Alignment Scores:
Pred. No.: 0.365 Length: 2745
Score: 103.50 Matches: 68
Percent Similarity: 40.16% Conservative: 34
Best Local Similarity: 26.77% Mismatches: 102
Query Match: 7.23% Indels: 52
DB: 4 Gaps: 13

US-10-015-388A-54 (1-280) x US-09-902-540-4835 (1-2745)

Qy 75 SerTrpValSerGlySerSerGlyArgSerGlyGlyPheMetArgLysIleThrProThr 94
Db 1445 ACCTGGACAACCGCATGATGACGACGCGCGCGAGGTGGACGCGA-----ACGCGCGCT 1498
Qy 95 ThrThrThrSerLeuGlyAla-----GlnProSerGlnThr----- 106
Db 1499 GCAAGACGACGCGGTGAGCCCTGCTGTCGCGCTCAACCTCGCGAGGTGTCGCGCACCC 1558
Qy 107 -----SerGlnGlyLeuGlnAlaGlnLeuAlaGlnAlaPhePhe-----HisAsn 121
Db 1559 GGCGGAGACCGAGGGGAC-GAGGCGTGTCTGCGGAGGCGCCCTCACGTGGCGGCAACACACAGC 1617
Qy 122 GlnPro-----ProSer-----LeuArgArgThrValGlu-----PheValAlaGlu 135
Db 1618 AACCCCATGCGCAGGACGCGGTGTATGCCGTGTACGTGGAGGGCGGCTTCTGCTGGAT 1677
Qy 136 ArgIleGlySerAsnCysValLysHisIleLysAlaThrLeuValAla----- 151
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Db 1678 TCCGACAGAGCCCGGGGCTGGCGCTGCTGGCGGAGACCATCACCGAGCGGAGGSCATTG 1737
Qy 152 -----AspLeuValArgGlnAlaGluSerLeuLeuGlnGlnLeuValThr 167
Db 1738 CCTCGGGAGATTCACTGGCGCGGAGCGCTGGGGGCTGAGCTATTCTGCTGCTGACG 1797
Qy 168 GlnGlyGluGluGlyAspProAlaGlnLeuLeuGluLeuLeuCysSerGlnLeuCys 187
Db 1798 GACGCGGCAAGCGGCGGAGTACACCCAGGCGTTGGAGTTGATGGCGCGCAGCTTGCC 1857
Qy 188 ProHisGlyAlaGlnAlaLeuAlaLeuGlyArgGlu-----PheCysGlnArgLysSerPro 206
Db 1858 ACGCCGCTGCCCCAGCGCTGCGCCCTTTCGCGCGGCTGATGCGAGCGAC-GGTGCT 1916
Qy 207 GlyAlaValArgAlaLeuLeuPro-----GluGluThrProAlaAlaVal 221
Db 1917 GGTGGCGCGGAGCGCAAGCCAGGTGCTGGGCCACTACGAGACGGACCGCAGGGGCC 1976
Qy 222 LeuSerSerAlaGluAsnIleAlaValGlyLeuAlaThrGluLys---AlaCysAlaTrp 240
Db 1977 ATTCATCGCGCGACACCTCGCGCTGGTCCGATCGGCTGCGTGGAGTGTTCGCTGG 2036
Qy 241 LeuSerAlaAsnIleThrAlaLeuIleArgArgGluValLys----- 254
Db 2037 CTGCGAGCGGTGAGCGTGTGCTGCGCGCCCGCTTTCGCGCACACGACGACCTGTGTC 2096
Qy 255 -----AlaAlaValSerArgThrLeuArgAlaGlnGlyProGlu----- 267
Db 2097 GCGGAGGTGCGCTGGAGCTTCCGCTGCGCGCGCAGCGCGCCGCGCACCGCCAC 2156
Qy 268 ---ProAlaAlaArgGlyGluArgArgGlyCysSerArgAla 280
Db 2157 GGCCCGCGGCTGCTGCTCCAGCGTGGATGTCGCGCGCT 2198

RESULT 13
US-09-902-540-1237/c
; Sequence 1237, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1237
; LENGTH: 26659
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1237

Alignment Scores:
Pred. No.: 13.4 Length: 26659
Score: 103.50 Matches: 68
Percent Similarity: 40.16% Conservative: 34
Best Local Similarity: 26.77% Mismatches: 102
Query Match: 7.23% Indels: 52
DB: 4 Gaps: 13

US-10-015-388A-54 (1-280) x US-09-902-540-1237 (1-26659)

Qy 75 SerTrpValSerGlySerSerGlyArgSerGlyGlyPheMetArgLysIleThrProThr 94
Db 20267 ACCTGGACAACCGCATGATGACGACGCGCGCGAGGTGGACGCGA-----ACGCGCGCT 20214
Qy 95 ThrThrThrSerLeuGlyAla-----GlnProSerGlnThr----- 106
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Db 20213 GCAAGAACGAGCGCTGAGCTGCTGCTTCCCGCTCAACCTCGCGAGTGTGCGGCACCC 20154  
Qy 107 -----SerGluGluGlnAlaGlnLeuAlaGlnAlaPhe-----HisAsn 121  
Db 20153 GCGCGAAGCAGGGGAC-GAGCGGTGCTGCGCGACGGCCCTCACGTGGGCCCAACACACAGC 20095  
Qy 122 GlnPro---ProSer-----LeuArgArgThrValGlu-----PheValAlaGlu 135  
Db 20094 AACCCCATGCCAGCGAGCGGTGTATGCCGTACGTGAGAGGGCGCTTCTGCTGGAT 20035  
Qy 136 ArgIleGlySerAsnCysValIleHisIleLysAlaThrLeuValAla----- 151  
Db 20034 TCCGACAGAGCCGGGGCTGCGCTGCTGCGCGACACCATCATCGAGCGGAGGATG 19975  
Qy 152 -----AspLeuValArgGlnAlaGlnLeuGlnLeuGlnLeuValThr 167  
Db 19974 CTGCGGGAGATTCACTGCGCGGAGGCGCTGGCGCTGAGTATTCGTCGCTGTCAG 19915  
Qy 168 GlnGluGluGlyGlyAspProAlaGlnLeuLeuGluLeuLeuCysSerGlnLeuCys 187  
Db 19914 GACGCGGCGAAGCGCGGAGTACACCCAGGCGTTGGAGTTGATGCGCGGAGCTTGGC 19855  
Qy 188 ProHisGlyAlaGlnAlaLeuAlaLeuGlyArgGlu-----PheCysGlnArgLysSerPro 206  
Db 19854 ACGCCGCTGCCCCAGCGCTGCGCCCTTTCGCGCGCGGTGTCATGGCGAGCGCAC-GGTGCT 19796  
Qy 207 GlyAlaValArgAlaLeuLeuPro-----GluGluThrProAlaAlaVal 221  
Db 19795 GTGCGCGCGGAGCGAAGCGAGGTGCTGGGCCACTACGAGACGGACCGGCGAGGGCC 19736  
Qy 222 LeuSerSerAlaGluAsnIleAlaValGlyLeuAlaThrGluLys---AlaCysAlaTrp 240  
Db 19735 ATTCAATCGCGCGGACACCTCGCGCTGTCGCGATCGCTGCGTGGAGTGTTCGCTGG 19676  
Qy 241 LeuSerAlaAsnIleThrAlaLeuIleArgArgGluValLys----- 254  
Db 19675 CTCGAGCGGTGGAGCGTGTTCGCGCGCGCTGCTTCGCGCCACAGGACCTGTTGCC 19616  
Qy 255 -----AlaAlaValSerArgThrLeuArgAlaGlnGlyProGlu----- 267  
Db 19615 GCGGAGGTGCCCTCGAGCTTCGCGCTCGGCGCAGCGGCCGCGCCAGCCAC 19556  
Qy 268 ---ProAlaArgGlyGluArgArgGlyCysSerArgAla 280  
Db 19555 GCGCGCGCGGTGCTGCTGCTCCAGCGGTGATGCGCGCGCT 19514

## RESULT 14

US-09-252-991A-8061/c  
; Sequence 8061, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 8061  
; LENGTH: 1236  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-8061

## Alignment Scores:

Pred. No.:	0.117	Length:	1236
Score:	103.00	Matches:	74
Percent Similarity:	32.81%	Conservative:	31
Best Local Similarity:	23.12%	Mismatches:	114

Query Match: 7.19% Indels: 101  
Db: 4 Gaps: 15

US-10-015-388A-54 (1-280) x US-09-252-991A-8061 (1-1236)

Qy 29 LeuGluGluGlyProSerTyrrAlaPheGluValAspThrValAlaProGluHisGlyLeu 48  
Db 1123 CTTGACGAGGCGCGGGTTTCTTGGCGG-----CCTTGGCCCGACCGCGGGTCT 1073  
Qy 49 AspAsnAlaProValValAspGlnLeuLeuTyrrCysCysProTyrrIleGlyGlu 68  
Db 1072 TCTTCGTCGCG-----CCGCGGCGGCTTCG 1046  
Qy 69 LeuArgLysLeuLeuAlaSerTrpValSerGly---SerSerGlyArgSerGlyGly--- 86  
Db 1045 CTTGCGCAGTTGCGCGGCGCATGCGCCAGTTCGCTGCGCTGGCGCTGCGGCGACGCCCT 986  
Qy 87 -----PheMetArgLysIleThrPro 93  
Db 985 CGGATTCACAGATCTGGTAGCGGAACTCTCGTATGCGTTTTCGTCGGCGC----- 935  
Qy 94 ThrThrThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGln 113  
Db 934 -----TCATGGGTGTCCTCTGCGCGAGCGCGTAAAGACAGGTTTACGCGGAAA 887  
Qy 114 LeuAlaGlnAlaPhePheHisAsnGlnProPro----- 124  
Db 886 GTGCGCGAGCACTTCGGACAGGCTCAGTCCCTGCTGGGCGAGCGCATGTTGGGAAAA 827  
Qy 125 -----SerLeuArgArgThrValGluPheValAlaGlu 135  
Db 826 CAGCGCGCTGAGTGCATTTCGGAGAGACTCGCGCGCAGCAGCAGGAGGTGTCGCCCA 767  
Qy 136 ArgIleGlySerAsnCysValLysHisIleLysAlaThrLeuValAlaAspLeu---Val 154  
Db 766 GCGCTCGGC-----CGGCACCTGCGGTGCTGCGTGGCGAGCAGCGGCGCA 719  
Qy 155 ArgGlnAlaGluSerLeuLeuGlnGlnLeuValThrGlnGlyGlu---GluGlyGly 173  
Db 718 GCGCAGCGCGGACCAACACAGCAGCAACCTGACACTGCGCGCGCGGCGAGGCGCAG 659  
Qy 174 AspProAlaGlnLeuGluGluIle-LeuCysSerGlnLeuCysProHisGlyAlaGlnAl 193  
Db 658 GACCG-----CTCGGCATGCTCGCCGCTGACCTCCAGGGGCGAGGTATGTC 614  
Qy 193 aLeuAlaLeuGlyArgGluPheCysGlnArgLysSerProGly-----AlaValArgAl 211  
Db 613 GCGCTCGCGGAACAGGCGCGCTGCTCATCCGCGCAGCCCGCAGCACGCGGCGGATCAGG 554  
Qy 211 aLeuLeuProGluGluThrProAlaAlaValLeuSerSerAlaGluAsnIleAlaValG 231  
Db 553 CTGCTTCATCGCA-----CGTTCGCGCAGTGTCTCCAGCAGATTCCGCGGAAGGCGTCCG 500  
Qy 231 YLeuAlaThrGluLysAlaCys----- 238  
Db 499 CGCGCGCAGCGCGCGCGCTGCGCGGCGAAATCCACCGCGCTCGCGTTCGCGGTCCGAC 440  
Qy 239 -----AlaTrpLeuSerAlaAsnIleThrAlaLeuIleAr 250  
Db 439 CAGGCTGAAGTCCAGTCTCTCGCGCCCTCGTGGTAGATCGGGGATACCCGCGGAGGTGAG 380  
Qy 250 gArg-----GluValLysAlaAlaValSerArgThr----- 260  
Db 379 GCGCAGCAGCATTTGGCGGAGGCCATTTCAGGGCCCCCGCGGCATCATGTCGACCGCGCG 320  
Qy 261 -LeuArgAlaGlnGlyProGluProAlaAlaArgGlyGluArgArgGlyCysSerArg 279  
Db 319 GTTCCCGCAGCGACTGGCGCGAGGCGCTGGCGCAGTGGCGCGCAGGAGGTGTTCCAGA 262

## RESULT 15

US-09-252-991A-8202  
; Sequence 8202, Application US/09252991A  
; Patent No. 6551795

## ; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 8202  
 ; LENGTH: 2556  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-8202

## Alignment Scores:

Pred. No.: 0.371 Length: 2556  
 Score: 103.00 Matches: 74  
 Percent Similarity: 32.81% Conservative: 31  
 Best Local Similarity: 23.12% Mismatches: 114  
 Query Match: 7.19% Indels: 101  
 DB: 4 Gaps: 15

US-10-015-388a-54 (1-280) x US-09-252-991A-8202 (1-2556)

Qy 29 LeuGluGluGlyProSerTyAlaPheGluValAspThrValAlaProGluHisGlyLeu 48  
 Db ||||| : : : : : ||||| : : : : :  
 160 CTTGCGAGCGCGCGGGTTCCTTGGCGG-----CCTTGGCCCGACGCGGGTCT 210  
 Qy 49 AspAenAlaProValValAspGlnGlnLeuLeuTyThrCysCysProTyrlleGlyGlu 68  
 Db ||||| : : : : : ||||| : : : : :  
 211 TCTTCGGTGGCG-----CCGCGCGGGCTTCGG 237  
 Qy 69 LeuArgLysLeuLeuAlaSerTrpValSerGly---SerSerdGlyArgSerGlyGly--- 86  
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 238 CTTGCGCAGTTTCCGCGGCCATGGCCAGTGGCGGTTCGCGCTGGCGCTCGGGCAGCCCT 297  
 Qy 87 -----PheMetArgLysIleThrPro 93  
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 298 CGGATTCAGACTGTGGTAGGCGAACTCTGTAATCGTTTTCGTGGCGC----- 348  
 Qy 94 ThrThrThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGln 113  
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 349 -----TCATGGGGTGTCTCTCTGGCGAGGCGGTAAAGCAGGTTGACGGGAAA 396  
 Qy 114 LeuAlaGlnAlaPhePheHisIleAsnGlnProPro----- 124  
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 397 GTGGCGAGCACTTCGGACAGGCTCAGGTGCCGCTGGCGAGCGGCGCATGGTGGA 456  
 Qy 125 -----SerLeuArgArgThrValGluPheValAlaGlu 135  
 Db ||||| : : : : : ||||| : : : : :  
 457 CAGCGCGCTGTAGTGTGCAATTCGAGAGACTCGCGCGGACGACGAGGAGTGTGCGCCCA 516  
 Qy 136 ArgIleGlySerAsnCysValLysHisIleLysAlaThrLeuValAlaAspLeu---Val 154  
 Db ||||| : : : : : ||||| : : : : :  
 517 GCCTTCGGC-----CGGCACCTCGGGTGGCGTGGCGGCGAGCGGGCGCA 564  
 Qy 155 ArgGlnAlaGluSerLeuGlnGlnGlnLeuValThrGlnGlyGlu---GluGlyGly 173  
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 625 GACCG-----CTCGGCATGCTCGCCGCTGACCTCCAGGGGCGAGGTAGTC 669  
 Qy 193 aLeuAlaLeuGlyArgGluPheCysGlnArgLysSerProGly-----AlaValArgAl 211  
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 Qy 211 aLeuLeuProGluGluThrProAlaAlaValLeuSerSerAlaGluAsnIleAlaValGl 231

Search completed: March 29, 2005, 12:39:38

Job time : 2385 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 29, 2005, 12:03:46 ; Search time 521 Seconds  
(without alignments)  
3202.712 Million cell updates/sec

Perfect score: 1432

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Searched: 5552208 seqs, 2379665951 residues

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Post-processing: Minimum Match 0%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB ID	Description
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c 68	112	7.8	17761	9	US-09-764-847-1596
c 69	112	7.8	17761	14	US-10-092-154-1596
70	111.5	7.8	1104	17	US-10-282-122A-26537
71	111.5	7.8	1104	18	US-10-481-265-42
72	111.5	7.8	1107	17	US-10-282-122A-28487
73	109	7.6	9025608	15	US-10-156-761-1
c 74	108.5	7.6	1457	9	US-09-954-531-982
c 75	107.5	7.5	1678	16	US-10-240-365-119
76	105.5	7.4	1664	18	US-10-723-860-5164
77	104.5	7.3	1122	15	US-10-156-761-5336
c 78	104.5	7.3	9025608	15	US-10-156-761-1
79	103.5	7.2	2054	18	US-10-425-115-163963
80	103	7.2	1594	17	US-10-425-114-32954
c 81	102.5	7.2	1467	17	US-10-062-674-1950
c 82	102	7.1	1101	17	US-10-369-493-39041
c 83	102	7.1	1104	17	US-10-369-493-39408
c 84	102	7.1	1374	17	US-10-369-493-39794
85	102	7.1	1649	17	US-10-425-114-26399
c 86	102	7.1	2031	15	US-10-156-761-26399
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92	101.5	7.1	9301	17	US-10-095-248A-18
93	101.5	7.1	9301	18	US-10-788-606-18
94	101.5	7.1	21501	17	US-10-377-315-1
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96	101.5	7.1	130320	17	US-10-408-168-1
c 97	101	7.1	1810	19	US-09-814-353-19133
98	101	7.1	2064	19	US-10-741-600-440
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c 103	100	7.0	6825	17	US-10-367-502-156
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c 105	100	7.0	100000	15	US-10-156-761-15103
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c 108	99.5	6.9	1756	18	US-10-425-115-138078
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c 113	99.5	6.9	27189	13	US-10-087-192-1828
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c 124	97.5	6.8	1308	17	US-10-425-114-24302
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c 133	97.5	6.8	36778	10	US-09-836-821-5
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C 138	97.5	6.8	38506	16	US-10-160-539-19	Sequence 19, Appl	211	94	6.6	1832	17	US-10-425-114-2852	Sequence 2852, Ap
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C 140	97	6.8	1347	17	US-10-282-122A-14155	Sequence 14155, A	C 213	94	6.6	2215	17	US-10-282-122A-33208	Sequence 33208, A
C 141	97	6.8	1499	17	US-10-131-410-4	Sequence 4, Appl	214	94	6.6	3118	18	US-10-425-115-104412	Sequence 104412, A
C 142	97	6.8	1328	15	US-10-156-761-4392	Sequence 4392, Ap	215	94	6.6	4248	17	US-10-282-122A-30505	Sequence 30505, A
C 143	97	6.8	3130	15	US-10-207-655-1036	Sequence 106, App	216	94	6.6	5159	17	US-10-334-143-111	Sequence 111, App
C 144	97	6.8	3120	18	US-10-717-597-84	Sequence 84, Appl	217	94	6.6	20311	18	US-10-719-993-7068	Sequence 7068, Ap
C 145	97	6.8	3223	18	US-10-742-161-9	Sequence 9, Appl	C 218	93.5	6.5	1078	18	US-10-767-701-658	Sequence 658, App
C 146	97	6.8	3223	18	US-10-742-372-9	Sequence 9, Appl	219	93.5	6.5	1224	18	US-10-437-963-21764	Sequence 21764, A
C 147	97	6.8	3223	18	US-10-646-308-3	Sequence 3, Appl	220	93.5	6.5	1284	15	US-10-156-761-3832	Sequence 3832, Ap
C 148	97	6.8	7438	16	US-10-359-050-11	Sequence 11, Appl	C 221	93.5	6.5	1495	17	US-10-425-114-20830	Sequence 20830, A
C 149	97	6.8	7438	17	US-10-014-099F-5	Sequence 5, Appl	C 222	93.5	6.5	1553	18	US-10-425-115-52255	Sequence 52255, A
C 150	97	6.8	7523	17	US-10-014-099F-79	Sequence 79, Appl	C 223	93.5	6.5	3542	15	US-10-037-270-2233	Sequence 233, App
C 151	97	6.8	7608	17	US-10-014-099F-78	Sequence 78, Appl	C 224	93.5	6.5	3542	17	US-10-117-722-233	Sequence 233, App
C 152	97	6.8	7803	17	US-10-014-099F-82	Sequence 82, Appl	C 225	93.5	6.5	3768	15	US-10-156-761-2190	Sequence 2190, Ap
C 153	97	6.8	8167	17	US-10-014-099F-83	Sequence 83, Appl	C 226	93.5	6.5	5630	9	US-09-871-388-1	Sequence 1, Appl
C 154	97	6.8	20574	18	US-10-719-993-7067	Sequence 7067, Ap	C 227	93.5	6.5	17596	18	US-10-611-442-2	Sequence 2, Appl
C 155	97	6.8	30624	18	US-10-719-993-6888	Sequence 6888, Ap	C 228	93	6.5	1119	15	US-10-156-761-4303	Sequence 4303, Ap
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C 157	96.5	6.7	1263	15	US-10-156-761-2071	Sequence 2071, Ap	C 230	93	6.5	2211	18	US-10-437-963-63253	Sequence 63253, A
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C 161	96	6.7	1458	16	US-10-029-386-20288	Sequence 20288, A	C 234	93	6.5	137560	18	US-10-481-112-1	Sequence 1, Appl
C 162	96	6.7	1813	10	US-09-993-731-11	Sequence 11, Appl	C 235	92.5	6.5	1224	18	US-10-767-701-12453	Sequence 12453, A
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C 173	95.5	6.7	1011	17	US-10-440-523-345	Sequence 345, App	C 246	92.5	6.5	3750	17	US-10-389-647-147	Sequence 147, App
C 174	95.5	6.7	1011	17	US-10-461-925-345	Sequence 345, App	C 247	92.5	6.5	4551	15	US-10-156-761-7163	Sequence 7163, Ap
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C 178	95.5	6.7	2940	15	US-10-156-761-3172	Sequence 3172, Ap	C 251	92.5	6.5	50552	18	US-10-719-993-6905	Sequence 6905, Ap
C 179	95.5	6.7	64492	17	US-10-378-083-1	Sequence 1, Appl	C 252	92.5	6.5	63158	16	US-10-392-198-1	Sequence 1, Appl
C 180	95	6.6	875	16	US-10-029-386-20568	Sequence 20568, A	C 253	92.5	6.5	86941	17	US-10-461-194-2	Sequence 2, Appl
C 181	95	6.6	957	11	US-09-758-759-88	Sequence 88, Appl	C 254	92.5	6.5	493999	18	US-10-719-993-6787	Sequence 6787, Ap
C 182	95	6.6	1534	18	US-10-425-115-67410	Sequence 67410, A	C 255	92.5	6.5	786431	16	US-10-412-277-3	Sequence 3, Appl
C 183	95	6.6	1950	18	US-10-767-701-15092	Sequence 15092, A	C 256	92	6.4	1321	17	US-10-428-275-77	Sequence 77, Appl
C 184	95	6.6	2612	18	US-10-425-115-116024	Sequence 116024, A	C 257	92	6.4	1469	17	US-10-425-114-31292	Sequence 31292, A
C 185	95	6.6	5960	17	US-10-172-118-16	Sequence 16, Appl	C 258	92	6.4	1608	17	US-10-282-122A-30209	Sequence 30209, A
C 186	95	6.6	5960	17	US-10-342-887-16	Sequence 16, Appl	C 259	92	6.4	1608	17	US-10-389-647-178	Sequence 178, App
C 187	95	6.6	6075	17	US-10-161-927-7	Sequence 7, Appl	C 260	92	6.4	1644	18	US-10-425-115-14950	Sequence 14950, A
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C 189	95	6.6	17493	19	US-10-211-028-10	Sequence 10, Appl	C 262	92	6.4	2094	17	US-10-369-493-43107	Sequence 43107, A
C 190	95	6.6	30000	13	US-09-980-217-3	Sequence 3, Appl	C 263	92	6.4	2224	17	US-10-104-047-1325	Sequence 1325, App
C 191	95	6.6	68750	11	US-10-014-717-1	Sequence 1, Appl	C 264	92	6.4	2646	15	US-10-156-761-139	Sequence 139, App
C 192	95	6.6	90597	19	US-10-211-028-1	Sequence 1, Appl	C 265	92	6.4	2973	15	US-10-156-761-2660	Sequence 2660, Ap
C 193	95	6.6	90597	19	US-10-211-028-1	Sequence 1, Appl	C 266	92	6.4	3029	17	US-10-108-260A-1476	Sequence 1476, Ap
C 194	95	6.6	109519	11	US-09-758-759-1	Sequence 1, Appl	C 267	92	6.4	2452	9	US-09-764-868-1487	Sequence 1487, Ap
C 195	94.5	6.6	640	17	US-10-424-599-52734	Sequence 52734, A	C 268	92	6.4	22452	9	US-09-764-868-1489	Sequence 1489, Ap
C 196	94.5	6.6	1050	9	US-09-955-597-20	Sequence 20, Appl	C 269	92	6.4	22783	10	US-09-990-613-6	Sequence 6, Appl
C 197	94.5	6.6	1607	18	US-10-425-115-58267	Sequence 58267, A	C 270	91.5	6.4	820	18	US-10-425-115-179178	Sequence 179178, A
C 198	94.5	6.6	1629	17	US-10-282-122A-14086	Sequence 14086, A	C 271	91.5	6.4	956	13	US-10-087-192-506	Sequence 506, App
C 199	94.5	6.6	2286	17	US-10-282-122A-33104	Sequence 33104, A	C 272	91.5	6.4	1113	18	US-10-437-963-84153	Sequence 84153, A
C 200	94.5	6.6	7033	18	US-10-678-816-5	Sequence 5, Appl	C 273	91.5	6.4	1174	18	US-10-437-963-38585	Sequence 38585, A
C 201	94.5	6.6	12523	9	US-09-955-597-1	Sequence 1, Appl	C 274	91.5	6.4	1182	18	US-10-425-115-153333	Sequence 153333, A
C 202	94.5	6.6	12523	9	US-09-955-597-1	Sequence 1, Appl	C 275	91.5	6.4	1185	18	US-10-739-930-2475	Sequence 2475, Ap
C 203	94.5	6.6	88624	16	US-10-292-081A-1	Sequence 1, Appl	C 276	91.5	6.4	1287	18	US-10-425-115-171088	Sequence 171088, A
C 204	94.5	6.6	88624	17	US-10-608-397-1	Sequence 1, Appl	C 277	91.5	6.4	1425	17	US-10-282-122A-37790	Sequence 37790, A
C 205	94.5	6.6	1980090	18	US-10-719-993-6815	Sequence 6815, Ap	C 278	91.5	6.4	1623	18	US-10-437-963-2083	Sequence 2083, Ap
C 206	94.5	6.6	1980090	19	US-10-741-600-17676	Sequence 17676, Ap	C 279	91.5	6.4	2792	17	US-10-104-047-458	Sequence 458, App
C 207	94	6.6	1026	15	US-10-156-761-4890	Sequence 4890, Ap	C 280	91.5	6.4	3044	17	US-10-108-260A-938	Sequence 938, App
C 208	94	6.6	1339	17	US-10-425-114-35313	Sequence 35313, A	C 281	91.5	6.4	3073	18	US-10-479-435-39	Sequence 39, Appl

282	91.5	6.4	3393	15	US-10-224-356-14	Sequence 14, Appl	c 355	90	6.3	2055	17	US-10-389-647-125	Sequence 125, App
283	91.5	6.4	3393	15	US-10-224-356-15	Sequence 15, Appl	c 356	90	6.3	2442	17	US-10-369-493-40548	Sequence 40548, A
c 284	91.5	6.4	7140	19	US-10-211-028-3	Sequence 3, Appl	c 357	90	6.3	2694	14	US-10-050-704-40	Sequence 40, Appl
c 285	91.5	6.4	8321	16	US-10-329-079-17	Sequence 17, Appl	c 358	90	6.3	2694	17	US-10-798-512-40	Sequence 40, Appl
c 286	91.5	6.4	20956	13	US-10-087-192-505	Sequence 505, App	c 359	90	6.3	2878	17	US-10-453-420-7	Sequence 7, Appl
c 287	91.5	6.4	23580	9	US-09-764-860-990	Sequence 990, App	c 360	90	6.3	2878	17	US-10-295-027-259	Sequence 259, App
c 288	91.5	6.4	23580	14	US-10-074-095-990	Sequence 990, App	c 361	90	6.3	3090	15	US-10-156-761-7457	Sequence 7457, App
c 289	91.5	6.4	23580	17	US-10-212-872-990	Sequence 990, App	c 362	90	6.3	3090	15	US-10-156-761-7457	Sequence 7457, App
c 290	91.5	6.4	70689	19	US-10-741-600-17775	Sequence 17775, A	c 363	90	6.3	7282	15	US-10-213-948-11	Sequence 11, Appl
c 291	91.5	6.4	86080	18	US-10-450-826-71	Sequence 71, Appl	c 364	90	6.3	59816	17	US-10-084-846A-1	Sequence 1, Appl
c 292	91.5	6.4	86080	18	US-10-723-860-1697	Sequence 1697, App	c 365	90	6.3	59816	17	US-10-084-846A-2	Sequence 2, Appl
c 293	91	6.4	748	18	US-10-425-115-2506	Sequence 2506, App	c 366	90	6.3	59856	13	US-10-087-192-664	Sequence 664, App
c 294	91	6.4	866	18	US-10-437-963-92621	Sequence 92621, App	c 367	90	6.3	94001	17	US-10-210-638-20	Sequence 20, Appl
c 295	91	6.4	1113	17	US-10-282-122A-25330	Sequence 25330, A	c 368	90	6.3	536165	10	US-09-339-964-1	Sequence 1, Appl
c 296	91	6.4	1171	18	US-10-739-930-4421	Sequence 4421, App	c 369	89.5	6.2	614	17	US-10-425-114-15293	Sequence 15293, A
c 297	91	6.4	1315	17	US-10-425-114-19238	Sequence 19238, A	c 370	89.5	6.2	688	18	US-10-437-963-71008	Sequence 71008, A
c 298	91	6.4	1538	18	US-10-425-115-20700	Sequence 20700, A	c 371	89.5	6.2	843	15	US-10-156-761-5578	Sequence 5578, App
c 299	91	6.4	1555	18	US-10-767-701-11840	Sequence 11840, A	c 372	89.5	6.2	854	18	US-10-425-115-25512	Sequence 25512, A
c 300	91	6.4	1590	16	US-10-271-889-1	Sequence 1, Appl	c 373	89.5	6.2	1145	18	US-10-425-115-136719	Sequence 136719, A
c 301	91	6.4	1713	18	US-10-425-115-58909	Sequence 58909, A	c 374	89.5	6.2	1227	17	US-10-458-201-23	Sequence 23, Appl
c 302	91	6.4	1727	18	US-10-437-963-10917	Sequence 10917, A	c 375	89.5	6.2	1374	17	US-10-236-417-7	Sequence 7, Appl
c 303	91	6.4	1807	17	US-10-425-114-28103	Sequence 28103, A	c 376	89.5	6.2	1422	19	US-10-472-928-2227	Sequence 2227, App
c 304	91	6.4	1943	18	US-10-425-115-122168	Sequence 122168, A	c 377	89.5	6.2	1468	9	US-09-822-830A-34	Sequence 34, Appl
c 305	91	6.4	2064	17	US-10-282-122A-11588	Sequence 11588, A	c 378	89.5	6.2	1527	17	US-10-474-776-506	Sequence 506, App
c 306	91	6.4	2088	18	US-10-425-115-46920	Sequence 46920, A	c 379	89.5	6.2	1590	8	US-08-961-527-184	Sequence 5462, App
c 307	91	6.4	2367	17	US-10-104-047-1297	Sequence 1297, App	c 380	89.5	6.2	1624	18	US-10-158-844-184	Sequence 184, App
c 308	91	6.4	2997	13	US-10-106-534-3	Sequence 3, Appl	c 381	89.5	6.2	1624	18	US-10-425-115-28237	Sequence 28237, A
c 309	91	6.4	3144	18	US-10-437-963-82347	Sequence 82347, A	c 382	89.5	6.2	1637	19	US-10-211-028-20	Sequence 20, Appl
c 310	91	6.4	3158	13	US-10-106-534-1	Sequence 1, Appl	c 383	89.5	6.2	1767	18	US-10-437-963-4185	Sequence 4185, App
c 311	91	6.4	3241	17	US-10-108-260A-937	Sequence 937, App	c 384	89.5	6.2	3003	9	US-09-820-155-1	Sequence 1, Appl
c 312	91	6.4	3255	19	US-10-660-811A-17	Sequence 17, Appl	c 385	89.5	6.2	3054	18	US-10-437-963-82264	Sequence 82264, A
c 313	91	6.4	4257	15	US-10-161-403-30	Sequence 30, Appl	c 386	89.5	6.2	3114	17	US-10-188-248-39	Sequence 39, Appl
c 314	91	6.4	4257	18	US-10-161-408-22	Sequence 22, Appl	c 387	89.5	6.2	4320	15	US-10-156-761-595	Sequence 595, App
c 315	91	6.4	4346	15	US-10-161-403-113	Sequence 113, App	c 388	89.5	6.2	5192	15	US-10-161-403-88	Sequence 88, Appl
c 316	91	6.4	4346	18	US-10-161-408-26	Sequence 26, App	c 389	89.5	6.2	5754	18	US-10-437-963-59723	Sequence 59723, A
c 317	91	6.4	4608	17	US-10-172-118-14	Sequence 14, Appl	c 390	89.5	6.2	6280	18	US-10-672-764A-64	Sequence 64, Appl
c 318	91	6.4	4608	17	US-10-342-887-14	Sequence 14, Appl	c 391	89.5	6.2	6502	18	US-10-672-764A-41	Sequence 41, Appl
c 319	91	6.4	24081	16	US-10-132-134-13	Sequence 13, Appl	c 392	89.5	6.2	9249	17	US-10-389-120-2	Sequence 2, Appl
c 320	91	6.4	52101	16	US-10-132-134-1	Sequence 1, Appl	c 393	89.5	6.2	15120	17	US-10-458-201-1	Sequence 1, Appl
c 321	91	6.4	84830	19	US-10-660-811A-2	Sequence 2, Appl	c 394	89.5	6.2	26173	14	US-10-114-170-69	Sequence 69, Appl
c 322	90.5	6.3	1017	15	US-10-146-772-283	Sequence 283, App	c 395	89.5	6.2	53799	19	US-10-042-665A-3	Sequence 3, Appl
c 323	90.5	6.3	1017	17	US-10-241-742-283	Sequence 283, App	c 396	89.5	6.2	2362598	19	US-10-472-928-4979	Sequence 4979, App
c 324	90.5	6.3	1017	17	US-10-440-523-283	Sequence 283, App	c 397	89.5	6.2	2731748	18	US-10-297-465A-1	Sequence 1, Appl
c 325	90.5	6.3	1017	17	US-10-440-503-283	Sequence 283, App	c 398	89	6.2	1164	15	US-10-156-761-2298	Sequence 2298, App
c 326	90.5	6.3	1017	17	US-10-461-925-283	Sequence 283, App	c 399	89	6.2	1370	17	US-10-437-963-82464	Sequence 82464, A
c 327	90.5	6.3	1170	18	US-10-425-115-162747	Sequence 162747, A	c 400	89	6.2	1370	17	US-10-425-114-35579	Sequence 35579, A
c 328	90.5	6.3	1179	17	US-10-369-493-24240	Sequence 24240, A	c 401	89	6.2	1407	17	US-10-369-493-41593	Sequence 41593, A
c 329	90.5	6.3	1248	17	US-10-369-493-32441	Sequence 32441, A	c 402	89	6.2	1459	18	US-10-425-115-124308	Sequence 124308, A
c 330	90.5	6.3	1426	18	US-10-437-963-34832	Sequence 34832, A	c 403	89	6.2	1720	18	US-10-437-963-31539	Sequence 31539, A
c 331	90.5	6.3	2268	18	US-10-437-963-39626	Sequence 39626, A	c 404	89	6.2	1827	18	US-10-411-910A-211	Sequence 211, App
c 332	90.5	6.3	2853	18	US-10-425-115-172942	Sequence 172942, A	c 405	89	6.2	2193	18	US-10-425-115-114963	Sequence 114963, A
c 333	90.5	6.3	2960	18	US-10-483-512-71	Sequence 71, Appl	c 406	89	6.2	2351	17	US-10-425-114-2510	Sequence 2510, App
c 334	90.5	6.3	9272	18	US-10-723-860-1784	Sequence 1784, App	c 407	89	6.2	2407	18	US-10-437-963-59093	Sequence 59093, A
c 335	90.5	6.3	9287	10	US-09-960-706-633	Sequence 633, App	c 408	89	6.2	2684	18	US-10-425-115-137279	Sequence 137279, A
c 336	90.5	6.3	9287	10	US-09-873-319-396	Sequence 396, App	c 409	89	6.2	2713	17	US-10-015-115-17	Sequence 17, Appl
c 337	90.5	6.3	9456	18	US-10-723-860-6147	Sequence 6147, App	c 410	89	6.2	3318	17	US-10-369-493-44592	Sequence 44592, A
c 338	90.5	6.3	18435	15	US-10-156-761-412	Sequence 412, App	c 411	89	6.2	3438	17	US-10-312-352-60	Sequence 60, Appl
c 339	90.5	6.3	34875	18	US-10-775-169-316	Sequence 316, App	c 412	89	6.2	3470	16	US-10-209-059-25	Sequence 25, Appl
c 340	90.5	6.3	48908	14	US-10-114-170-137	Sequence 137, App	c 413	89	6.2	3470	17	US-10-627-132-25	Sequence 25, Appl
c 341	90.5	6.3	85915	18	US-10-647-196-1	Sequence 1, Appl	c 422	89	6.2	3476	14	US-10-237-535-51	Sequence 51, Appl
c 342	90.5	6.3	100000	15	US-10-156-761-15103	Sequence 15103, A	c 431	89	6.2	3476	14	US-10-239-196-51	Sequence 51, Appl
c 343	90.5	6.3	276820	17	US-10-271-416-9	Sequence 9, Appl	c 522	89	6.2	3699	17	US-10-362-571-7	Sequence 7, Appl
c 344	90	6.3	507	18	US-10-437-963-73604	Sequence 73604, A	c 523	89	6.2	5468	17	US-10-363-616-69	Sequence 69, Appl
c 345	90	6.3	813	18	US-10-425-115-104528	Sequence 104528, A	c 524	89	6.2	7095	15	US-10-156-761-7340	Sequence 7340, App
c 346	90	6.3	1097	17	US-10-425-115-12462	Sequence 12462, A	c 525	89	6.2	8009	10	US-09-373-658-34	Sequence 34, Appl
c 347	90	6.3	1099	17	US-10-425-114-1540	Sequence 1540, App	c 526	89	6.2	8009	11	US-09-989-687-34	Sequence 34, Appl
c 348	90	6.3	1188	18	US-10-437-963-48852	Sequence 48852, A	c 527	89	6.2	12951	17	US-10-282-122A-31678	Sequence 31678, A
c 349	90	6.3	1195	15	US-10-304-928-7	Sequence 7, Appl	c 528	89	6.2	73467	9	US-09-740-026-3	Sequence 3, Appl
c 350	90	6.3	1212	17	US-10-282-122A-11640	Sequence 11640, A	c 529	89	6.2	73467	14	US-10-237-859-3	Sequence 3, Appl
c 351	90	6.3	1240	18	US-10-425-115-43278	Sequence 43278, A	c 530	89	6.2	135638	16	US-10-314-657-1	Sequence 1, Appl
c 352	90	6.3	1422	17	US-10-389-647-347	Sequence 347, App	c 531	88.5	6.2	657	10	US-09-814-353-14012	Sequence 14012, A
c 353	90	6.3	1874	18	US-10-437-963-44429	Sequence 44429, A	c 532	88.5	6.2	918	17	US-10-369-493-44153	Sequence 44153, A
c 354	90	6.3	1976	17	US-10-425-114-660	Sequence 660, App	c 533	88.5	6.2	1123	18	US-10-425-115-70246	Sequence 70246, A

534	88.5	6.2	1221	18	US-10-437-963-95456	Sequence 95456, A	c 607	88	6.1	3132	9	US-09-737-149-7	Sequence 7, Appli
535	88.5	6.2	1245	18	US-10-425-115-120267	Sequence 120267, A	c 608	88	6.1	3132	17	US-10-701-283-7	Sequence 7, Appli
536	88.5	6.2	1290	18	US-10-437-963-81097	Sequence 81097, A	c 609	88	6.1	3506	18	US-10-425-115-103557	Sequence 103557, A
537	88.5	6.2	1296	18	US-10-372-966-1	Sequence 1, Appli	c 610	88	6.1	5732	18	US-10-437-963-35518	Sequence 35518, A
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c 539	88.5	6.2	1630	17	US-10-425-114-28166	Sequence 28166, A	c 612	88	6.1	6961	18	US-10-723-860-7512	Sequence 7512, Ap
c 540	88.5	6.2	1650	18	US-10-425-115-108881	Sequence 108881, A	c 613	88	6.1	8496	18	US-10-451-467A-667	Sequence 667, App
c 541	88.5	6.2	1803	18	US-10-437-963-5740	Sequence 5740, Ap	c 614	88	6.1	10232	17	US-10-282-122A-25487	Sequence 25487, A
c 542	88.5	6.2	2006	18	US-10-437-963-7948	Sequence 7948, Ap	c 615	88	6.1	10283	10	US-09-938-795A-3	Sequence 130, Appli
c 543	88.5	6.2	2891	18	US-10-425-115-99415	Sequence 99415, A	c 616	87.5	6.1	6285	9	US-09-921-397-130	Sequence 13316, A
544	88.5	6.2	2316	18	US-10-437-963-54479	Sequence 54479, A	c 617	87.5	6.1	634	13	US-10-027-632-113316	Sequence 113316, A
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c 546	88.5	6.2	3072	14	US-10-198-848-14019	Sequence 14019, A	c 619	87.5	6.1	650	18	US-10-767-701-29530	Sequence 29530, A
c 547	88.5	6.2	4470	18	US-10-877-645-1	Sequence 1, Appli	c 620	87.5	6.1	1210	18	US-10-425-115-167270	Sequence 167270, A
c 548	88.5	6.2	6233	18	US-10-790-455-10	Sequence 10, Appli	c 621	87.5	6.1	1308	17	US-10-425-114-32476	Sequence 32476, A
c 549	88.5	6.2	6233	18	US-10-811-1368-10	Sequence 10, Appli	c 622	87.5	6.1	1419	18	US-10-437-963-60050	Sequence 60050, A
c 550	88.5	6.2	6233	19	US-10-940-318-10	Sequence 10, Appli	c 623	87.5	6.1	1646	18	US-10-755-889-355	Sequence 355, App
c 551	88.5	6.2	9379	9	US-09-916-359-1	Sequence 1, Appli	c 624	87.5	6.1	1659	18	US-10-425-115-176344	Sequence 176344, A
c 552	88.5	6.2	9401	18	US-10-445-724-1	Sequence 5, Appli	c 625	87.5	6.1	1816	11	US-09-968-007A-521	Sequence 521, App
c 553	88.5	6.2	12980	10	US-09-938-076-5	Sequence 5, Appli	c 626	87.5	6.1	1816	11	US-10-802-432-13	Sequence 13, Appli
c 554	88.5	6.2	12980	10	US-09-995-937-5	Sequence 5, Appli	c 627	87.5	6.1	1864	17	US-10-305-720-1161	Sequence 1161, Ap
c 555	88.5	6.2	12980	10	US-09-917-563-5	Sequence 5, Appli	c 628	87.5	6.1	1890	9	US-09-880-107-3390	Sequence 3390, Ap
c 556	88.5	6.2	16175	19	US-10-741-600-17596	Sequence 17596, A	c 629	87.5	6.1	1956	18	US-10-482-706-164	Sequence 164, App
c 557	88.5	6.2	17402	18	US-10-790-453-8	Sequence 8, Appli	c 630	87.5	6.1	1991	18	US-10-425-115-113652	Sequence 113652, A
c 558	88.5	6.2	17402	18	US-10-811-1368-8	Sequence 8, Appli	c 631	87.5	6.1	2053	18	US-10-425-115-97974	Sequence 97974, A
c 559	88.5	6.2	17402	19	US-10-940-315-8	Sequence 8, Appli	c 632	87.5	6.1	2102	19	US-10-473-451-22	Sequence 22, Appli
c 560	88.5	6.2											



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681	6.1	5902	14	US-10-152-886-84	Sequence 84, Appl	c 754	86.5	6.0	2394	15	US-10-156-761-11	Sequence 11, Appl
682	6.1	5860	17	US-09-798-883B-14	Sequence 14, Appl	755	86.5	6.0	2484	17	US-10-264-049-752	Sequence 752, Appl
683	6.1	5960	10	US-09-326-885-14	Sequence 14, Appl	756	86.5	6.0	2486	15	US-10-106-698-11989	Sequence 1989, Appl
684	6.1	5967	17	US-10-120-988-405	Sequence 405, Appl	757	86.5	6.0	2655	17	US-10-369-493-31950	Sequence 31990, A
c 685	6.1	38764	11	US-09-997-722-286	Sequence 286, Appl	758	86.5	6.0	2655	18	US-10-723-860-5461	Sequence 5461, Appl
686	6.1	40668	18	US-10-450-826-57	Sequence 57, Appl	759	86.5	6.0	2709	9	US-09-922-199A-3	Sequence 3, Appl
687	6.1	70082	18	US-10-715-066-1	Sequence 1, Appl	760	86.5	6.0	2772	18	US-10-425-115-93681	Sequence 93681, A
688	6.1	66765	18	US-10-715-066-4	Sequence 4, Appl	761	86.5	6.0	2811	18	US-10-437-963-35886	Sequence 35886, A
689	6.1	117985	18	US-10-719-993-7053	Sequence 7053, Appl	c 762	86.5	6.0	3094	9	US-09-925-297-320	Sequence 290, Appl
c 690	6.1	158001	17	US-10-211-179-11	GENERAL INFORMATI	763	86.5	6.0	3189	9	US-09-815-242-4056	Sequence 4056, Appl
691	6.0	717	17	US-10-262-445-3	Sequence 3, Appl	764	86.5	6.0	3189	17	US-10-282-122A-7343	Sequence 7343, Appl
c 692	6.0	832	18	US-10-437-963-44583	Sequence 44583, A	765	86.5	6.0	3220	14	US-10-103-313-100	Sequence 100, Appl
c 693	6.0	1023	17	US-10-389-647-172	Sequence 172, Appl	766	86.5	6.0	3318	18	US-10-425-115-115973	Sequence 115973, A
c 694	6.0	1068	17	US-10-437-963-94656	Sequence 94656, A	767	86.5	6.0	3440	18	US-10-357-930-21306	Sequence 21306, A
695	6.0	1086	17	US-10-282-122A-40919	Sequence 40919, A	768	86.5	6.0	3440	18	US-10-357-930-22150	Sequence 22150, A
c 696	6.0	1098	17	US-10-282-122A-25587	Sequence 25587, A	769	86.5	6.0	3440	18	US-10-357-930-27148	Sequence 27148, A
c 697	6.0	1191	17	US-10-369-493-40731	Sequence 40731, A	770	86.5	6.0	3440	18	US-10-357-930-28011	Sequence 28011, A
698	6.0	1289	18	US-10-437-963-97181	Sequence 97181, A	c 771	86.5	6.0	3462	17	US-10-369-493-35433	Sequence 35433, A
699	6.0	1296	13	US-10-076-421-1	Sequence 1, Appl	772	86.5	6.0	3636	18	US-10-474-792-37	Sequence 37, Appl
c 700	6.0	1358	18	US-10-739-930-2535	Sequence 2535, Appl	773	86.5	6.0	3691	9	US-09-922-199A-1	Sequence 1, Appl
701	6.0	1475	9	US-09-735-705-122	Sequence 122, Appl	774	86.5	6.0	3729	17	US-10-671-403-86	Sequence 86, Appl
702	6.0	1475	9	US-09-850-716A-122	Sequence 122, Appl	775	86.5	6.0	3729	17	US-10-671-419-86	Sequence 86, Appl
703	6.0	1475	9	US-09-897-778-122	Sequence 122, Appl	776	86.5	6.0	3729	17	US-10-670-844-86	Sequence 86, Appl
704	6.0	1475	10	US-09-466-396A-122	Sequence 122, Appl	777	86.5	6.0	3729	17	US-10-671-134-86	Sequence 86, Appl
705	6.0	1475	14	US-10-007-700-122	Sequence 122, Appl	778	86.5	6.0	3729	17	US-10-673-120-86	Sequence 86, Appl
706	6.0	1475	15	US-10-117-982-122	Sequence 122, Appl	779	86.5	6.0	3729	17	US-10-673-098-86	Sequence 86, Appl
707	6.0	1475	15	US-10-101-510-159	Sequence 159, Appl	780	86.5	6.0	3729	17	US-10-673-127-86	Sequence 86, Appl
708	6.0	1475	17	US-10-313-986-122	Sequence 122, Appl	781	86.5	6.0	3729	18	US-10-670-817-86	Sequence 86, Appl
709	6.0	1475	17	US-10-411-037-33	Sequence 33, Appl	782	86.5	6.0	3729	18	US-10-673-119-86	Sequence 86, Appl
710	6.0	1475	17	US-10-411-026-33	Sequence 33, Appl	783	86.5	6.0	3729	18	US-10-671-207-86	Sequence 86, Appl
711	6.0	1475	17	US-10-410-962-33	Sequence 33, Appl	784	86.5	6.0	3729	19	US-10-673-120-86	Sequence 86, Appl
712	6.0	1475	17	US-10-411-049-33	Sequence 33, Appl	785	86.5	6.0	3729	19	US-10-673-120-86	Sequence 86, Appl
713	6.0	1475	18	US-10-410-930-33	Sequence 33, Appl	786	86.5	6.0	5628	16	US-10-311-626-15	Sequence 15, Appl
714	6.0	1475	18	US-10-410-997-33	Sequence 33, Appl	787	86.5	6.0	5871	14	US-10-152-886-24	Sequence 24, Appl
715	6.0	1475	18	US-10-410-012-33	Sequence 33, Appl	788	86.5	6.0	5892	18	US-10-437-963-52962	Sequence 52962, A
716	6.0	1475	18	US-10-287-394-33	Sequence 33, Appl	c 789	86.5	6.0	10011	18	US-10-563-433-3	Sequence 3, Appl
717	6.0	1475	18	US-10-410-913-33	Sequence 33, Appl	c 790	86.5	6.0	10725	18	US-10-723-860-7789	Sequence 7789, Appl
718	6.0	1475	18	US-10-775-972-122	Sequence 122, Appl	c 791	86.5	6.0	10877	14	US-10-263-788-1	Sequence 1, Appl
719	6.0	1475	19	US-10-410-980-33	Sequence 33, Appl	c 792	86.5	6.0	12300	11	US-10-167-034-11	Sequence 11, Appl
720	6.0	1884	17	US-10-041-018-113	Sequence 113, Appl	c 793	86.5	6.0	16951	18	US-10-181-174B-72	Sequence 72, Appl
c 721	6.0	1896	18	US-10-181-174B-10	Sequence 10, Appl	794	86.5	6.0	18876	16	US-10-329-079-42	Sequence 42, Appl
722	6.0	1964	16	US-10-131-985-22	Sequence 22, Appl	c 795	86.5	6.0	23810	19	US-10-741-600-17925	Sequence 17925, A
723	6.0	1964	17	US-10-432-989-2	Sequence 2, Appl	796	86.5	6.0	19444	16	US-10-329-079-34	Sequence 34, Appl
724	6.0	1968	19	US-10-901-417-22	Sequence 22, Appl	797	86.5	6.0	85915	18	US-10-647-196-1	Sequence 1, Appl
c 725	6.0	2054	17	US-10-369-493-24298	Sequence 24298, A	798	86.5	6.0	88400	9	US-09-967-768A-314	Sequence 314, Appl
726	6.0	2175	17	US-10-425-114-15621	Sequence 15621, A	c 799	86.5	6.0	174424	18	US-09-960-706-969	Sequence 969, Appl
727	6.0	2211	17	US-10-425-114-1166	Sequence 1166, Appl	c 800	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
728	6.0	2211	17	US-10-425-114-7049	Sequence 7049, Appl	c 801	86	6.0	786	18	US-10-437-963-62697	Sequence 62697, A
729	6.0	2294	9	US-09-735-705-123	Sequence 123, Appl	c 802	86	6.0	837	18	US-10-425-115-60329	Sequence 60329, A
730	6.0	2294	9	US-09-850-716A-123	Sequence 123, Appl	c 803	86	6.0	864	17	US-10-282-122A-11310	Sequence 11310, A
731	6.0	2294	9	US-09-897-778-123	Sequence 123, Appl	c 804	86	6.0	1101	15	US-10-156-761-4292	Sequence 4292, Appl
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733	6.0	2294	14	US-10-007-700-123	Sequence 123, Appl	c 806	86	6.0	1137	18	US-10-437-963-68538	Sequence 68538, A
734	6.0	2294	15	US-10-117-982-123	Sequence 123, Appl	c 807	86	6.0	1207	18	US-10-437-963-64776	Sequence 64776, A
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736	6.0	2294	18	US-10-641-643-1217	Sequence 1217, Appl	c 809	86	6.0	1352	17	US-10-767-701-15096	Sequence 15096, A
737	6.0	2294	18	US-10-775-972-123	Sequence 123, Appl	c 810	86	6.0	1359	17	US-10-432-989-3	Sequence 3, Appl
738	6.0	2297	13	US-10-087-192-593	Sequence 593, Appl	c 811	86	6.0	1365	17	US-10-369-493-45476	Sequence 45476, A
739	6.0	2304	14	US-10-171-311-183	Sequence 183, Appl	c 812	86	6.0	1407	17	US-10-282-122A-31839	Sequence 31839, A
740	6.0	2304	15	US-10-301-822-160	Sequence 160, Appl	c 813	86	6.0	1413	17	US-10-282-122A-33369	Sequence 33369, A
741	6.0	2304	17	US-10-388-360-335	Sequence 335, Appl	c 814	86	6.0	1480	17	US-10-282-122A-29943	Sequence 29943, A
742	6.0	2304	17	US-10-295-027-413	Sequence 413, Appl	c 815	86	6.0	1491	9	US-09-938-842A-2620	Sequence 2620, Appl
743	6.0	2304	17	US-10-295-027-1058	Sequence 1058, Appl	c 816	86	6.0	1491	11	US-09-938-842A-2620	Sequence 2620, Appl
744	6.0	2304	17	US-10-159-563-121	Sequence 121, Appl	c 817	86	6.0	1500	9	US-09-881-165-1	Sequence 1, Appl
745	6.0	2304	17	US-10-665-216-3	Sequence 3, Appl	c 818	86	6.0	1500	15	US-10-164-775-4	Sequence 4, Appl
746	6.0	2304	19	US-10-645-756-37	Sequence 37, Appl	c 819	86	6.0	1500	15	US-10-252-732-1	Sequence 1, Appl
747	6.0	2325	18	US-10-425-115-114835	Sequence 114835, A	c 820	86	6.0	1728	13	US-10-029-180-101	Sequence 101, Appl
748	6.0	2328	16	US-10-247-671-34	Sequence 34, Appl	c 821	86	6.0	1728	17	US-10-149-310-307	Sequence 307, Appl
749	6.0	2336	10	US-09-971-392-46	Sequence 46, Appl	c 822	86	6.0	1878	18	US-10-425-114-3637	Sequence 3637, Appl
750	6.0	2336	15	US-10-101-510-458	Sequence 458, Appl	c 823	86	6.0	1878	18	US-10-437-963-35998	Sequence 35998, A
751	6.0	2336	16	US-10-252-157-358	Sequence 358, Appl	c 824	86	6.0	1924	17	US-10-369-493-31575	Sequence 31575, A
752	6.0	2341	14	US-10-116-802-163	Sequence 163, Appl	c 825	86	6.0	1943	15	US-10-156-761-6069	Sequence 6069, Appl



826	Sequence 27270, A	18	3502	18	US-10-437-963-50940	Sequence 50940, A
827	Sequence 116, App	15	3786	15	US-10-303-685-8	Sequence 8, Appli
828	Sequence 1241, Ap	18	4031	18	US-10-437-963-66469	Sequence 64669, A
829	Sequence 115966,	17	4135	17	US-10-369-493-27067	Sequence 27067, A
830	Sequence 108837,	17	4347	17	US-10-282-122A-30284	Sequence 30284, A
831	Sequence 92, Appl	17	4483	17	US-10-114-270-145	Sequence 145, App
832	Sequence 531, App	17	4758	17	US-10-437-963-97719	Sequence 97719, A
833	Sequence 30446, A	9	4932	9	US-09-920-300A-1688	Sequence 1688, Ap
834	Sequence 52862, A	13	4932	13	US-10-033-528-1688	Sequence 1688, Ap
835	Sequence 30812, A	16	4932	16	US-10-099-926-1688	Sequence 1688, Ap
836	Sequence 13, Appl	6	5352	6	US-10-188-832-85	Sequence 85, Appl
837	Sequence 93, Appl	18	7564	18	US-10-476-397-15	Sequence 15, Appl
838	Sequence 708, App	19	19462	19	US-10-741-600-17715	Sequence 17715, A
839	Sequence 8, Appli	9	23668	9	US-09-741-148A-3	Sequence 3, Appli
840	Sequence 36, Appl	14	2668	14	US-10-254-577-3	Sequence 3, Appli
841	Sequence 7449, Ap	19	28512	19	US-10-741-600-17963	Sequence 17963, A
842	Sequence 58, Appl	19	28769	19	US-10-741-600-17894	Sequence 17894, A
843	Sequence 1, Appli	16	32767	16	US-10-004-113-4	Sequence 4, Appli
844	Sequence 280, App	17	32767	17	US-10-394-948-4	Sequence 4, Appli
845	Sequence 1, Appli	10	75270	10	US-09-790-852-1	Sequence 1, Appli
846	Sequence 24, Appl	18	75270	18	US-10-723-860-2554	Sequence 2554, Ap
847	Sequence 205, App	17	80161	17	US-10-329-148A-1	Sequence 1, Appli
848	Sequence 1, Appli	17	80161	17	US-10-723-860-3426	Sequence 3426, Ap
849	Sequence 921	18	195917	18	US-10-723-860-3426	Sequence 5, Appli
850	Sequence 1, Appli	17	207433	17	US-10-277-216-5	Sequence 5, Appli
851	Sequence 1, Appli	17	207433	17	US-10-126-022-5	Sequence 5, Appli
852	Sequence 161681,	85	59	401	US-09-814-353-59	Sequence 59, Appl
853	Sequence 5411, Ap	85	59	401	US-09-814-353-59	Sequence 59, Appl
854	Sequence 119, App	85	59	455	US-10-439-388-17	Sequence 17, Appl
855	Sequence 66726, A	85	59	458	US-09-814-353-12841	Sequence 12841, A
856	Sequence 143334, A	85	59	460	US-09-864-761-10781	Sequence 10781, A
857	Sequence 74985, A	85	59	547	US-10-425-115-80937	Sequence 80937, A
858	Sequence 2398, Ap	85	59	569	US-10-029-386-24905	Sequence 24905, A
859	Sequence 2398, Ap	85	59	733	US-10-027-632-15602	Sequence 15602, A
860	Sequence 5343, Ap	85	59	733	US-10-027-632-15602	Sequence 15602, A
861	Sequence 1444, A	85	59	825	US-10-128-714-2348	Sequence 2348, Ap
862	Sequence 14191, A	85	59	1047	US-10-282-122A-33709	Sequence 33709, A
863	Sequence 23028, A	85	59	1141	US-10-437-963-27314	Sequence 27314, A
864	Sequence 22934, A	85	59	1205	US-09-425-026-4	Sequence 4, Appli
865	Sequence 84404, A	85	59	1215	US-10-425-114-8357	Sequence 8357, Ap
866	Sequence 8044, Ap	85	59	1215	US-10-282-122A-26482	Sequence 26482, A
867	Sequence 30665, A	85	59	1215	US-10-482-706-182	Sequence 182, App
868	Sequence 1780, Ap	85	59	1215	US-10-282-122A-28600	Sequence 28600, A
869	Sequence 36454, A	85	59	1227	US-10-767-701-10385	Sequence 10385, A
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871	Sequence 2, Appli	85	59	1346	US-10-425-115-50056	Sequence 50056, A
872	Sequence 1, Appli	85	59	1350	US-10-425-114-17538	Sequence 17538, A
873	Sequence 34455, A	85	59	1350	US-09-815-242-7965	Sequence 7965, Ap
874	Sequence 75028, A	85	59	1425	US-10-282-122A-30556	Sequence 30556, A
875	Sequence 35960, A	85	59	1425	US-09-815-242-7981	Sequence 7981, Ap
876	Sequence 5, Appli	85	59	1473	US-10-282-122A-30585	Sequence 30585, A
877	Sequence 103, App	85	59	1473	US-10-425-114-32731	Sequence 32731, A
878	Sequence 79872, A	85	59	1488	US-10-739-930-4080	Sequence 4080, Ap
879	Sequence 4138, Ap	85	59	1565	US-10-425-114-21839	Sequence 21839, A
880	Sequence 16, Appl	85	59	1577	US-10-425-114-6021	Sequence 6021, Ap
881	Sequence 85002, A	85	59	1634	US-10-302-172-167	Sequence 167, App
882	Sequence 33989, A	85	59	1654	US-10-425-115-86634	Sequence 86634, A
883	Sequence 33989, A	85	59	1683	US-10-205-032-3	Sequence 3, Appli
884	Sequence 2241, Ap	85	59	1701	US-10-425-115-110590	Sequence 110590, A
885	Sequence 20309, A	85	59	1769	US-10-437-963-66435	Sequence 66435, A
886	Sequence 34008, A	85	59	1916	US-10-437-963-66435	Sequence 7, Appli
887	Sequence 32749, A	85	59	1916	US-10-887-233-7	Sequence 7, Appli
888	Sequence 77, Appl	85	59	1917	US-10-369-493-35775	Sequence 35775, A
889	Sequence 33345, A	85	59	1932	US-10-425-114-10320	Sequence 10320, A
890	Sequence 647, App	85	59	1964	US-10-425-114-10825	Sequence 10825, A
891	Sequence 31709, A	85	59	2131	US-09-764-864-250	Sequence 250, App
892	Sequence 235, App	85	59	2135	US-10-425-115-73164	Sequence 73164, A
893	Sequence 48158, A	85	59	2231	US-10-289-757-19	Sequence 19, Appl
894	Sequence 111013, A	85	59	2262	US-10-094-749-441	Sequence 441, App
895	Sequence 111013, A	85	59	2305	US-10-296-606-17	Sequence 17, Appl
896	Sequence 95, Appl	85	59	2355	US-10-437-963-90379	Sequence 90379, A
897	Sequence 23968, A	85	59	2372	US-10-437-963-72431	Sequence 72431, A
898	Sequence 44171, A	85	59	2427	US-10-156-761-3395	Sequence 3395, Ap
		85	59	2612	US-10-425-115-160028	Sequence 160028, A

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c 973	85	5.9	2758	17	US-10-094-749-1267	Sequence 1267, Ap	1046	84.5	5.9	1674	9	US-09-808-387-3	Sequence 3, Appli
974	85	5.9	2848	13	US-10-002-344-60	Sequence 60, Appl	1047	84.5	5.9	1677	17	US-10-369-493-34258	Sequence 34258, A
975	85	5.9	2848	17	US-10-958-862-60	Sequence 60, Appl	c1048	84.5	5.9	1679	13	US-10-044-090-316	Sequence 316, App
976	85	5.9	2929	17	US-10-425-114-11279	Sequence 11279, A	1049	84.5	5.9	1725	9	US-09-808-387-1	Sequence 1, Appli
c 977	85	5.9	2937	15	US-10-156-761-1581	Sequence 1581, Ap	c1050	84.5	5.9	1725	10	US-09-814-353-20589	Sequence 20589, A
978	85	5.9	3008	10	US-09-373-658-3	Sequence 3, Appli	1051	84.5	5.9	1725	10	US-10-437-963-100495	Sequence 100495, A
979	85	5.9	3008	11	US-09-989-687-3	Sequence 3, Appli	c1052	84.5	5.9	1826	18	US-09-971-992-91	Sequence 91, Appl
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c 981	85	5.9	3148	18	US-10-437-963-80145	Sequence 80145, A	1054	84.5	5.9	1860	17	US-10-369-493-38468	Sequence 38468, A
982	85	5.9	3307	17	US-10-424-599-116102	Sequence 116102, A	c1055	84.5	5.9	1860	17	US-10-411-910A-124	Sequence 124, App
c 983	85	5.9	3404	18	US-10-602-494-70	Sequence 70, Appl	1056	84.5	5.9	1869	17	US-10-369-493-38622	Sequence 38622, A
984	85	5.9	3711	18	US-10-283-975A-398	Sequence 398, App	1057	84.5	5.9	1949	17	US-10-369-493-35060	Sequence 35060, A
c 985	85	5.9	3937	14	US-10-198-846-13985	Sequence 13985, A	1058	84.5	5.9	2174	17	US-10-282-122A-14290	Sequence 14290, A
c 986	85	5.9	4145	9	US-09-911-781-3	Sequence 3, Appli	1059	84.5	5.9	2377	18	US-10-425-115-176394	Sequence 176394, A
c 987	85	5.9	4145	14	US-09-976-800-82	Sequence 82, Appl	c1060	84.5	5.9	2463	18	US-10-425-115-170656	Sequence 170656, A
c 988	85	5.9	4145	14	US-10-138-838-82	Sequence 82, Appl	c1061	84.5	5.9	2478	18	US-10-322-281-381	Sequence 381, App
c 989	85	5.9	4145	14	US-10-139-031-82	Sequence 82, Appl	c1062	84.5	5.9	2550	18	US-10-425-115-111107	Sequence 111107, A
c 990	85	5.9	4145	14	US-10-138-905-82	Sequence 82, Appl	1063	84.5	5.9	2917	18	US-10-343-903-44	Sequence 44, Appl
c 991	85	5.9	4145	14	US-10-138-916-82	Sequence 82, Appl	1064	84.5	5.9	3096	18	US-10-476-597-70	Sequence 70, Appl
c 992	85	5.9	4145	15	US-10-139-296-82	Sequence 82, Appl	1065	84.5	5.9	3096	18	US-10-476-597-71	Sequence 71, Appl
c 993	85	5.9	4145	16	US-10-139-218-82	Sequence 82, Appl	c1066	84.5	5.9	3186	18	US-10-425-115-114129	Sequence 114129, A
c 994	85	5.9	4145	16	US-10-400-902-3	Sequence 3, Appli	1067	84.5	5.9	3291	18	US-10-723-860-1367	Sequence 1367, Ap
c 995	85	5.9	4145	16	US-10-405-660-82	Sequence 82, Appl	1068	84.5	5.9	3343	17	US-10-257-022-19	Sequence 19, Appl
c 996	85	5.9	4145	17	US-10-138-898-82	Sequence 82, Appl	1069	84.5	5.9	3408	9	US-09-795-693-16	Sequence 16, Appl
c 997	85	5.9	4212	13	US-10-194-163-39	Sequence 39, Appl	1070	84.5	5.9	3408	14	US-10-156-239-16	Sequence 16, Appl
998	85	5.9	4341	15	US-10-156-761-1074	Sequence 1074, Ap	1071	84.5	5.9	3408	14	US-10-199-485-16	Sequence 16, Appl
999	85	5.9	4512	10	US-09-792-616-2	Sequence 2, Appli	1072	84.5	5.9	3411	17	US-10-374-979-67	Sequence 67, Appl
1000	85	5.9	4512	18	US-10-764-328-2	Sequence 2, Appli	1073	84.5	5.9	3411	17	US-10-182-936A-67	Sequence 67, Appl
1001	85	5.9	4535	19	US-10-741-600-755	Sequence 755, App	1074	84.5	5.9	3411	18	US-10-477-238A-646	Sequence 646, App
c1002	85	5.9	4551	15	US-10-156-761-5715	Sequence 5715, Ap	1075	84.5	5.9	3411	18	US-10-680-287A-646	Sequence 646, App
c1003	85	5.9	5360	18	US-10-467-506A-13	Sequence 13, Appl	1076	84.5	5.9	3414	14	US-10-074-475-36	Sequence 36, Appl
c1004	85	5.9	5491	18	US-10-723-860-5914	Sequence 5914, Ap	1077	84.5	5.9	3512	13	US-10-072-621-1	Sequence 1, Appli
c1005	85	5.9	9320	18	US-10-471-065-20	Sequence 20, Appl	1078	84.5	5.9	3536	18	US-10-802-513-1	Sequence 1, Appli
1006	85	5.9	9369	16	US-10-200-562-190	Sequence 190, App	c1079	84.5	5.9	3575	9	US-09-796-858-41	Sequence 41, Appli
1007	85	5.9	9369	16	US-10-237-551-190	Sequence 190, App	c1080	84.5	5.9	3600	9	US-09-875-338-3	Sequence 3, Appli
c1008	85	5.9	9369	16	US-10-237-551-247	Sequence 247, App	c1081	84.5	5.9	3600	14	US-10-077-023-3	Sequence 3, Appli
1009	85	5.9	71989	9	US-09-727-889-2	Sequence 2, Appli	c1082	84.5	5.9	3616	19	US-10-890-789-5	Sequence 5, Appli
1010	85	5.9	125746	15	US-10-849-462-2	Sequence 2, Appli	c1083	84.5	5.9	3660	10	US-09-814-353-19604	Sequence 19604, A
c1011	85	5.9	154746	10	US-10-156-761-15102	Sequence 15102, A	1084	84.5	5.9	4432	17	US-10-120-988-148	Sequence 148, App
c1012	85	5.9	593	16	US-10-029-386-5929	Sequence 8, Appli	1085	84.5	5.9	4548	15	US-10-156-761-6166	Sequence 6166, Ap
c1013	84.5	5.9	618	9	US-09-738-626-3423	Sequence 5229, Ap	c1086	84.5	5.9	4862	15	US-10-161-403-87	Sequence 87, Appl
1014	84.5	5.9	688	18	US-10-437-963-59927	Sequence 3423, Ap	1087	84.5	5.9	5179	18	US-10-437-963-25554	Sequence 25554, A
c1015	84.5	5.9	867	18	US-10-437-963-59927	Sequence 5927, A	1088	84.5	5.9	5679	14	US-10-152-886-74	Sequence 74, Appl
1016	84.5	5.9	870	18	US-10-425-115-48092	Sequence 48092, A	1089	84.5	5.9	6754	17	US-10-240-425-350	Sequence 350, App
c1017	84.5	5.9	870	19	US-10-890-789-2	Sequence 2, Appli	1090	84.5	5.9	6754	18	US-10-473-974-118	Sequence 118, App
c1018	84.5	5.9	873	9	US-09-910-174A-22	Sequence 22, Appl	1091	84.5	5.9	7080	17	US-10-276-774-729	Sequence 729, App
c1019	84.5	5.9	873	18	US-10-644-671-22	Sequence 22, Appl	1092	84.5	5.9	10846	9	US-09-923-109-5	Sequence 5, Appli
1020	84.5	5.9	899	17	US-10-425-114-7134	Sequence 7134, Ap	1093	84.5	5.9	10846	15	US-10-164-204-5	Sequence 5, Appli
c1021	84.5	5.9	967	9	US-09-898-570-33	Sequence 33, Appl	1094	84.5	5.9	10846	17	US-10-705-430-5	Sequence 5, Appli
1022	84.5	5.9	967	10	US-09-839-446-33	Sequence 33, Appl	1095	84.5	5.9	10900	9	US-09-923-109-6	Sequence 6, Appli
c1023	84.5	5.9	1161	18	US-10-425-115-3106	Sequence 3106, Ap	1096	84.5	5.9	10900	15	US-10-164-204-6	Sequence 6, Appli
c1024	84.5	5.9	1178	17	US-10-425-114-22293	Sequence 22293, Ap	1097	84.5	5.9	10900	17	US-10-705-430-6	Sequence 6, Appli
1025	84.5	5.9	1179	17	US-10-282-122A-14447	Sequence 14447, A	1098	84.5	5.9	11606	18	US-10-602-475A-9	Sequence 9, Appli
c1026	84.5	5.9	1207	18	US-10-437-963-62054	Sequence 62054, A	1099	84.5	5.9	13116	17	US-10-499-406-2	Sequence 2, Appli
c1027	84.5	5.9	1286	14	US-10-132-829-3	Sequence 3, Appli	c1100	84.5	5.9	14061	17	US-10-093-463-73	Sequence 73, Appl
c1028	84.5	5.9	1286	16	US-10-136-819-1	Sequence 1, Appli	c1101	84.5	5.9	14109	17	US-10-093-463-71	Sequence 71, Appl
1029	84.5	5.9	1286	15	US-10-133-907-3	Sequence 3, Appli	1102	84.5	5.9	45191	15	US-10-080-170-649	Sequence 649, App
c1030	84.5	5.9	1314	17	US-10-282-122A-30204	Sequence 30204, A	1103	84.5	5.9	45191	18	US-10-080-170-649	Sequence 649, App
c1031	84.5	5.9	1323	17	US-10-369-493-44491	Sequence 44491, A	1104	84.5	5.9	45191	18	US-10-468-356-649	Sequence 649, App
c1032	84.5	5.9	1406	18	US-10-726-699-56	Sequence 56, Appl	1105	84.5	5.9	71292	13	US-10-087-192-1942	Sequence 1942, Ap
c1033	84.5	5.9	1413	17	US-10-369-493-40672	Sequence 40672, A	c1106	84.5	5.9	74868	14	US-10-175-523-67	Sequence 67, Appl
1034	84.5	5.9	1366	15	US-10-437-963-32627	Sequence 32627, Ap	1107	84.5	5.9	98474	13	US-10-087-192-175	Sequence 175, App
c1035	84.5	5.9	1395	18	US-10-723-860-8124	Sequence 8124, Ap	1108	84.5	5.9	101209	13	US-10-087-192-460	Sequence 460, App
c1036	84.5	5.9	1406	18	US-10-726-699-27	Sequence 27, Appl	c1109	84.5	5.9	104729	18	US-10-723-860-1434	Sequence 1434, Ap
c1037	84.5	5.9	1406	18	US-10-726-699-56	Sequence 56, Appl	1110	84	5.9	714	17	US-10-282-122A-26405	Sequence 26405, A
c1038	84.5	5.9	1413	17	US-10-369-493-40672	Sequence 40672, A	1111	84	5.9	750	17	US-10-282-122A-28206	Sequence 28206, A
1039	84.5	5.9	1545	17	US-10-282-122A-14095	Sequence 14095, A	1112	84	5.9	765	18	US-10-425-115-58352	Sequence 58352, A
c1040	84.5	5.9	1553	13	US-10-002-775-3	Sequence 3, Appli	1113	84	5.9	831	17	US-10-437-963-41149	Sequence 41149, A
c1041	84.5	5.9	1553	14	US-10-115-615-3	Sequence 3, Appli	1114	84	5.9	876	17	US-10-369-493-32649	Sequence 32649, A
c1042	84.5	5.9	1604	9	US-09-875-338-1	Sequence 1, Appli	c1115	84	5.9	947	18	US-10-425-115-13959	Sequence 13959, A
c1043	84.5	5.9	1604	14	US-10-077-023-1	Sequence 1, Appli	1116	84	5.9	1117	18	US-10-437-963-46167	Sequence 46167, A
c1044	84.5	5.9	1662	10	US-09-292-862-1	Sequence 1, Appli	c1117	84	5.9	1132	18	US-10-425-115-48054	Sequence 48054, A

c1118	84	5.9	1296	18	US-10-739-930-4335	Sequence 4335, Ap	1191	83.5	5.8	1240	11	US-09-729-821-2	Sequence 2, Appli
c1119	84	5.9	1299	18	US-10-739-930-2323	Sequence 2323, Ap	1192	83.5	5.8	1240	18	US-10-734-282-2	Sequence 2, Appli
c1120	84	5.9	1352	18	US-10-425-115-64812	Sequence 64812, A	1193	83.5	5.8	1265	15	US-10-037-770-892	Sequence 892, App
c1121	84	5.9	1388	17	US-10-282-122A-25610	Sequence 25610, A	1194	83.5	5.8	1265	17	US-10-117-722-892	Sequence 213, App
c1122	84	5.9	1497	17	US-10-282-122A-25610	Sequence 11595, A	1195	83.5	5.8	1332	11	US-09-997-722-213	Sequence 213, App
c1123	84	5.9	1589	18	US-10-767-701-12146	Sequence 12146, A	1196	83.5	5.8	1339	17	US-10-282-122A-29995	Sequence 29995, A
c1124	84	5.9	1602	18	US-10-425-115-124288	Sequence 124288, A	1197	83.5	5.8	1446	17	US-10-369-493-35956	Sequence 35956, A
c1125	84	5.9	1609	14	US-10-082-830-48	Sequence 48, Appl	1198	83.5	5.8	1480	17	US-10-282-122A-29943	Sequence 29943, A
c1126	84	5.9	1629	17	US-10-282-122A-14919	Sequence 14919, A	1199	83.5	5.8	1525	17	US-10-291-172-66	Sequence 66, Appl
c1127	84	5.9	1827	15	US-10-156-761-4695	Sequence 4695, Ap	1200	83.5	5.8	1525	17	US-10-221-278-66	Sequence 66, Appl
c1128	84	5.9	1847	18	US-10-411-910A-104	Sequence 104, App	1201	83.5	5.8	1557	15	US-10-119-926-18	Sequence 18, Appl
c1129	84	5.9	2028	18	US-10-425-115-94597	Sequence 94597, A	1202	83.5	5.8	1613	18	US-10-425-115-166627	Sequence 166627, A
c1130	84	5.9	2291	17	US-10-094-749-218	Sequence 218, App	1203	83.5	5.8	1649	15	US-10-278-945-1	Sequence 1, Appli
c1131	84	5.9	2436	17	US-10-260-238-1510	Sequence 1510, Ap	1204	83.5	5.8	1678	18	US-10-425-115-96353	Sequence 96353, A
c1132	84	5.9	2601	17	US-10-369-493-33730	Sequence 33730, A	1205	83.5	5.8	1767	17	US-10-425-114-16419	Sequence 16419, A
c1133	84	5.9	2667	10	US-09-895-298-12	Sequence 12, Appl	1206	83.5	5.8	1772	17	US-10-425-114-26363	Sequence 26363, A
c1134	84	5.9	2667	18	US-10-885-039-12	Sequence 12, Appl	1207	83.5	5.8	1811	17	US-10-425-114-17717	Sequence 17717, A
c1135	84	5.9	2780	9	US-09-864-864-318	Sequence 318, Appl	1208	83.5	5.8	1914	18	US-10-441-949-60	Sequence 60, Appl
c1136	84	5.9	2788	18	US-10-723-860-6037	Sequence 6037, Ap	1209	83.5	5.8	1923	18	US-09-746-660A-105	Sequence 105, App
c1137	84	5.9	2828	18	US-10-723-860-6037	Sequence 6037, Ap	1210	83.5	5.8	1923	18	US-10-441-949-61	Sequence 61, Appl
c1138	84	5.9	2919	17	US-10-359-493-44751	Sequence 44751, A	1211	83.5	5.8	1923	18	US-10-441-949-62	Sequence 62, Appl
c1139	84	5.9	2961	18	US-10-425-115-93677	Sequence 93677, A	1212	83.5	5.8	1923	18	US-10-441-949-65	Sequence 65, Appl
c1140	84	5.9	3008	17	US-10-108-260A-1736	Sequence 1736, Ap	1213	83.5	5.8	1923	18	US-10-441-949-66	Sequence 66, Appl
c1141	84	5.9	3336	15	US-10-156-761-376	Sequence 376, App	1214	83.5	5.8	1929	17	US-10-425-114-25324	Sequence 5578, Ap
c1142	84	5.9	3831	17	US-10-282-122A-30485	Sequence 30485, A	1215	83.5	5.8	2020	17	US-10-425-114-25324	Sequence 5578, Ap
c1143	84	5.9	4248	17	US-10-282-122A-30485	Sequence 30485, A	1216	83.5	5.8	2088	18	US-10-425-115-22868	Sequence 22868, A
c1144	84	5.9	4818	17	US-10-282-122A-26430	Sequence 26430, A	1217	83.5	5.8	2103	18	US-10-425-115-177617	Sequence 177617, A
c1145	84	5.9	5470	18	US-10-723-860-7477	Sequence 7477, Ap	1218	83.5	5.8	2106	18	US-10-437-963-39568	Sequence 39568, A
c1146	84	5.9	6816	16	US-10-021-660-12	Sequence 12, Appl	1219	83.5	5.8	2194	9	US-09-738-626-1261	Sequence 678, App
c1147	84	5.9	6816	17	US-10-211-462-31	Sequence 31, Appl	1220	83.5	5.8	2235	9	US-09-738-626-1261	Sequence 1261, App
c1148	84	5.9	6822	18	US-10-437-963-82458	Sequence 82458, A	1221	83.5	5.8	2261	13	US-10-425-115-35617	Sequence 35617, A
c1149	84	5.9	6822	19	US-10-780-002-31	Sequence 31, Appl	1222	83.5	5.8	2268	13	US-10-087-192-935	Sequence 935, App
c1150	84	5.9	7068	18	US-10-437-963-86105	Sequence 86105, A	1223	83.5	5.8	2328	10	US-09-746-660A-103	Sequence 103, App
c1151	84	5.9	7536	17	US-10-282-122A-26585	Sequence 26585, A	1224	83.5	5.8	2339	18	US-10-405-877-116	Sequence 116, App
c1152	84	5.9	7539	17	US-10-282-122A-26585	Sequence 26585, A	1225	83.5	5.8	2402	17	US-10-405-877-116	Sequence 116, App
c1153	84	5.9	8010	17	US-10-016-248-3	Sequence 3, Appli	1226	83.5	5.8	2430	15	US-10-157-031-396	Sequence 396, App
c1154	84	5.9	9748	17	US-10-282-122A-31388	Sequence 31388, A	1227	83.5	5.8	2479	18	US-10-723-860-5318	Sequence 5318, App
c1155	84	5.9	10136	17	US-10-016-248-1	Sequence 1, Appli	1228	83.5	5.8	2574	14	US-10-167-749-101	Sequence 101, App
c1156	84	5.9	10296	17	US-10-282-122A-33665	Sequence 33665, A	1229	83.5	5.8	2574	17	US-10-170-481A-101	Sequence 101, App
c1157	84	5.9	1427	15	US-10-156-761-1540	Sequence 1540, Ap	1230	83.5	5.8	2574	17	US-10-210-028-101	Sequence 101, App
c1158	84	5.9	59554	17	US-10-052-482-202	Sequence 202, App	1231	83.5	5.8	2574	17	US-10-162-521A-101	Sequence 101, App
c1159	84	5.9	60196	15	US-10-205-032-1	Sequence 1, Appli	1232	83.5	5.8	2574	17	US-10-918-851-101	Sequence 101, App
c1160	84	5.9	86114	15	US-10-080-170-648	Sequence 648, App	1233	83.5	5.8	2574	19	US-10-805-667-101	Sequence 101, App
c1161	84	5.9	86114	18	US-10-080-170-648	Sequence 648, App	1234	83.5	5.8	2574	19	US-10-897-359-101	Sequence 101, App
c1162	84	5.9	86114	18	US-10-468-356-648	Sequence 648, App	1235	83.5	5.8	2589	15	US-10-242-576-1	Sequence 1, Appli
c1163	84	5.9	176080	17	US-10-235-192A-43	Sequence 43, Appl	1236	83.5	5.8	2772	17	US-10-108-260A-169	Sequence 169, App
c1164	84	5.9	347001	18	US-10-319-908-16	Sequence 16, Appl	1237	83.5	5.8	2772	9	US-09-738-626-2944	Sequence 2944, Ap
c1165	83.5	5.8	576	15	US-10-156-761-205	Sequence 205, App	1238	83.5	5.8	2810	9	US-09-919-835-1	Sequence 1, Appli
c1166	83.5	5.8	579	14	US-10-198-846-9350	Sequence 9350, Ap	1239	83.5	5.8	2824	18	US-10-322-281-337	Sequence 337, App
c1167	83.5	5.8	688	18	US-10-767-701-768	Sequence 768, App	1240	83.5	5.8	2824	18	US-10-322-281-339	Sequence 339, App
c1168	83.5	5.8	706	18	US-10-425-115-120383	Sequence 120383, A	1241	83.5	5.8	2873	9	US-09-925-300-287	Sequence 287, App
c1169	83.5	5.8	747	9	US-09-764-877-2387	Sequence 2387, Ap	1242	83.5	5.8	2899	17	US-10-120-988-112	Sequence 112, App
c1170	83.5	5.8	747	17	US-10-242-515-2387	Sequence 2387, Ap	1243	83.5	5.8	2923	15	US-10-242-576-3	Sequence 3, Appli
c1171	83.5	5.8	770	9	US-09-974-300-2057	Sequence 2057, Ap	1244	83.5	5.8	3130	11	US-09-997-722-212	Sequence 212, App
c1172	83.5	5.8	834	18	US-10-425-115-176763	Sequence 176763, A	1245	83.5	5.8	3144	16	US-10-270-845-2	Sequence 2, Appli
c1173	83.5	5.8	874	9	US-09-925-301-191	Sequence 191, App	1246	83.5	5.8	3144	16	US-10-440-366-8	Sequence 8, Appli
c1174	83.5	5.8	897	17	US-10-424-599-127609	Sequence 127609, A	1247	83.5	5.8	3183	9	US-09-949-036-1	Sequence 88438, A
c1175	83.5	5.8	972	15	US-10-156-761-6533	Sequence 6533, Ap	1248	83.5	5.8	3240	9	US-10-425-115-88438	Sequence 1, Appli
c1176	83.5	5.8	976	18	US-10-425-115-177697	Sequence 177697, A	1249	83.5	5.8	3336	15	US-10-156-761-376	Sequence 376, App
c1177	83.5	5.8	990	17	US-10-260-238-4176	Sequence 4176, Ap	1250	83.5	5.8	3451	17	US-10-369-493-38914	Sequence 38914, A
c1178	83.5	5.8	991	17	US-10-114-270-135	Sequence 135, App	1251	83.5	5.8	3466	17	US-10-369-493-38432	Sequence 38432, A
c1179	83.5	5.8	991	17	US-10-114-270-137	Sequence 137, App	1252	83.5	5.8	3554	18	US-10-437-963-49449	Sequence 49449, A
c1180	83.5	5.8	993	9	US-09-876-216-1	Sequence 1, Appli	1253	83.5	5.8	3709	18	US-10-335-053-92	Sequence 92, Appli
c1181	83.5	5.8	993	15	US-10-359-076-1	Sequence 1, Appli	1254	83.5	5.8	3720	18	US-10-473-126-26	Sequence 26, Appli
c1182	83.5	5.8	1004	17	US-10-425-114-15631	Sequence 15631, A	1255	83.5	5.8	3789	18	US-10-437-963-69323	Sequence 69323, A
c1183	83.5	5.8	1080	9	US-09-815-242-4061	Sequence 4061, Ap	1256	83.5	5.8	3789	18	US-10-322-281-335	Sequence 335, App
c1184	83.5	5.8	1080	17	US-10-282-122A-7305	Sequence 7305, Ap	1257	83.5	5.8	3905	18	US-10-322-281-333	Sequence 333, App
c1185	83.5	5.8	1116	15	US-10-156-761-1283	Sequence 1283, Ap	1258	83.5	5.8	4200	17	US-10-093-463-139	Sequence 139, App
c1186	83.5	5.8	1162	18	US-10-437-963-73894	Sequence 73894, A	1259	83.5	5.8	4350	16	US-10-285-976-40	Sequence 40, Appli
c1187	83.5	5.8	1216	18	US-10-767-701-7988	Sequence 7988, Ap	1260	83.5	5.8	4350	18	US-10-473-974-124	Sequence 124, App
c1188	83.5	5.8	1224	17	US-10-282-122A-27529	Sequence 27529, A	1261	83.5	5.8	4350	18	US-10-473-974-125	Sequence 125, App
c1189	83.5	5.8	1239	18	US-10-425-115-162441	Sequence 162441, A	1262	83.5	5.8	4350	18	US-10-473-974-205	Sequence 205, App
c1190	83.5	5.8	1240	9	US-09-729-821-2	Sequence 2, Appli	1263	83.5	5.8	4402	18	US-10-437-963-35915	Sequence 35915, A

c1348	83.5	5.8	4694	18	US-10-723-860-5310	Sequence 5310, Ap	83	1614	17	US-10-616-187-45	Sequence 45, Appl
c1349	83.5	5.8	4719	17	US-10-258-106-25	Sequence 25, Appl	83	1614	17	US-10-671-242-45	Sequence 45, Appl
c1350	83.5	5.8	4837	17	US-10-062-674-1978	Sequence 1978, Ap	83	1832	18	US-10-437-963-76365	Sequence 76365, A
c1351	83.5	5.8	4933	17	US-10-172-118-1539	Sequence 1539, Ap	83	1884	18	US-10-425-115-24959	Sequence 24959, A
c1352	83.5	5.8	4933	17	US-10-342-887-1539	Sequence 1539, Ap	83	1924	18	US-10-437-963-29436	Sequence 29436, A
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 29, 2005, 04:18:08 ; Search time 3093 Seconds  
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Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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93	98	6.8	913	5	BQ677169	AGENCOURT	BQ677169	AGENCOURT	c 166	96	6.7	928	3	CR595839	full-leng
94	98	6.8	920	5	BK459175	BK459175	BK459175	BK459175	c 167	96	6.7	958	5	BQ675598	AGENCOURT
95	98	6.8	928	2	BE216278	HV CEB001	BE216278	HV CEB001	c 168	96	6.7	963	4	BF973201	602241458
96	98	6.8	931	5	BQ919623	AGENCOURT	BQ919623	AGENCOURT	c 169	96	6.7	1003	5	BQ065289	AGENCOURT
97	98	6.8	939	5	BUI190831	AGENCOURT	BUI190831	AGENCOURT	c 170	96	6.7	1077	4	BG745757	602723880
98	98	6.8	959	5	BK355802	EX355802	BK355802	EX355802	c 171	96	6.7	1046	4	BI522308	603081343
99	98	6.8	1058	5	BQ956152	AGENCOURT	BQ956152	AGENCOURT	c 172	96	6.7	1092	5	BK335155	EX335155
100	98	6.8	1093	3	CR621877	full-leng	CR621877	full-leng	c 173	96	6.7	1099	2	BE909994	601498028
101	98	6.8	1116	4	BM544687	AGENCOURT	BM544687	AGENCOURT	c 174	96	6.7	1112	5	BM924220	AGENCOURT
102	98	6.8	1347	3	CR617514	full-leng	CR617514	full-leng	c 175	96	6.7	1178	2	BE730977	601570936
103	98	6.8	1373	3	CR603866	full-leng	CR603866	full-leng	c 176	95.5	6.7	689	7	CN145409	WOUND1.28
104	98	6.8	1385	3	CR619388	full-leng	CR619388	full-leng	c 177	95.5	6.7	751	7	CK452666	908314-MA
105	98	6.8	1392	3	CR606004	full-leng	CR606004	full-leng	c 178	95.5	6.7	842	8	BZ574058	msb.3488
106	98	6.8	1399	3	CR596948	full-leng	CR596948	full-leng	c 179	95.5	6.7	846	9	CC638581	OGVBC68TH
107	98	6.8	1399	3	CR625424	full-leng	CR625424	full-leng	c 180	95.5	6.7	1043	8	CC263986	CH261-79M
108	98	6.8	1402	3	CR591537	full-leng	CR591537	full-leng	c 181	95.5	6.7	1048	9	CNS02K25	Tetraodon
109	98	6.8	1409	3	CR619887	full-leng	CR619887	full-leng	c 182	95.5	6.7	1053	5	BM921737	AGENCOURT
110	98	6.8	1411	3	CR607197	full-leng	CR607197	full-leng	c 183	95.5	6.7	1112	7	CK161523	FGAS01409
111	98	6.8	1418	3	CR616455	full-leng	CR616455	full-leng	c 184	95.5	6.7	1171	4	BM544885	AGENCOURT
112	98	6.8	1427	3	CR618610	full-leng	CR618610	full-leng	c 185	95.5	6.7	1225	8	CC227413	CH261-156
113	98	6.8	1430	3	CR607312	full-leng	CR607312	full-leng	c 186	95.5	6.7	1578	3	CR639830	Tetraodon
114	98	6.8	1439	3	CR624552	full-leng	CR624552	full-leng	c 187	95.5	6.7	2682	9	CL950368	OGJRU000
115	98	6.8	1442	3	CR625692	full-leng	CR625692	full-leng	c 188	95	6.6	580	4	BJ698899	BJ698899
116	98	6.8	1444	3	CR605376	full-leng	CR605376	full-leng	c 189	95	6.6	641	6	CD234821	SSI.34.B0
117	98	6.8	1449	3	CR597384	full-leng	CR597384	full-leng	c 190	95	6.6	660	5	BK352671	BK352671
118	98	6.8	1449	3	CR601788	full-leng	CR601788	full-leng	c 191	95	6.6	679	8	BZ310292	IC52b10.b
119	98	6.8	1449	3	CR611476	full-leng	CR611476	full-leng	c 192	95	6.6	721	2	BF628992	HVSMEM000
120	98	6.8	1451	3	CR604735	full-leng	CR604735	full-leng	c 193	95	6.6	728	8	BZ749747	PUPBP40TD
121	98	6.8	1451	3	CR625232	full-leng	CR625232	full-leng	c 194	95	6.6	731	4	BG390225	602415971
122	98	6.8	1454	3	CR603821	full-leng	CR603821	full-leng	c 195	95	6.6	767	5	BUI23113	603149412
123	98	6.8	1456	3	CR591442	full-leng	CR591442	full-leng	c 196	95	6.6	768	2	BE558830	HV_CEB002
124	98	6.8	1456	3	CR599568	full-leng	CR599568	full-leng	c 197	95	6.6	800	5	BU220426	603756441
125	98	6.8	1460	3	CR604363	full-leng	CR604363	full-leng	c 198	95	6.6	808	7	CK973012	4103586.B
126	98	6.8	1460	3	CR614498	full-leng	CR614498	full-leng	c 199	95	6.6	808	9	CC674603	OGWJ79TV
127	98	6.8	1463	3	CR626102	full-leng	CR626102	full-leng	c 200	95	6.6	816	2	BF264593	HV_CEB000
128	98	6.8	1464	3	CR607263	full-leng	CR607263	full-leng	c 201	95	6.6	848	7	CK193385	FGAS00179
129	98	6.8	1465	3	CR613053	full-leng	CR613053	full-leng	c 202	95	6.6	875	4	BG472142	602313865
130	98	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 203	95	6.6	880	5	BUI22710	603149245
131	97.5	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 204	95	6.6	912	5	BU421161	603962368
132	97.5	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 205	95	6.6	915	9	CG251394	OGXEG26TV
133	97.5	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 206	95	6.6	1013	9	CNS03QC2	Tetraodon
134	97.5	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 207	95	6.6	1062	5	BQ957073	AGENCOURT
135	97.5	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 208	95	6.6	1076	4	BG114843	602315602
136	97.5	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 209	95	6.6	1083	5	BM923030	AGENCOURT
137	97.5	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 210	95	6.6	1125	4	BM453590	AGENCOURT
138	97	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 211	95	6.6	1419	9	CL949615	OGIFSB001
139	97	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 212	95	6.6	3762	3	CL970829	OsiFCC020
140	97	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 213	95	6.6	4560	3	AV539866	Rattus no
141	97	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 214	94.5	6.6	508	6	CA711206	wdk2c.pko
142	97	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 215	94.5	6.6	622	4	BI598168	603451526
143	97	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 216	94.5	6.6	664	1	AV699757	AV699757
144	97	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 217	94.5	6.6	668	5	BU278540	603865278
145	97	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 218	94.5	6.6	700	7	CN289276	170005999
146	97	6.8	1465	3	CR749557	Homo sapi	CR749557	Homo sapi	c 219	94.5	6.6	706	7	CF774655	UI-D-GC1-
147	96.5	6.7	654	8	CC337207	FUHBV31TH	CC337207	FUHBV31TH	c 220	94.5	6.6	756	9	CL158521	104.347.1
148	96.5	6.7	773	8	CC332844	OGPAP40TH	CC332844	OGPAP40TH	c 221	94.5	6.6	761	9	CL288236	ZMWB063
149	96.5	6.7	794	4	BI918874	603180926	BI918874	603180926	c 222	94.5	6.6	763	4	BI517781	603042027
150	96.5	6.7	803	2	BE873246	601451783	BE873246	601451783	c 223	94.5	6.6	880	4	BI517781	603042027
151	96.5	6.7	869	7	CO365894	RTK1.19.H	CO365894	RTK1.19.H	c 224	94.5	6.6	885	4	BG490498	602519638
152	96.5	6.7	969	5	BQ954766	AGENCOURT	BQ954766	AGENCOURT	c 225	94.5	6.6	910	9	CG629635	OGUIJ70TH
153	96.5	6.7	974	5	BK336087	EX336087	BK336087	EX336087	c 226	94.5	6.6	1176	5	BQ645037	AGENCOURT
154	96.5	6.7	1468	5	BQ962374	AGENCOURT	BQ962374	AGENCOURT	c 227	94	6.6	409	4	BM818650	K-EST0085
155	96	6.7	424	4	BM818694	K-EST0086	BM818694	K-EST0086	c 228	94	6.6	479	2	AW512070	xu54d07.x



C 229	94	6.6	607	4	BG117685	602349648	C 302	93	6.5	1136	8	B2559274	pac2-164
C 230	94	6.6	628	7	CK971039	4086715 B	C 303	93	6.5	1245	8	B2579393	msb2 6335
C 231	94	6.6	673	4	BI960378	HVSMEM002	C 304	93	6.5	2121	9	CL969972	OiIFCC019
C 232	94	6.6	674	7	CK962937	4077615 B	C 305	93	6.5	3642	9	CL978063	CL978063
C 233	94	6.6	682	7	CK963478	4078160 B	C 306	92.5	6.5	458	7	CF732839	UI-M-HB0-
C 234	94	6.6	683	6	BY747887	BY747887	C 307	92.5	6.5	622	6	CA197731	SCAGAD107
C 235	94	6.6	683	7	CK965556	4080546 B	C 308	92.5	6.5	651	6	CA094082	SCCCL400
C 236	94	6.6	684	7	CK967503	4083019 B	C 309	92.5	6.5	672	4	BI955459	HVSMEM002
C 237	94	6.6	684	7	CK982840	4072199 B	C 310	92.5	6.5	686	4	BG274868	WHE2118 C
C 238	94	6.6	685	7	CK977695	4109059 B	C 311	92.5	6.5	726	4	BG231184	BG231184
C 239	94	6.6	686	7	CK963769	4078138 B	C 312	92.5	6.5	728	6	CD908518	G468.110C
C 240	94	6.6	686	7	CK976981	4108149 B	C 313	92.5	6.5	759	2	BF627397	HVSMEM000
C 241	94	6.6	686	7	CK982973	4107710 B	C 314	92.5	6.5	774	6	CB955159	AGENCOURT
C 242	94	6.6	687	7	CK977860	4108947 B	C 315	92.5	6.5	809	5	BX337592	BX337592
C 243	94	6.6	688	7	CK940248	4113805 B	C 316	92.5	6.5	816	4	BI952395	HVSMEM000
C 244	94	6.6	688	7	CK978955	4110694 B	C 317	92.5	6.5	876	9	CG607156	QGWCF04TH
C 245	94	6.6	688	7	CK979852	4111376 B	C 318	92.5	6.5	876	9	CG281803	OGWMP04TH
C 246	94	6.6	690	7	CK968289	4083636 B	C 319	92.5	6.5	948	4	BI462234	603205552
C 247	94	6.6	690	7	CK976266	4107326 B	C 320	92.5	6.5	951	2	BE214936	HV_CEB000
C 248	94	6.6	700	7	CK981811	4114501 B	C 321	92.5	6.5	953	4	BI456794	603174688
C 249	94	6.6	720	7	CK968952	4084506 B	C 322	92.5	6.5	1000	4	BM552624	AGENCOURT
C 250	94	6.6	727	7	CK966403	4081494 B	C 323	92.5	6.5	1008	4	BI670332	603292701
C 251	94	6.6	766	7	CK973716	4104380 B	C 324	92.5	6.5	1029	9	CG211302	QG1DK33TV
C 252	94	6.6	781	3	CR641149	Tetraodon	C 325	92.5	6.5	1097	3	AK047780	Mus muscu
C 253	94	6.6	838	4	BI952373	HVSMEM000	C 326	92.5	6.5	3597	3	AK085684	Mus muscu
C 254	94	6.6	846	7	CK974254	4105208 B	C 327	92	6.4	452	2	AW013240	Sp190f W1
C 255	94	6.6	870	5	BU225793	603946725	C 328	92	6.4	643	9	CC478416	CH240 304
C 256	94	6.6	891	2	BF312847	601896991	C 329	92	6.4	649	4	BI955246	HVSMEM002
C 257	94	6.6	906	5	BU155418	AGENCOURT	C 330	92	6.4	667	1	AV910604	AV910604
C 258	94	6.6	912	5	BX334692	BX334692	C 331	92	6.4	682	3	CR648452	Tetraodon
C 259	94	6.6	934	5	BQ680655	AGENCOURT	C 332	92	6.4	686	8	B2415333	if54a12.9
C 260	94	6.6	934	5	BU179046	AGENCOURT	C 333	92	6.4	690	5	BQ257892	NISC kp07
C 261	94	6.6	1357	8	B2548495	pac21-60	C 334	92	6.4	693	2	BE216255	BE216255
C 262	94	6.6	2682	9	CL969033	OsiIFCC017	C 335	92	6.4	698	5	BU397697	603536254
C 263	94	6.6	3735	3	AK043669	Mus muscu	C 336	92	6.4	713	2	BF628666	BF628666
C 264	93.5	6.5	604	5	BU092442	AV6130F07	C 337	92	6.4	746	7	CO517983	3530 1 11
C 265	93.5	6.5	629	1	AV609635	AV609635	C 338	92	6.4	756	2	BF266955	HV_CEA001
C 266	93.5	6.5	712	4	BG328765	602427047	C 339	92	6.4	760	2	BF627589	HVSMEM000
C 267	93.5	6.5	774	4	BI762380	603049047	C 340	92	6.4	809	7	CO799872	AGENCOURT
C 268	93.5	6.5	837	5	BU329791	603494564	C 341	92	6.4	811	6	CA243740	SCQGF407
C 269	93.5	6.5	857	6	CB659131	OSJNEC15N	C 342	92	6.4	814	7	CF132151	UI-HF-F00
C 270	93.5	6.5	844	8	CC344924	OGTAN21TV	C 343	92	6.4	820	2	BF624789	HVSMEM001
C 271	93.5	6.5	861	4	BG751793	602730727	C 344	92	6.4	827	2	BF264782	HV_CEA001
C 272	93.5	6.5	866	8	BH702422	BOMMQ06TF	C 345	92	6.4	827	2	BF267532	HV_CEA001
C 273	93.5	6.5	889	6	CD358942	AGENCOURT	C 346	92	6.4	829	2	BF263229	HV_CEA000
C 274	93.5	6.5	892	2	BF623079	HVSMEM001	C 347	92	6.4	834	5	BX438268	BX438268
C 275	93.5	6.5	918	5	BU554267	AGENCOURT	C 348	92	6.4	900	5	BX357722	BX357722
C 276	93.5	6.5	975	5	BU197207	AGENCOURT	C 349	92	6.4	920	4	BM013414	603635165
C 277	93.5	6.5	1049	5	BM919417	AGENCOURT	C 350	92	6.4	922	2	BF066038	HV_CEB001
C 278	93.5	6.5	3153	9	CL982154	OsiIFC046	C 351	92	6.4	973	2	BE548456	601076021
C 279	93	6.5	594	2	BF090297	QV0-NN114	C 352	92	6.4	1117	2	BE620421	601483628
C 280	93	6.5	618	1	AL507561	AL507561	C 353	92	6.4	1219	8	BZ579066	msb2 6164
C 281	93	6.5	620	1	AV557154	AV557154	C 354	92	6.4	1252	4	BM555633	BM555633
C 282	93	6.5	626	6	CB840366	M15B-0844	C 355	92	6.4	2472	3	HSM804344	AGENCOURT
C 283	93	6.5	653	6	CB518630	UI-M-GH0-	C 356	91.5	6.4	481	2	BF702235	MI-P-A2-a
C 284	93	6.5	661	7	CK597927	AGENCOURT	C 357	91.5	6.4	538	2	BE759652	BB759652
C 285	93	6.5	670	7	CK266010	170005316	C 358	91.5	6.4	541	8	BZ580999	3590 1 36
C 286	93	6.5	677	4	BJ482168	BJ482168	C 359	91.5	6.4	568	6	CA624151	w11n.pk01
C 287	93	6.5	783	4	BM018953	603646907	C 360	91.5	6.4	595	6	CD661366	CD661366
C 288	93	6.5	797	5	BM009027	BM009027	C 361	91.5	6.4	619	4	BI134742	UI-M-BH3-
C 289	93	6.5	797	6	CB900781	tr1c024xd	C 362	91.5	6.4	634	7	CF115309	Shu1tzm01
C 290	93	6.5	797	7	CF870590	tr1c024xd	C 363	91.5	6.4	640	4	BI953782	HVSMEM001
C 291	93	6.5	797	7	CK776543	CK776543	C 364	91.5	6.4	660	8	BZ895801	NaRP2 019
C 292	93	6.5	831	2	BF628948	BF628948	C 365	91.5	6.4	663	6	CA320541	UI-M-FW0-
C 293	93	6.5	863	4	BI118103	BI118103	C 366	91.5	6.4	678	4	BI716214	1031007H0
C 294	93	6.5	886	5	BU186573	AGENCOURT	C 367	91.5	6.4	688	5	BU400273	603481274
C 295	93	6.5	887	4	BI655389	603285033	C 368	91.5	6.4	741	5	BX862108	BX862108
C 296	93	6.5	891	5	BQ690378	AGENCOURT	C 369	91.5	6.4	745	5	BE265787	BE265787
C 297	93	6.5	917	6	CA984114	AGENCOURT	C 370	91.5	6.4	773	9	CG198048	CG198048
C 298	93	6.5	960	5	BX423119	BX423119	C 371	91.5	6.4	786	9	CL980410	CL980410
C 299	93	6.5	972	9	CHS040VA	Tetraodon	C 372	91.5	6.4	876	8	CC332343	CC332343
C 300	93	6.5	992	7	CF880802	tr1c024xe	C 373	91.5	6.4	877	4	BG865243	BG865243
C 301	93	6.5	1077	8	BZ551827	pac21-60	C 374	91.5	6.4	877	9	CG259213	CG259213



C 375	91.5	6.4	908	4	BI150114	602849342	448	90.5	6.3	696	4	BM608888	170006870
376	91.5	6.4	931	3	AY106485	Zea mays	449	90.5	6.3	697	6	CB055230	NISC gm08
377	91.5	6.4	932	3	BM561466	AGENCOURT	C 450	90.5	6.3	711	6	CB322421	UI-R-DV0-
378	91.5	6.4	1063	5	BM903637	AGENCOURT	C 451	90.5	6.3	741	7	CN237338	RJB132C02
C 379	91.5	6.4	1095	3	BC006189	Mus muscu	452	90.5	6.3	754	7	CV114366	AGENCOURT
380	91.5	6.4	1182	3	AY108490	Zea mays	453	90.5	6.3	774	7	CO402970	AGENCOURT
C 381	91.5	6.4	1206	3	BC028330	Mus muscu	454	90.5	6.3	782	7	CO388439	AGENCOURT
382	91.5	6.4	1224	9	CL965137	OsIFCC011	455	90.5	6.3	786	4	BI767295	603057986
C 383	91.5	6.4	1501	3	CR617424	full-leng	456	90.5	6.3	818	7	CO554206	AGENCOURT
C 384	91.5	6.4	1550	3	CR601928	full-leng	457	90.5	6.3	822	7	CO395878	AGENCOURT
C 385	91.5	6.4	1868	3	BC012904	Homo sapi	458	90.5	6.3	829	7	CK731115	961720 MA
C 386	91.5	6.4	3750	9	AY414005	Mus muscu	459	90.5	6.3	847	4	BG541318	602569821
C 387	91	6.4	438	4	BM748764	K-EST0019	460	90.5	6.3	863	7	CO388794	AGENCOURT
C 388	91	6.4	499	6	CB878764	HP09L157	461	90.5	6.3	868	5	BX929045	BX929045
C 389	91	6.4	507	8	BZ580639	3590_1_39	462	90.5	6.3	871	5	BU123191	603003133
C 390	91	6.4	585	4	BM501813	952036C08	463	90.5	6.3	885	9	CG373673	CG4BK517C
C 391	91	6.4	615	4	BG369112	HVSMB1002	464	90.5	6.3	886	5	BQ882836	AGENCOURT
C 392	91	6.4	643	9	CG246867	OG0AB737H	C 465	90.5	6.3	906	2	AW982788	HVSMG9000
C 393	91	6.4	672	8	CK396334	PUHP171TB	466	90.5	6.3	916	4	BQ432053	AGENCOURT
C 394	91	6.4	687	7	CK975303	4106527 B	467	90.5	6.3	915	4	BG335095	602403573
C 395	91	6.4	690	7	CN161339	950622 MA	C 468	90.5	6.3	950	5	BQ641398	AGENCOURT
C 396	91	6.4	706	6	CA122120	SCJFIR107	C 469	90.5	6.3	963	9	CC631613	OGU8811TV
C 397	91	6.4	729	5	BX456257	BX456257	C 470	90.5	6.3	971	6	CA275555	SCBFS103
398	91	6.4	738	9	CG246859	OG0AB737H	C 471	90.5	6.3	974	5	BU540661	AGENCOURT
399	91	6.4	758	5	BU249423	603592154	C 472	90.5	6.3	986	3	CR694341	Tetraodon
400	91	6.4	779	6	CA512710	UI-R-FJ0-	473	90.5	6.3	999	5	BX334546	BX334546
401	91	6.4	795	9	CC734191	OGUME20TV	474	90.5	6.3	1056	5	BM922613	AGENCOURT
402	91	6.4	796	2	BF859402	963002C07	475	90.5	6.3	1070	9	CNS08R21	UI-R-DV0-
C 403	91	6.4	817	2	BF264482	HV_CEA000	476	90.5	6.3	1088	4	BM544272	AGENCOURT
C 404	91	6.4	836	9	CG247683	OGICV91TH	C 477	90.5	6.3	1089	9	CL944703	AGENCOURT
405	91	6.4	847	2	BE908929	601497867	478	90.5	6.3	1170	5	BQ896744	AGENCOURT
406	91	6.4	852	5	BQ890164	AGENCOURT	479	90.5	6.3	1214	2	B4222245	HWM022CA
407	91	6.4	856	7	CN162742	952158 MA	C 480	90.5	6.3	1303	8	BZ570288	msb2_1301
408	91	6.4	890	9	CG370784	OGYCH50TV	C 481	90.5	6.3	1464	3	CR653497	Tetraodon
409	91	6.4	898	9	CC680929	OGYAT35TH	C 482	90.5	6.3	1577	3	CR694327	Tetraodon
410	91	6.4	914	9	CG250633	CG3CK44TH	C 483	90.5	6.3	1623	3	AK043787	Mus muscu
411	91	6.4	920	7	CF580423	AGENCOURT	484	90.5	6.3	1717	3	CR620892	full-leng
C 412	91	6.4	964	4	BG023947	602303640	485	90.5	6.3	1774	4	BG743567	602633914
C 413	91	6.4	972	5	BQ619005	RNOSEQ2E1	C 486	90.5	6.3	1810	3	CR623164	full-leng
C 414	91	6.4	981	8	BZ570784	msb2_1534	C 487	90.5	6.3	1843	3	BC032475	Homo sapi
C 415	91	6.4	1005	9	CL970274	OsIFCC041	C 488	90.5	6.3	1894	3	CR621766	full-leng
416	91	6.4	1027	9	BM458216	AGENCOURT	C 489	90.5	6.3	2004	9	AY407914	Pan trogl
C 417	91	6.4	1039	5	BQ060881	AGENCOURT	C 490	90.5	6.3	2127	9	CL504232	SAIL 734
418	91	6.4	1103	4	BM558891	AGENCOURT	491	90.5	6.3	2730	3	AK030866	Mus muscu
419	91	6.4	1110	8	CG305860	CH261-113	C 492	90.5	6.3	3042	9	CL960537	OsIFCC004
420	91	6.4	1350	9	CL970977	OsIFCC020	C 493	90.5	6.3	7874	9	AY420498	Homo sapi
C 421	91	6.4	1476	3	CNSLTI1AK	human ful	C 494	90	6.3	505	5	BQ326397	CM3-CN009
C 422	91	6.4	1492	3	CR621008	full-leng	495	90	6.3	568	4	BI682896	464093 MA
C 423	91	6.4	1503	3	CR623408	full-leng	496	90	6.3	577	6	CB249755	UI-M-EX0-
C 424	91	6.4	1530	3	CNSLTI1AJ	human ful	497	90	6.3	582	5	BP297132	BP297132
C 425	91	6.4	1551	3	CNSLTI1AL	human ful	C 498	90	6.3	608	2	BE452946	894066H06
C 426	91	6.4	1574	3	CR616658	full-leng	C 499	90	6.3	611	2	BP251191	ESF418451
C 427	91	6.4	1630	3	CR623931	full-leng	C 500	90	6.3	627	9	CG348471	OGOCF72TV
C 428	91	6.4	1639	3	CR602316	full-leng	501	90	6.3	627	7	CN788353	4122685 B
C 429	91	6.4	1647	3	CR618931	full-leng	C 502	90	6.3	650	7	CN366219	170004706
C 430	91	6.4	1664	3	CR601083	full-leng	503	90	6.3	654	2	BF863865	963047C03
C 431	91	6.4	1763	3	CR626376	full-leng	504	90	6.3	677	7	CR655376	Tetraodon
C 432	91	6.4	1784	3	CNSLTI1AM	human ful	505	90	6.3	678	7	CN157469	946180 MA
C 433	91	6.4	1845	3	CR621976	full-leng	C 506	90	6.3	678	7	CN159412	948484 MA
434	91	6.4	2340	9	CL972081	OsIFCC022	507	90	6.3	679	3	CR649445	Tetraodon
C 435	91	6.4	2345	3	BC008814	Homo sapi	508	90	6.3	683	3	CR652460	Tetraodon
C 436	91	6.4	2348	3	BC062565	Homo sapi	509	90	6.3	684	3	CR642393	Tetraodon
C 437	91	6.4	2848	3	AK016522	Mus muscu	510	90	6.3	688	3	CR634043	Tetraodon
C 438	91	6.4	2994	9	CL972758	OsIFCC023	511	90	6.3	688	3	CR651789	Tetraodon
C 439	91	6.4	3051	3	CNS0ALP6	Arabidops	512	90	6.3	689	3	CR642553	Tetraodon
C 440	91	6.4	3231	3	AY724521	Rattus no	513	90	6.3	690	3	CR647097	Tetraodon
C 441	91	6.4	4930	3	CR749837	Homo sapi	514	90	6.3	690	3	CR647556	Tetraodon
C 442	90.5	6.3	615	7	CO513881	s13dSG73F	515	90	6.3	692	3	CR640044	Tetraodon
443	90.5	6.3	647	9	CM372673	CH240_449	516	90	6.3	694	3	CR637526	Tetraodon
C 444	90.5	6.3	651	4	BM388938	UI-R-D20-	517	90	6.3	694	3	CR645308	Tetraodon
C 445	90.5	6.3	657	5	BQ208529	UI-R-DX1-	518	90	6.3	694	3	CR652067	Tetraodon
C 446	90.5	6.3	666	6	CA225062	SCCAMP2C0	519	90	6.3	695	3	CR638115	Tetraodon
C 447	90.5	6.3	677	4	BI285583	UI-R-CW08	520	90	6.3	695	3	CR652304	Tetraodon

521	90	6.3	597	3	CR652825	Tetraodon	594	89.5	6.2	833	6	CB652492	OSJNEC021
522	90	6.3	707	6	CA283389	SCBGSD105	595	89.5	6.2	862	2	BF104612	BF104612
523	90	6.3	717	3	CR649811	Tetraodon	596	89.5	6.2	867	2	CO543777	LYS8T1143
524	90	6.3	730	3	CR650904	Tetraodon	c	89.5	6.2	870	5	BQ233203	AGENCOURT
525	90	6.3	737	8	AO631350	RPCI-11-4	598	89.5	6.2	886	5	BX424410	BX424410
526	90	6.3	748	9	CG664692	OGWEA07TV	599	89.5	6.2	893	9	CG338878	OGZBZ40TH
527	90	6.3	754	5	BU271251	603508354	600	89.5	6.2	911	2	BF692621	603248980
528	90	6.3	761	3	CR634795	Tetraodon	c	89.5	6.2	922	5	EX328285	EX328285
529	90	6.3	761	3	CR646944	Tetraodon	602	89.5	6.2	930	6	CNS0952K	AGENCOURT
530	90	6.3	762	3	CR644580	Tetraodon	603	89.5	6.2	930	6	CA976041	AGENCOURT
531	90	6.3	764	6	CB523440	UI-M-GH0-	604	89.5	6.2	953	4	BG443127	GA_Ea001
532	90	6.3	765	6	CB312195	AGENCOURT	c	89.5	6.2	956	6	BY716393	BY716393
533	90	6.3	766	2	BF265921	HV_CEA001	c	89.5	6.2	1042	6	CD507684	CD507684
534	90	6.3	768	7	CNI41776	WOUND1_1	607	89.5	6.2	1051	1	AL564056	AL564056
535	90	6.3	773	4	BI181855	603033078	608	89.5	6.2	1102	5	BM908109	BM908109
536	90	6.3	776	3	CR638058	Tetraodon	c	89.5	6.2	1128	6	CD498522	CD498522
537	90	6.3	777	3	CR638828	Tetraodon	610	89.5	6.2	1206	3	AK011926	AK011926
538	90	6.3	777	3	CR640383	Tetraodon	611	89.5	6.2	1423	9	CL460782	CL460782
539	90	6.3	777	7	CNI48568	WOUND1_57	c	89.5	6.2	1484	3	CR603169	full-lang
540	90	6.3	778	3	CR636585	Tetraodon	613	89.5	6.2	2198	3	AK038734	Mus muscu
541	90	6.3	781	3	CR638807	Tetraodon	614	89.5	6.2	3098	3	AK044016	Mus muscu
542	90	6.3	778	3	CR654110	Tetraodon	615	89.5	6.2	3127	3	AK084631	Mus muscu
543	90	6.3	779	3	CR649270	Tetraodon	616	89.5	6.2	3358	3	AK048691	Mus muscu
544	90	6.3	779	3	CR651938	Tetraodon	617	89	6.2	375	7	CN031190	UMC-PGYO2
545	90	6.3	782	3	CR636544	Tetraodon	618	89	6.2	405	7	CN300678	170006008
546	90	6.3	782	3	CR647795	Tetraodon	619	89	6.2	485	1	AL1634694	AL1634694
547	90	6.3	786	6	CR629660	OSIIEB06B	620	89	6.2	514	5	EX280101	EX280101
548	90	6.3	787	3	CR636642	Tetraodon	621	89	6.2	550	8	BZ580996	BZ580996
549	90	6.3	789	3	CR651423	Tetraodon	622	89	6.2	562	8	BZ917191	CH240_102
550	90	6.3	792	4	BI193608	Tetraodon	c	89	6.2	581	5	BP365751	BP365751
551	90	6.3	794	3	CR644935	Tetraodon	624	89	6.2	596	5	BQ463683	HG01B18r
552	90	6.3	794	3	CR646272	Tetraodon	c	89	6.2	606	9	AY408969	AY408969
553	90	6.3	794	3	CR649219	Tetraodon	626	89	6.2	609	4	BG705699	602668929
554	90	6.3	811	4	BG537371	Tetraodon	627	89	6.2	611	9	CS526396	CH240_401
555	90	6.3	820	7	CO883041	BoVGen_11	c	89	6.2	616	6	CB878361	HP08E09T
556	90	6.3	822	7	CR348885	Tetraodon	c	89	6.2	620	5	BQ468275	HP01K22T
557	90	6.3	856	4	BI768085	Tetraodon	630	89	6.2	621	7	CN481338	hw06d04.Y
558	90	6.3	880	9	CS522797	Tetraodon	c	89	6.2	631	1	AY924399	AY924399
559	90	6.3	886	7	CV212131	EST871841	c	89	6.2	634	6	CB877867	HP06H12T
560	90	6.3	932	4	BI771877	603055278	c	89	6.2	635	6	CB879862	HP02P01T
561	90	6.3	935	2	BF533003	Tetraodon	c	89	6.2	637	6	CB877021	HP03E14T
562	90	6.3	953	6	BY717668	Tetraodon	c	89	6.2	648	9	CL156955	CL156955
563	90	6.3	979	5	BQ961288	AGENCOURT	636	89	6.2	654	7	CF789740	CF789740
564	90	6.3	1044	5	BA424076	AGENCOURT	c	89	6.2	665	4	BG280961	BG280961
565	90	6.3	1139	8	BZ563497	pacs2-164	638	89	6.2	667	9	CS559311	CH240_468
566	90	6.3	1179	2	BF307229	601891393	639	89	6.2	668	2	BE949497	UI-M-CO-
567	90	6.3	2485	3	BC023209	Homo sapi	c	89	6.2	695	2	BF621894	HVSMEa000
568	90	6.3	3295	3	BC029348	Homo sapi	641	89	6.2	714	3	CR646145	Tetraodon
569	90	6.3	3365	3	BSM803244	Homo sapi	c	89	6.2	716	7	CN135400	CN135400
570	89.5	6.2	491	1	AA424076	AGENCOURT	c	89	6.2	728	7	BE519877	HV_CEB002
571	89.5	6.2	549	1	AI807514	wf48f05.x	644	89	6.2	730	2	BE519877	CS_hyp_45
572	89.5	6.2	573	8	BZ310697	ic57d08.b	645	89	6.2	730	2	BE274037	601104335
573	89.5	6.2	576	2	BE357931	DG1_23_E0	c	89	6.2	748	7	CN139561	Ox1_22_G0
574	89.5	6.2	581	9	CG674595	OGWCUT9TH	647	89	6.2	764	5	BU595554	BU595554
575	89.5	6.2	589	4	BJ769002	BJ769002	648	89	6.2	765	4	BI836384	BI836384
576	89.5	6.2	589	4	BJ806535	BJ806535	c	89	6.2	765	7	CN134141	603082901
577	89.5	6.2	662	9	CE171457	tigr-g88-	c	89	6.2	766	7	CN138735	Ox1_13_D0
578	89.5	6.2	664	1	AV609758	AV609758	c	89	6.2	780	8	BZ577903	mh2_5629
579	89.5	6.2	670	9	CS533360	CH240_412	c	89	6.2	784	9	CG017514	ZUACH49TV
580	89.5	6.2	674	9	CS572653	CH240_449	c	89	6.2	799	4	BI772181	603056121
581	89.5	6.2	675	4	BI955087	HVSMEM002	654	89	6.2	803	9	CG318499	CG318499
582	89.5	6.2	689	7	CN134142	Ox1_20_B0	c	89	6.2	806	9	CL301193	CL301193
583	89.5	6.2	695	7	CN133695	Ox1_17_F0	c	89	6.2	819	9	CC482572	CH240_311
584	89.5	6.2	707	8	AZ569578	262FvH05	657	89	6.2	823	5	BQ425155	AGENCOURT
585	89.5	6.2	732	7	CNO60788	A06_Ag2_P	c	89	6.2	827	2	BF623285	BF623285
586	89.5	6.2	733	7	CK433144	UI-D-GC1	c	89	6.2	832	4	BI949179	BI949179
587	89.5	6.2	796	4	BG911734	602808202	c	89	6.2	837	4	BG571235	BG571235
588	89.5	6.2	796	9	CC690766	OGUKB63TH	c	89	6.2	839	2	BF262287	BF262287
589	89.5	6.2	797	6	CB650217	OSJNEB141	c	89	6.2	844	9	CL526997	CL526997
590	89.5	6.2	801	4	BG367903	HVSMEL1001	c	89	6.2	856	4	BI952488	BI952488
591	89.5	6.2	820	8	BZ655107	OGCCS57TM	664	89	6.2	858	7	CN163976	CN163976
592	89.5	6.2	825	5	BM944207	UI-M-HOP	c	89	6.2	869	2	BF033230	BF033230
593	89.5	6.2	830	6	CB630998	OSIIEB08E	c	89	6.2	869	4	BG968296	BG968296

C 667	89	6.2	870	5	BX336730	BX336730	BX336730	740	88.5	6.2	1803	3	AK009709	Mus muscu
C 668	89	6.2	878	8	CG337734	OGPBE18TH	C 741	88.5	6.2	1884	9	CI487289	CI487289	
C 669	89	6.2	880	4	BI550580	603197628	C 742	88.5	6.2	2327	7	CV068994	F2_new_ch	
C 670	89	6.2	891	5	BUL61097	BUL61097	C 743	88.5	6.2	2538	9	CU980030	OSIFCC034	
C 671	89	6.2	891	7	CV069595	WPAEHUX15	C 744	88.5	6.2	3454	3	AK028441	Mus muscu	
C 672	89	6.2	892	5	BQ441122	AGENCOURT	C 745	88.5	6.2	5262	9	CL967637	OSIFCC015	
C 673	89	6.2	909	5	BQ894222	BQ894222	C 746	88.5	6.2	10655	3	AK090136	Mus muscu	
C 674	89	6.2	923	9	CG702023	OGGAC07TM	C 747	88	6.1	388	2	BF441044	257154 MA	
C 675	89	6.2	937	8	BZ561320	pac82-164	C 748	88	6.1	463	2	BF063267	7h87c12.x	
C 676	89	6.2	940	4	BI770311	603056215	C 749	88	6.1	463	2	BI057918	PM4-GN049	
C 677	89	6.2	947	8	BZ571199	msh2_1773	C 750	88	6.1	575	6	CA186190	SCSGT311	
C 678	89	6.2	968	9	CG881640	ZMMEB049	C 751	88	6.1	579	4	BI407794	602919167	
C 679	89	6.2	977	5	BX327801	BX327801	C 752	88	6.1	595	5	BU648465	111206900	
C 680	89	6.2	990	8	BZ564269	pac82-164	C 753	88	6.1	597	6	CD887832	G118_106G	
C 681	89	6.2	1006	4	BG425099	602452679	C 754	88	6.1	620	4	EG300930	HVSNEM001	
C 682	89	6.2	1032	6	CD105894	AGENCOURT	C 755	88	6.1	630	4	BM601221	170006870	
C 683	89	6.2	1051	2	BF384507	602046471	C 756	88	6.1	631	4	BJ453452	BJ453452	
C 684	89	6.2	1078	8	BZ563432	pac82-164	C 757	88	6.1	632	1	AA511080	vh61d05_r	
C 685	89	6.2	1107	5	BX377454	BX377454	C 758	88	6.1	635	6	CD898877	G174_110F	
C 686	89	6.2	1119	5	BQ681628	AGENCOURT	C 759	88	6.1	638	4	BI953729	HVSNEM001	
C 687	89	6.2	1128	8	BZ558882	pac82-164	C 760	88	6.1	638	6	CD898686	G174_109M	
C 688	89	6.2	1165	8	BZ562536	pac82-164	C 761	88	6.1	643	6	CD886350	G118_102B	
C 689	89	6.2	1168	4	BI951926	HVSNEM000	C 762	88	6.1	655	7	CK979040	4110528 B	
C 690	89	6.2	1211	5	BH510035	AGENCOURT	C 763	88	6.1	660	5	BU647624	1112060A0	
C 691	89	6.2	1220	3	CR662193	Tetraodon	C 764	88	6.1	669	7	CV434385	CS_hyp_33	
C 692	89	6.2	1221	5	BM926108	AGENCOURT	C 765	88	6.1	671	5	BM114846	BX114846	
C 693	89	6.2	1267	3	CG677011	Tetraodon	C 766	88	6.1	672	5	BM949540	UI-M-EGOP	
C 694	89	6.2	1361	8	BZ580081	msh2_928	C 767	88	6.1	673	6	CA118767	SCBGLR111	
C 695	89	6.2	1409	3	CR727990	Tetraodon	C 768	88	6.1	685	8	BZ872430	CH240_192	
C 696	89	6.2	1616	9	AG075498	Pan trogl	C 769	88	6.1	685	9	CC562085	CH240_472	
C 697	89	6.2	1820	9	AY415784	Mus muscu	C 770	88	6.1	690	3	CR656616	Tetraodon	
C 698	89	6.2	2759	3	BC029313	BC029313	C 771	88	6.1	695	7	CK581028	IST_W15_3	
C 699	89	6.2	3270	3	BC035457	BC035457	C 772	88	6.1	702	5	BM445000	BM445000	
C 700	88.5	6.2	573	4	BJ104203	BJ104203	C 773	88	6.1	708	7	CV303090	CS_hyp_28	
C 701	88.5	6.2	590	9	CG302675	CG302675	C 774	88	6.1	710	3	CR654957	Tetraodon	
C 702	88.5	6.2	600	4	BI799827	BI799827	C 775	88	6.1	711	7	CN149436	WOUNDI_62	
C 703	88.5	6.2	623	8	BZ885549	CH240_244	C 776	88	6.1	711	7	CV463384	CS_hyp_57	
C 704	88.5	6.2	628	7	CO662703	CO662703	C 777	88	6.1	718	5	BM444963	BM444963	
C 705	88.5	6.2	678	7	CV479788	CS_hyp_40	C 778	88	6.1	742	4	EG177866	602314277	
C 706	88.5	6.2	694	7	CN133843	CN133843	C 779	88	6.1	764	9	CM506871	OP_Ba000	
C 707	88.5	6.2	768	8	BH529737	BH529737	C 780	88	6.1	765	4	BU583378	BU583378	
C 708	88.5	6.2	783	8	BH564792	BH564792	C 781	88	6.1	793	7	CK193516	CK193516	
C 709	88.5	6.2	792	4	BM046604	BM046604	C 782	88	6.1	796	6	CA214548	SCSPSB110	
C 710	88.5	6.2	800	8	BZ574638	BZ574638	C 783	88	6.1	802	7	CO063690	est_k_bre	
C 711	88.5	6.2	812	4	BG417631	BG417631	C 784	88	6.1	815	2	BF267926	HV_CEA001	
C 712	88.5	6.2	831	7	CK635363	CK635363	C 785	88	6.1	818	9	CG281398	OGWFE03TV	
C 713	88.5	6.2	841	4	BI258457	BI258457	C 786	88	6.1	824	4	EG345164	HVSNEM001	
C 714	88.5	6.2	843	2	BF264360	BF264360	C 787	88	6.1	825	2	BF267638	HV_CEA001	
C 715	88.5	6.2	849	4	BG751460	BG751460	C 788	88	6.1	825	9	CG324936	OG0BJ87TV	
C 716	88.5	6.2	877	4	BM015034	BM015034	C 789	88	6.1	847	8	BZ863664	CH240_210	
C 717	88.5	6.2	885	2	BE747335	BE747335	C 790	88	6.1	864	8	BZ559802	pac82-164	
C 718	88.5	6.2	888	4	BF984969	BF984969	C 791	88	6.1	871	6	CB960458	AGENCOURT	
C 719	88.5	6.2	888	5	BQ687705	BQ687705	C 792	88	6.1	894	4	BF979661	602287964	
C 720	88.5	6.2	894	5	BQ685576	BQ685576	C 793	88	6.1	909	5	BQ956203	AGENCOURT	
C 721	88.5	6.2	899	4	BI909673	BI909673	C 794	88	6.1	916	9	CG281070	OG3AU02TH	
C 722	88.5	6.2	906	9	CL963217	CL963217	C 795	88	6.1	926	9	CC625298	OGUKO53TV	
C 723	88.5	6.2	915	6	CB589793	CB589793	C 796	88	6.1	929	5	BU528425	AGENCOURT	
C 724	88.5	6.2	932	9	CG649322	CG649322	C 797	88	6.1	930	4	BI519339	AGENCOURT	
C 725	88.5	6.2	950	8	BZ549147	pac81-60	C 798	88	6.1	942	4	EG030352	602297468	
C 726	88.5	6.2	951	9	CNS060JOY	AL421289 T7 end of	C 799	88	6.1	972	5	EX375933	EX375933	
C 727	88.5	6.2	956	5	BU503920	AGENCOURT	C 800	88	6.1	977	8	CC199125	ZMMEB0332	
C 728	88.5	6.2	970	2	BE792500	BE792500	C 801	88	6.1	991	9	CNS03MTR	AL251208 Tetraodon	
C 729	88.5	6.2	999	9	CL949374	CL949374	C 802	88	6.1	992	5	BM404307	BM404307	
C 730	88.5	6.2	1000	1	AL524279	AL524279	C 803	88	6.1	1042	7	CK211974	FGAS02383	
C 731	88.5	6.2	1012	5	BU146208	BU146208	C 804	88	6.1	1062	4	BI410932	BI410932	
C 732	88.5	6.2	1023	5	EX438826	EX438826	C 805	88	6.1	1098	5	BQ880280	AGENCOURT	
C 733	88.5	6.2	1029	5	BM919894	BM919894	C 806	88	6.1	1101	3	CR623119	CR623119	
C 734	88.5	6.2	1037	4	BG519654	BG519654	C 807	88	6.1	1136	5	BU163413	AGENCOURT	
C 735	88.5	6.2	1044	3	AK020150	AK020150	C 808	88	6.1	1202	3	CR725876	Tetraodon	
C 736	88.5	6.2	1046	5	BQ056949	BQ056949	C 809	88	6.1	1226	4	BI411327	602964426	
C 737	88.5	6.2	1076	5	BX359507	BX359507	C 810	88	6.1	1234	5	BU856206	AGENCOURT	
C 738	88.5	6.2	1158	2	BF578719	BF578719	C 811	88	6.1	1262	8	BZ578229	msh2_5755	
C 739	88.5	6.2	1724	3	AK077751	AK077751	C 812	88	6.1	1276	2	BF337756	602037535	

C 813	88	6.1	1452	9	CL968968	886	87.5	6.1	2901	3	AK031120	AK031120 Mus muscu
C 814	88	6.1	1462	4	BG032875	887	87.5	6.1	3104	3	AK044719	AK044719 Mus muscu
C 815	88	6.1	1535	9	AG065661	888	87.5	6.1	3251	3	AK039337	AK039337 Mus muscu
C 816	88	6.1	1578	9	CL945954	889	87	6.1	402	5	BX102955	BX102955 BX102955
C 817	88	6.1	2253	9	CL980455	890	87	6.1	409	5	CG045303	CG045303 PUGBW66TB
C 818	87.5	6.1	503	8	BZ781911	891	87	6.1	413	5	BP614180	BP614180 BP614180
C 819	87.5	6.1	538	4	BM258866	892	87	6.1	478	1	AI620687	AI620687 tu85g02.x
C 820	87.5	6.1	597	9	CE056928	893	87	6.1	564	5	BP742257	BP742257 BP742257
C 821	87.5	6.1	614	4	BJ096164	894	87	6.1	597	8	CN788819	CN788819 4123196 B
C 822	87.5	6.1	636	9	CE050464	895	87	6.1	597	8	AG689304	AG689304 nbxb0079C
C 823	87.5	6.1	641	5	BP766024	896	87	6.1	599	4	CF940161	CF940161 NESTTgab3
C 824	87.5	6.1	650	2	BE360349	897	87	6.1	600	4	BI986557	BI986557 3173-24 M
C 825	87.5	6.1	656	5	BZ287394	898	87	6.1	604	9	CL743745	CL743745 OR_BBA008
C 826	87.5	6.1	667	4	BD779634	899	87	6.1	611	4	BG300690	BG300690 HVSMED001
C 827	87.5	6.1	671	6	CD761542	900	87	6.1	616	4	BM669774	BM669774 UI-B-DX1-
C 828	87.5	6.1	674	6	CA070113	901	87	6.1	622	9	CC473143	CC473143 CH240_297
C 829	87.5	6.1	683	7	CN848704	902	87	6.1	624	9	CN134980	CN134980 OX1_25_F1
C 830	87.5	6.1	684	7	CN133868	903	87	6.1	631	6	CD442675	CD442675 EL01N0414
C 831	87.5	6.1	697	9	CG958668	904	87	6.1	651	5	BQ257103	BQ257103 NISC.k010
C 832	87.5	6.1	712	5	BQ865793	905	87	6.1	651	5	CK972541	CK972541 4103395 B
C 833	87.5	6.1	716	6	CB247533	906	87	6.1	655	2	AM757596	AM757596 874002D01
C 834	87.5	6.1	719	8	BZ858386	907	87	6.1	655	4	BI959218	BI959218 HVSMEN001
C 835	87.5	6.1	721	6	CA212718	908	87	6.1	665	4	BI765133	BI765133 603051356
C 836	87.5	6.1	724	4	BI908181	909	87	6.1	667	7	CK982658	CK982658 4115240 B
C 837	87.5	6.1	736	8	BZ634998	910	87	6.1	679	4	BI939098	BI939098 p9pln.pk0
C 838	87.5	6.1	746	5	BP139755	911	87	6.1	679	7	CK947889	CK947889 4072576 B
C 839	87.5	6.1	755	4	BI836321	912	87	6.1	679	7	CN853814	CN853814 Ha.mx0_17
C 840	87.5	6.1	762	4	BI768197	913	87	6.1	683	9	CG436783	CG436783 OGVGM35TH
C 841	87.5	6.1	765	4	BG765688	914	87	6.1	688	6	CA156029	CA156029 SCBPR2300
C 842	87.5	6.1	766	4	BI149125	915	87	6.1	705	3	CF648705	CF648705 Tetraodon
C 843	87.5	6.1	775	9	CNS02852	916	87	6.1	706	7	CN144154	CN144154 WOUND1_20
C 844	87.5	6.1	776	5	BU408345	917	87	6.1	729	6	CA231656	CA231656 SCQSF1303
C 845	87.5	6.1	785	8	BH383930	918	87	6.1	730	8	BZ520704	BZ520704 BOMQ32TR
C 846	87.5	6.1	788	9	CG631607	919	87	6.1	731	5	CN150983	CN150983 WOUND1_72
C 847	87.5	6.1	796	9	CG244005	920	87	6.1	731	5	BX922736	BX922736 BX922736
C 848	87.5	6.1	800	7	C0386693	921	87	6.1	749	7	CN137496	CN137496 OX1_57_E0
C 849	87.5	6.1	803	4	BI770839	922	87	6.1	760	7	CN134678	CN134678 OX1_27_F1
C 850	87.5	6.1	840	9	CG514203	923	87	6.1	762	2	BF265661	BF265661 HV_CEA001
C 851	87.5	6.1	854	5	BU171653	924	87	6.1	763	6	CA237471	CA237471 SCRFEL504
C 852	87.5	6.1	862	8	BZ799254	925	87	6.1	769	9	CG436790	CG436790 OGVGM35TV
C 853	87.5	6.1	868	2	BZ788300	926	87	6.1	769	8	BZ458224	BZ458224 BONGV25TF
C 854	87.5	6.1	868	6	CA291678	927	87	6.1	772	7	CN132717	CN132717 OX1_7_F10
C 855	87.5	6.1	885	6	CD244547	928	87	6.1	778	7	CN144331	CN144331 WOUND1_21
C 856	87.5	6.1	887	5	BQ731339	929	87	6.1	785	3	CR641779	CR641779 Tetraodon
C 857	87.5	6.1	898	9	CG333766	930	87	6.1	788	3	CR644268	CR644268 Tetraodon
C 858	87.5	6.1	902	8	CG376684	931	87	6.1	791	8	BZ853044	BZ853044 CH240_253
C 859	87.5	6.1	907	7	CF593730	932	87	6.1	832	9	CP752360	CP752360 om_1000_9
C 860	87.5	6.1	908	5	BQ45604	933	87	6.1	841	9	CG630803	CG630803 OGVST88TH
C 861	87.5	6.1	909	2	BE797774	934	87	6.1	846	6	CB995082	CB995082 AGENCOURT
C 862	87.5	6.1	920	2	CG683070	935	87	6.1	849	9	CG674894	CG674894 tr82626 t
C 863	87.5	6.1	930	2	BE732984	936	87	6.1	851	8	BZ704179	BZ704179 PUCDR94TD
C 864	87.5	6.1	938	9	CG445765	937	87	6.1	856	5	BX916091	BX916091 BX916091
C 865	87.5	6.1	939	2	BF300876	938	87	6.1	872	6	CD050939	CD050939 AGENCOURT
C 866	87.5	6.1	940	8	BZ556971	939	87	6.1	887	7	CF585066	CF585066 SCJPLA10
C 867	87.5	6.1	948	9	CG665915	940	87	6.1	887	6	CA253395	CA253395 AGENCOURT
C 868	87.5	6.1	1012	4	BM550191	941	87	6.1	888	4	BG682602	BG682602 602626737
C 869	87.5	6.1	1015	5	BQ888762	942	87	6.1	891	2	BF663980	BF663980 602145649
C 870	87.5	6.1	1024	5	BQ058226	943	87	6.1	894	4	BF6762140	BF6762140 602717727
C 871	87.5	6.1	1037	5	BQ900677	944	87	6.1	928	5	BX396548	BX396548 BX396548
C 872	87.5	6.1	1059	9	CL991800	945	87	6.1	929	9	CG117193	CG117193 PUKAT53TD
C 873	87.5	6.1	1061	5	CNS03290	946	87	6.1	933	9	CG297832	CG297832 OGI8187TV
C 874	87.5	6.1	1067	5	BM920114	947	87	6.1	950	5	BQ918792	BQ918792 AGENCOURT
C 875	87.5	6.1	1135	4	BM803335	948	87	6.1	953	5	BX336948	BX336948 BX336948
C 876	87.5	6.1	1174	5	BM914761	949	87	6.1	960	5	BM903732	BM903732 AGENCOURT
C 877	87.5	6.1	1311	3	CR607553	950	87	6.1	973	5	BQ073527	BQ073527 AGENCOURT
C 878	87.5	6.1	1419	9	CL973598	951	87	6.1	996	9	CL961407	CL961407 OGI8187TV
C 879	87.5	6.1	1479	4	BG862470	952	87	6.1	1029	4	BM544473	BM544473 AGENCOURT
C 880	87.5	6.1	1479	9	AG356852	953	87	6.1	1031	5	BUS02796	BUS02796 AGENCOURT
C 881	87.5	6.1	1510	9	AG356852	954	87	6.1	1045	5	CL471991	CL471991 SAIL_171
C 882	87.5	6.1	1524	3	AK077719	955	87	6.1	1072	5	BQ217632	BQ217632 AGENCOURT
C 883	87.5	6.1	1670	4	BF975317	956	87	6.1	1073	1	AL519958	AL519958 AL519958
C 884	87.5	6.1	2259	9	CL965071	957	87	6.1	1098	5	BUS27314	BUS27314 AGENCOURT
C 885	87.5	6.1	2305	3	BC044627	958	87	6.1	1122	6	CD507271	CD507271 CDA84-A03

c 959	87	6.1	1257	9	AG066326	Pan trogl	AG066326	1403	9	AG186950	AG186950	Pan trogl
960	87	6.1	1337	7	COG35720	AGENT9292	COG35720	1563	3	CNS0A6QF	CNS0A6QF	Arabidops
961	87	6.1	1360	4	BM552690	AGENCOURT	BM552690	1679	3	AK011229	AK011229	Mus muscu
962	87	6.1	1414	3	CR643446	Tetraodon	CR643446	1823	3	CR633902	CR633902	Tetraodon
963	87	6.1	1506	9	CL961254	ObiFCC005	CL961254	1870	9	CG758664	CG758664	P051-4-D0
c 964	87	6.1	1733	3	BC024308	Homo sapi	BC024308	1923	9	CL979626	CL979626	ObiFCC033
c 965	87	6.1	1811	5	BU103687	SCEQRT102	BU103687	1933	7	CO635679	CO635679	Contig276
c 966	87	6.1	2841	3	AK044765	Mus muscu	AK044765	2415	9	CL944530	CL944530	ObiFSCB004
c 967	87	6.1	3167	3	BC024102	Homo sapi	BC024102	3289	3	AK029933	AK029933	Mus muscu
c 968	87	6.1	3860	3	CR749395	Homo sapi	CR749395	3791	9	AY400807	AY400807	Pan trogl
c 969	87	6.1	6285	3	CR749818	Homo sapi	CR749818	3823	3	AK031712	AK031712	Mus muscu
c 970	86.5	6.0	369	7	CK342275	K0418D05-	CK342275	3947	3	BC048169	BC048169	Mus muscu
c 971	86.5	6.0	404	4	BG945069	RC6-AN006	BG945069	299	1	AA622698	AA622698	np36509..B
c 972	86.5	6.0	491	4	BM255549	517317 MA	BM255549	409	5	BY419748	BY419748	BY419748
c 973	86.5	6.0	514	6	CD051515	d8159 P	CD051515	434	7	AA188733	AA188733	3D78C07..X
c 974	86.5	6.0	541	6	CA830804	1117009C1	CA830804	434	7	CK465159	CK465159	936237 MA
c 975	86.5	6.0	542	4	BU121236	BU121236	BU121236	434	7	CK467257	CK467257	938541 MA
c 976	86.5	6.0	548	7	CO219787	WS0107..B2	CO219787	469	6	CA616905	CA616905	w11n.pk00
c 977	86.5	6.0	573	5	BP214058	BP214058	BP214058	486	6	CB726880	CB726880	AMGNNUC:N
c 978	86.5	6.0	595	2	BF622001	HVSMEA000	BF622001	493	1	AV396713	AV396713	AV396713
c 979	86.5	6.0	600	9	CT767568	CH240_134	CT767568	520	4	BI5339757	BI5339757	452547 MA
c 980	86.5	6.0	605	6	CB469226	sn04_G10.	CB469226	520	9	CW011396	CW011396	ZMBELC000
c 981	86.5	6.0	617	9	CW012740	ZMBELC000	CW012740	561	7	CR287289	CR287289	CR287289
c 982	86.5	6.0	638	4	BI873687	963110E05	BI873687	561	8	BZ866306	BZ866306	CH240_235
c 983	86.5	6.0	638	7	CO517169	813GSG33D	CO517169	566	5	BU579630	BU579630	im88C01..X
c 984	86.5	6.0	647	7	CN141013	OX1_48..F1	CN141013	579	1	AV592949	AV592949	AV592949
c 985	86.5	6.0	670	5	BP460698	BP460698	BP460698	594	1	AI655373	AI655373	1898A09..X
c 986	86.5	6.0	670	7	CN217818	RJA018F09	CN217818	600	4	BI340290	BI340290	365514 MA
c 987	86.5	6.0	684	8	BZ395719	EINEBO16TR	BZ395719	605	5	BU619355	BU619355	UI-H-FU1-
c 988	86.5	6.0	690	4	BM684639	UI-E-EO1-	BM684639	605	8	BZ832394	BZ832394	CH240_222
c 989	86.5	6.0	699	7	CR835304	4059703 B	CR835304	609	5	BU644968	BU644968	mgn8017XM
c 990	86.5	6.0	699	7	CN220142	WLA013D03	CN220142	616	5	BU571866	BU571866	946185F12
c 991	86.5	6.0	705	2	BZ214076	HV..CEB000	BZ214076	623	9	CC489668	CC489668	CH240_322
c 992	86.5	6.0	712	8	BM528091	OGAJR28TM	BM528091	625	2	BE532956	BE532956	601232369
c 993	86.5	6.0	715	5	BM943102	UI-N-CG0P	BM943102	626	4	BI910072	BI910072	603067905
c 994	86.5	6.0	720	7	CK782207	UI-N-HJ0-	CK782207	636	8	BZ832152	BZ832152	CH240_234
c 995	86.5	6.0	725	9	CN432579	BE030002A	CN432579	641	9	CC762973	CC762973	CH240_3E1
c 996	86.5	6.0	728	9	CG198051	PU1AY67TD	CG198051	644	9	CC563308	CC563308	CH240_474
c 997	86.5	6.0	729	9	CC630762	OGUIG71TV	CC630762	644	4	BM001090	BM001090	103105380
c 998	86.5	6.0	730	7	CO217178	WS0047..B2	CO217178	656	9	CR831075	CR831075	GR0AAA3C
c 999	86.5	6.0	731	9	CC569846	CH240_445	CC569846	658	3	CR648458	CR648458	HVSAG001
1000	86.5	6.0	732	5	BM950513	UI-N-EHOP	BM950513	677	5	BM973798	BM973798	UI-CF-EC1
c1001	86.5	6.0	734	6	CA468398	AGENCOURT	CA468398	681	9	CC500845	CC500845	CH240_338
1002	86.5	6.0	734	7	CN225286	WLA069H10	CN225286	682	2	BE280853	BE280853	601155421
1003	86.5	6.0	737	6	CD370199	UI-H-FU1-	CD370199	685	9	CC589126	CC589126	CH240_387
1004	86.5	6.0	766	7	CO740445	S1LL07827	CO740445	691	7	CN137459	CN137459	OX1_57..A0
c1005	86.5	6.0	773	4	BM008340	603617316	BM008340	692	4	BI252769	BI252769	602952833
1006	86.5	6.0	776	5	BU122625	603149251	BU122625	694	7	CN140375	CN140375	OX1_35..F0
1007	86.5	6.0	791	5	BX352322	BX352322	BX352322	694	9	CC564280	CC564280	CH240_475
1008	86.5	6.0	798	6	CF066352	AC3912..AM	CF066352	694	9	CC564280	CC564280	CH240_475
c1009	86.5	6.0	801	7	CN148437	WOUND1_56	CN148437	695	7	CN149557	CN149557	WOUND1_63
1010	86.5	6.0	819	7	CP745353	UI-N-GV0-	CP745353	698	7	CN145724	CN145724	WOUND1_34
1011	86.5	6.0	824	6	CD439604	EL01N0526	CD439604	698	9	CL154052	CL154052	104_338..1
1012	86.5	6.0	830	6	CB670497	OSUNEEO3J	CB670497	702	9	CC585519	CC585519	CH240_382
c1013	86.5	6.0	864	6	CL109938	AGENCOURT	CL109938	703	4	BU167897	BU167897	BJ167897
1014	86.5	6.0	867	9	CL415688	ZMBBB042	CL415688	705	9	CC587560	CC587560	CH240_385
1015	86.5	6.0	894	6	CA185212	SCS8ST309	CA185212	707	7	CN139895	CN139895	OX1_24..G0
1016	86.5	6.0	895	5	BQ232886	AGENCOURT	BQ232886	707	7	CN140336	CN140336	OX1_35..C0
1017	86.5	6.0	925	5	BQ883149	AGENCOURT	BQ883149	707	7	CN399921	CN399921	170005321
c1018	86.5	6.0	925	2	BQ960337	AGENCOURT	BQ960337	711	7	CN147983	CN147983	WOUND1_53
1019	86.5	6.0	926	2	BE970559	601679765	BE970559	713	4	BG678096	BG678096	602625839
1020	86.5	6.0	926	6	CB204967	AGENCOURT	CB204967	713	8	BZ887660	BZ887660	CH240_221
1021	86.5	6.0	930	1	AL5566821	AL5566821	AL5566821	714	7	CR559093	CR559093	DKZP2468J
1022	86.5	6.0	963	9	CL970133	ObiFCC019	CL970133	716	7	CN146525	CN146525	WOUND1_41
c1023	86.5	6.0	972	5	BQ925595	AGENCOURT	BQ925595	716	1	AA983446	AA983446	oq69b06..B
1024	86.5	6.0	976	7	CF546891	AGENCOURT	CF546891	719	7	CN144341	CN144341	WOUND1_21
c1025	86.5	6.0	1020	9	CL018874	CH216-4D1	CL018874	724	9	CC554192	CC554192	CH240_460
1026	86.5	6.0	1023	5	BQ680487	AGENCOURT	BQ680487	725	7	CN138867	CN138867	OX1_14..B1
c1027	86.5	6.0	1080	5	BX334929	BX334929	BX334929	726	7	CN147855	CN147855	WOUND1_52
1028	86.5	6.0	1085	4	BM805302	AGENCOURT	BM805302	726	7	CN143327	CN143327	WOUND1_15
1029	86.5	6.0	1121	6	CB995357	AGENCOURT	CB995357	726	9	CC592505	CC592505	CH240_393
c1030	86.5	6.0	1161	8	BZ579434	msH2_6353	BZ579434	730	6	CA158440	CA158440	SCEZR2309
1031	86.5	6.0	1238	9	CG746469	P039-3-H0	CG746469					

1105	86	6.0	732	4	BJ171151	BJ171151	BJ171151	86	6.0	816	7	CN134585	CN134585	OX1_27_F0
1106	86	6.0	733	9	CS586672	CS586672	CH240_384	86	6.0	816	9	CC589396	CC589396	CH240_388
1107	86	6.0	734	9	CS509659	CS509659	CH240_352	86	6.0	818	4	BG702456	BG702456	602684518
1108	86	6.0	735	9	CE221501	CE221501	tigr-G8a-	86	6.0	819	7	CK791519	CK791519	AGENCOURT
1109	86	6.0	735	9	CN148623	CN148623	WOUND1_57	86	6.0	824	7	CN140221	CN140221	OX1_34_G0
1110	86	6.0	735	7	CN151158	CN151158	WOUND1_73	86	6.0	826	7	CK794617	CK794617	AGENCOURT
1111	86	6.0	738	5	BQ45468	BQ45468	UI-CF-ENI	86	6.0	832	9	CC536103	CC536103	CH240_415
1112	86	6.0	738	7	CN147720	CN147720	WOUND1_51	86	6.0	834	7	CN148634	CN148634	WOUND1_57
1113	86	6.0	739	7	CN148459	CN148459	WOUND1_56	86	6.0	837	7	CN152355	CN152355	WOUND1_81
1114	86	6.0	740	7	CN147623	CN147623	WOUND1_50	86	6.0	841	7	CN148754	CN148754	WOUND1_58
1115	86	6.0	741	7	CN148202	CN148202	WOUND1_54	86	6.0	841	9	CG367567	CG367567	QGXBH14TH
1116	86	6.0	741	7	CN150970	CN150970	WOUND1_72	86	6.0	842	7	CK193475	CK193475	FGAS00188
1117	86	6.0	742	1	AUI32766	AUI32766	AUI32766	86	6.0	842	9	CG251566	CG251566	OGZBG11TH
1118	86	6.0	742	7	CN132887	CN132887	OX1_8_G05	86	6.0	844	9	CN135725	CN135725	OX1_38_D0
1119	86	6.0	742	7	CN137824	CN137824	OX1_59_H05	86	6.0	844	9	CC520507	CC520507	CH240_367
1120	86	6.0	742	9	CC507175	CC507175	CH240_348	86	6.0	851	2	BF583262	BF583262	602101725
1121	86	6.0	742	9	CC981727	CC981727	ZUACD45TH	86	6.0	854	7	CN132986	CN132986	OX1_9_A07
1122	86	6.0	743	4	BJ167473	BJ167473	BJ167473	86	6.0	855	9	CNS033X2	AL465523	Tet-raodon
1123	86	6.0	743	4	BJ171757	BJ171757	BJ171757	86	6.0	857	9	CC474906	CC474906	CH240_300
1124	86	6.0	743	4	BJ602382	BJ602382	BJ602382	86	6.0	861	9	CC593836	CC593836	CH240_395
1125	86	6.0	744	9	CC489586	CC489586	CH240_322	86	6.0	862	5	BP172130	BP172130	BP172130
1126	86	6.0	745	9	CC478230	CC478230	CH240_304	86	6.0	862	7	CN148954	CN148954	WOUND1_59
1127	86	6.0	749	7	CN147043	CN147043	WOUND1_46	86	6.0	865	9	CG249561	CG249561	QGYBW01TH
1128	86	6.0	750	7	CN145375	CN145375	WOUND1_28	86	6.0	866	4	BG334285	BG334285	602461790
1129	86	6.0	751	7	CN147603	CN147603	WOUND1_50	86	6.0	866	5	BUS29044	BUS29044	AGENCOURT
1130	86	6.0	752	7	CN148219	CN148219	WOUND1_54	86	6.0	869	9	CC484829	CC484829	CH240_314
1131	86	6.0	753	4	BG684048	BG684048	602635658	86	6.0	870	5	BQ641748	BQ641748	AGENCOURT
1132	86	6.0	753	7	CN144666	CN144666	WOUND1_23	86	6.0	872	7	CN136367	CN136367	OX1_42_C0
1133	86	6.0	754	8	BZ859977	BZ859977	CH240_286	86	6.0	874	4	BG747965	BG747965	602705632
1134	86	6.0	756	7	CN140474	CN140474	OX1_36_B0	86	6.0	883	7	CN136692	CN136692	OX1_44_F0
1135	86	6.0	757	2	BF630737	BF630737	HVSMB001	86	6.0	887	4	CO063216	CO063216	est_k_bre
1136	86	6.0	759	7	CN140032	CN140032	OX1_33_D0	86	6.0	891	4	BG293666	BG293666	602390536
1137	86	6.0	759	7	CN144937	CN144937	WOUND1_25	86	6.0	893	9	CG255296	CG255296	OG3CV94TV
1138	86	6.0	760	7	CN134692	CN134692	OX1_27_H0	86	6.0	907	5	BK347595	BK347595	602347595
1139	86	6.0	761	5	BX840232	BX840232	BX840232	86	6.0	911	7	CN148961	CN148961	WOUND1_59
1140	86	6.0	762	6	CD432729	CD432729	ETH1_25_H	86	6.0	928	5	BQ674900	BQ674900	AGENCOURT
1141	86	6.0	764	2	BE277913	BE277913	601120290	86	6.0	933	6	CB181809	CB181809	AGENCOURT
1142	86	6.0	764	7	CN137689	CN137689	OX1_58_H1	86	6.0	935	5	BQ647364	BQ647364	AGENCOURT
1143	86	6.0	767	7	CN135930	CN135930	OX1_39_G0	86	6.0	940	5	BQ920746	BQ920746	AGENCOURT
1144	86	6.0	768	7	CN138408	CN138408	OX1_63_D0	86	6.0	949	7	CO581053	CO581053	ILLUMIGN
1145	86	6.0	768	7	CN150683	CN150683	WOUND1_70	86	6.0	953	5	BQ721531	BQ721531	AGENCOURT
1146	86	6.0	771	7	CN149388	CN149388	WOUND1_62	86	6.0	955	7	CK182866	CK182866	EST772181
1147	86	6.0	772	7	CN140057	CN140057	OX1_33_F0	86	6.0	969	6	BY716204	BY716204	BY716204
1148	86	6.0	773	7	CF132245	CF132245	UI-HF-FQ0	86	6.0	969	9	CC650477	CC650477	OGUAZ10TV
1149	86	6.0	775	7	CN149412	CN149412	WOUND1_62	86	6.0	975	5	BQ945751	BQ945751	AGENCOURT
1150	86	6.0	776	7	CN134505	CN134505	OX1_26_F0	86	6.0	982	5	BK331859	BK331859	OX1_31859
1151	86	6.0	776	7	CN136997	CN136997	OX1_54_C0	86	6.0	989	3	CG552848	CG552848	Tet-raodon
1152	86	6.0	778	2	BF866617	BF866617	963068E12	86	6.0	990	9	CC710075	CC710075	OGUHN69TV
1153	86	6.0	778	7	CN145718	CN145718	WOUND1_34	86	6.0	990	9	CL198217	CL198217	ZMMBBC024
1154	86	6.0	780	7	CN148894	CN148894	WOUND1_59	86	6.0	1020	5	BK343348	BK343348	EX343348
1155	86	6.0	781	4	BI520385	BI520385	603071863	86	6.0	1035	3	CR726723	CR726723	Tet-raodon
1156	86	6.0	783	7	CN136864	CN136864	OX1_53_F0	86	6.0	1036	9	CG434327	CG434327	ZMMBBC005
1157	86	6.0	785	7	CN136402	CN136402	OX1_42_G0	86	6.0	1040	4	BM559574	BM559574	AGENCOURT
1158	86	6.0	785	7	CN144467	CN144467	WOUND1_22	86	6.0	1048	5	BX438346	BX438346	EX438346
1159	86	6.0	788	7	CF932223	CF932223	TREST-B25	86	6.0	1068	5	BUI77863	BUI77863	AGENCOURT
1160	86	6.0	789	7	CN133059	CN133059	OX1_9_H05	86	6.0	1093	4	BM560965	BM560965	AGENCOURT
1161	86	6.0	790	7	CN136056	CN136056	OX1_40_C0	86	6.0	1098	4	BI912745	BI912745	603176136
1162	86	6.0	791	8	BZ870305	BZ870305	CH240_248	86	6.0	1098	5	BK337038	BK337038	EX337038
1163	86	6.0	793	7	CN151320	CN151320	WOUND1_74	86	6.0	1119	3	CG540777	CG540777	Tet-raodon
1164	86	6.0	796	9	CG285423	CG285423	OGSAU01TC	86	6.0	1125	4	BM551740	BM551740	AGENCOURT
1165	86	6.0	797	9	CC536552	CC536552	CH240_415	86	6.0	1142	9	AG081203	AG081203	Pan trogl
1166	86	6.0	798	7	CN148345	CN148345	WOUND1_55	86	6.0	1150	5	BQ721351	BQ721351	AGENCOURT
1167	86	6.0	801	7	CV463060	CV463060	CS_hyp_49	86	6.0	1243	5	BG811176	BG811176	AGENCOURT
1168	86	6.0	802	7	CN136880	CN136880	OX1_53_G1	86	6.0	1330	4	BM811176	BM811176	AGENCOURT
1169	86	6.0	804	7	CN143629	CN143629	WOUND1_17	86	6.0	1600	3	CNS03RAC0	BX320060	Arabidops
1170	86	6.0	806	7	CN145867	CN145867	WOUND1_35	86	6.0	1784	2	BF312396	BF312396	601898936
1171	86	6.0	807	9	CC581438	CC581438	CH240_376	86	6.0	1878	9	CL969921	CL969921	ObiFCC019
1172	86	6.0	808	7	CN134423	CN134423	OX1_26_F0	86	6.0	1894	4	BG328291	BG328291	602427267
1173	86	6.0	811	4	BI413618	BI413618	602987089	86	6.0	2091	3	AK017844	AK017844	Mus muscu
1174	86	6.0	812	7	CN134514	CN134514	OX1_26_G0	86	6.0	2283	3	AK011533	AK011533	Mus muscu
1175	86	6.0	812	7	CN136294	CN136294	OX1_42_C0	86	6.0	3598	3	AK030410	AK030410	Mus muscu
1176	86	6.0	812	7	CN136609	CN136609	OX1_44_F0	86	6.0	4532	3	AK090093	AK090093	Mus muscu
1177	86	6.0	813	9	CC521671	CC521671	CH240_369	85.5	6.0	491	1	AL039275	AL039275	DKF2p434A



c1251	1251	85.5	6.0	514	4	BJ803040	BJ803040	BJ803040	BJ803040	c1324	85.5	6.0	957	3	CR708534	Tetraodon
c1252	1252	85.5	6.0	530	8	BZ566382	pac82-164	AZ089498	RPC1-23-4	c1325	85.5	6.0	969	5	BUI93436	AGENCY
c1253	1253	85.5	6.0	536	8	BZ089498	RPC1-23-4	AI871505	w167h03.x	c1326	85.5	6.0	970	4	BUI93436	AGENCY
c1254	1254	85.5	6.0	559	1	AI871505	w167h03.x	AI871505	w167h03.x	c1327	85.5	6.0	973	4	BUI93436	AGENCY
c1255	1255	85.5	6.0	560	4	BI228759	1024093C0	BI228759	1024093C0	c1328	85.5	6.0	976	5	BM926289	AGENCY
c1256	1256	85.5	6.0	600	7	CF182341	UI-N-EYO-	CF182341	UI-N-EYO-	c1329	85.5	6.0	975	5	BM926289	AGENCY
c1257	1257	85.5	6.0	601	4	BI91853	1020053F0	BI91853	1020053F0	c1330	85.5	6.0	981	2	BE793251	AGENCY
c1258	1258	85.5	6.0	631	7	CF909004	A0530F03-	CF909004	A0530F03-	c1331	85.5	6.0	990	5	BO960405	AGENCY
c1259	1259	85.5	6.0	638	4	BM749316	K-EST0024	BM749316	K-EST0024	c1332	85.5	6.0	992	3	CF711939	Tetraodon
c1260	1260	85.5	6.0	639	6	CB469855	sn12_H07.	CB469855	sn12_H07.	c1333	85.5	6.0	998	5	EX342369	EX342369
c1261	1261	85.5	6.0	643	1	AA391499	sn10174.5	AA391499	sn10174.5	c1334	85.5	6.0	1001	2	BE548710	601073448
c1262	1262	85.5	6.0	645	4	BG043738	sv27e08.Y	BG043738	sv27e08.Y	c1335	85.5	6.0	1006	4	BG395869	602458658
c1263	1263	85.5	6.0	658	2	BB642617	BB642617	BB642617	BB642617	c1336	85.5	6.0	1001	3	CR716042	Tetraodon
c1264	1264	85.5	6.0	663	9	CG016859	ZUA3B32PH	CG016859	ZUA3B32PH	c1337	85.5	6.0	1007	3	CR716928	Tetraodon
c1265	1265	85.5	6.0	668	7	CK947906	4072583.B	CK947906	4072583.B	c1338	85.5	6.0	1008	9	CNS03CVT	Tetraodon
c1266	1266	85.5	6.0	675	9	CC480869	CH240.308	CC480869	CH240.308	c1339	85.5	6.0	1039	2	BF125415	601763541
c1267	1267	85.5	6.0	687	4	BG340132	602437713	BG340132	602437713	c1340	85.5	6.0	1049	4	BM561005	AGENCY
c1268	1268	85.5	6.0	697	7	CN142676	WOUND1.11	CN142676	WOUND1.11	c1341	85.5	6.0	1059	5	BQ691667	AGENCY
c1269	1269	85.5	6.0	698	4	BG859559	1024064A1	BG859559	1024064A1	c1342	85.5	6.0	1083	5	BQ879397	AGENCY
c1270	1270	85.5	6.0	700	6	CD053874	HO03D24S	CD053874	HO03D24S	c1343	85.5	6.0	1089	5	BM925969	AGENCY
c1271	1271	85.5	6.0	700	7	CN142583	WOUND1.10	CN142583	WOUND1.10	c1344	85.5	6.0	1096	4	BG746209	AGENCY
c1272	1272	85.5	6.0	704	1	AA790552	w17h03.r	AA790552	w17h03.r	c1345	85.5	6.0	1098	7	CK210787	FGAS02261
c1273	1273	85.5	6.0	717	6	CA243627	SCQFL407	CA243627	SCQFL407	c1346	85.5	6.0	1107	5	BQ686727	AGENCY
c1274	1274	85.5	6.0	719	2	BF220330	601296987	BF220330	601296987	c1347	85.5	6.0	1120	5	BM922869	AGENCY
c1275	1275	85.5	6.0	731	8	BZ342449	ic83e12.b	BZ342449	ic83e12.b	c1348	85.5	6.0	1126	4	BG293989	AGENCY
c1276	1276	85.5	6.0	739	7	CO001589	EST789924	CO001589	EST789924	c1349	85.5	6.0	1161	4	BG403494	602419184
c1277	1277	85.5	6.0	741	6	CD430898	ETH1.5.A0	CD430898	ETH1.5.A0	c1350	85.5	6.0	1204	8	BG403494	602419184
c1278	1278	85.5	6.0	748	7	CN136253	OX1_41_G0	CN136253	OX1_41_G0	c1351	85.5	6.0	1248	5	BM913610	AGENCY
c1279	1279	85.5	6.0	750	9	CL542158	OB_Ba006	CL542158	OB_Ba006	c1352	85.5	6.0	1296	9	CL972919	AGENCY
c1280	1280	85.5	6.0	754	7	CF748814	UI-N-HU0	CF748814	UI-N-HU0	c1353	85.5	6.0	1485	9	CL981424	AGENCY
c1281	1281	85.5	6.0	759	5	BQ572373	UI-N-PD0	BQ572373	UI-N-PD0	c1354	85.5	6.0	1713	3	AK044604	AGENCY
c1282	1282	85.5	6.0	760	2	BF616953	HVMEC001	BF616953	HVMEC001	c1355	85.5	6.0	1803	2	BM962810	Mus muscu
c1283	1283	85.5	6.0	760	7	CF429971	PH1.25.G0	CF429971	PH1.25.G0	c1356	85.5	6.0	2216	3	BC051962	Mus muscu
c1284	1284	85.5	6.0	770	7	CV463398	CS_FVD_53	CV463398	CS_FVD_53	c1357	85.5	6.0	2225	3	CF625324	full_leng
c1285	1285	85.5	6.0	771	9	CG439436	OG8AE41V	CG439436	OG8AE41V	c1358	85.5	6.0	2836	3	AK078023	Mus muscu
c1286	1286	85.5	6.0	773	9	CG325677	OGYAR51TH	CG325677	OGYAR51TH	c1359	85.5	6.0	2931	9	CL974984	AGENCY
c1287	1287	85.5	6.0	779	4	BG294850	602391675	BG294850	602391675	c1360	85.5	6.0	3097	3	AK035712	Mus muscu
c1288	1288	85.5	6.0	781	4	BF826410	EST703792	BF826410	EST703792	c1361	85.5	6.0	3209	3	AK046771	Mus muscu
c1289	1289	85.5	6.0	791	4	BI544438	603241951	BI544438	603241951	c1362	85.5	6.0	4659	3	AK031271	Mus muscu
c1290	1290	85.5	6.0	803	2	BF568250	602184626	BF568250	602184626	c1363	85.5	6.0	347	5	BY398894	AGENCY
c1291	1291	85.5	6.0	809	5	BF529628	EX329628	BF529628	EX329628	c1364	85.5	6.0	347	5	BY398894	AGENCY
c1292	1292	85.5	6.0	810	7	CF822687	EST700069	CF822687	EST700069	c1365	85.5	6.0	387	4	B1602750	60347102
c1293	1293	85.5	6.0	826	5	EX888923	EX888923	EX888923	EX888923	c1366	85.5	6.0	435	4	BG516671	ETESTed59
c1294	1294	85.5	6.0	833	5	EX881366	EX881366	EX881366	EX881366	c1367	85.5	6.0	447	2	BF563485	UI-R-BT1-
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c1296	1296	85.5	6.0	837	4	BI820511	603036140	BI820511	603036140	c1369	85.5	6.0	516	8	AQ847973	LMJFV1.1
c1297	1297	85.5	6.0	840	4	BG294497	602391821	BG294497	602391821	c1370	85.5	6.0	517	6	CD345223	ETESTe56
c1298	1298	85.5	6.0	841	7	CN138409	OX1_63_D0	CN138409	OX1_63_D0	c1371	85.5	6.0	522	8	BZ954941	CH240_94N
c1299	1299	85.5	6.0	847	5	BUI28145	603115136	BUI28145	603115136	c1372	85.5	6.0	523	8	BZ580619	3590_1_39
c1300	1300	85.5	6.0	848	7	CO812913	AGENCY	CO812913	AGENCY	c1373	85.5	6.0	539	2	AW786079	117701_MA
c1301	1301	85.5	6.0	851	7	CF446415	EST682760	CF446415	EST682760	c1374	85.5	6.0	581	5	BP226156	BP226156
c1302	1302	85.5	6.0	855	4	BG855139	1024041H0	BG855139	1024041H0	c1375	85.5	6.0	600	9	CC680905	OGUIT53TH
c1303	1303	85.5	6.0	858	7	CF240894	AGENCY	CF240894	AGENCY	c1376	85.5	6.0	602	6	CB878893	HP10D03T
c1304	1304	85.5	6.0	862	7	CO009250	EST797585	CO009250	EST797585	c1377	85.5	6.0	611	6	CB877026	HP03E19T
c1305	1305	85.5	6.0	864	5	BUI28145	603115136	BUI28145	603115136	c1378	85.5	6.0	613	6	CB877756	HP06A23T
c1306	1306	85.5	6.0	865	4	BI462355	603203712	BI462355	603203712	c1379	85.5	6.0	620	8	BH714932	BOMQ29TTR
c1307	1307	85.5	6.0	867	7	CN201023	Tor10693	CN201023	Tor10693	c1380	85.5	6.0	621	7	CK371597	zmrvw005
c1308	1308	85.5	6.0	869	5	BUI69535	AGENCY	BUI69535	AGENCY	c1381	85.5	6.0	632	9	CL543778	OB_Ba007
c1309	1309	85.5	6.0	879	9	CG248450	OGWB72TH	CG248450	OGWB72TH	c1382	85.5	6.0	639	5	BUI439505	60209425
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c1313	1313	85.5	6.0	897	7	CO009288	EST797623	CO009288	EST797623	c1386	85.5	6.0	654	2	BE985566	BE985566
c1314	1314	85.5	6.0	897	9	CG620871	OGUPW82TV	CG620871	OGUPW82TV	c1387	85.5	6.0	659	6	BY735116	BY735116
c1315	1315	85.5	6.0	900	9	CG439069	OGF7A123TV	CG439069	OGF7A123TV	c1388	85.5	6.0	668	7	CK434506	GQ0062_TB
c1316	1316	85.5	6.0	909	5	BUI69499	AGENCY	BUI69499	AGENCY	c1389	85.5	6.0	670	2	BF430820	OG05A05T3
c1317	1317	85.5	6.0	925	5	BQ366377	EST700677	BQ366377	EST700677	c1390	85.5	6.0	685	6	CA283181	SCBGS105
c1318	1318	85.5	6.0	932	7	CF823295	EST700677	CF823295	EST700677	c1391	85.5	6.0	690	6	CD763439	SCBGS105
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c1320	1320	85.5	6.0	935	7	CO059833	est_k.bre	CO059833	est_k.bre	c1393	85.5	6.0	691	9	AG091533	Pan trogl
c1321	1321	85.5	6.0	937	9	CG396735	ZMWBBC001	CG396735	ZMWBBC001	c1394	85.5	6.0	699	4	BI824709	603033873
c1322	1322	85.5	6.0	944	9	CG634016	OGUDQ82TV	CG634016	OGUDQ82TV	c1395	85.5	6.0	699	6	BY748737	BY748737
c1323	1323	85.5	6.0	955	5	BUI400172	603483777	BUI400172	603483777	c1396	85.5	6.0	702	5	EX627673	EX627673

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1398	85	5.9	707	8	BZ886360	CH240_198	1471	85	5.9	888	6	CD380658	PTMM05827
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1404	85	5.9	716	5	BM986267	EST531721	1477	85	5.9	899	9	CG318029	OGWFT46TV
1405	85	5.9	717	4	BG967679	602833484	1478	85	5.9	902	5	BUS28634	AGENCOURT
1406	85	5.9	717	7	CK149571	WOUND1_63	1479	85	5.9	903	2	BE798767	601585794
1407	85	5.9	719	9	CG437156	OGYAI20TV	1480	85	5.9	903	5	BQ879327	AGENCOURT
1408	85	5.9	722	9	CG437146	OGYAI20TV	1481	85	5.9	905	1	AL961556	AL961556
1409	85	5.9	738	4	BG705967	602669291	1482	85	5.9	906	6	CD556373	AGENCOURT
1410	85	5.9	739	9	CG259164	OGWKD80TH	1483	85	5.9	910	2	BF680343	602154124
1411	85	5.9	740	7	CF730613	UI-M-G20-	1484	85	5.9	922	7	CN509062	AGENCOURT
1412	85	5.9	741	9	CG487158	CH240_318	1485	85	5.9	922	9	CG836429	CG836429
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1414	85	5.9	746	9	CG318023	CG18023	1487	85	5.9	924	5	EX354149	EX354149
1415	85	5.9	749	7	CK788871	AGENCOURT	1488	85	5.9	925	8	CC334397	OGPBA41TV
1416	85	5.9	751	9	CL843639	OR_CBA007	1489	85	5.9	926	8	CNS033BC	AL237585
1417	85	5.9	755	7	CF589244	EST00H01	1490	85	5.9	930	8	CC114993	NDL_70C24
1418	85	5.9	758	4	BG722492	602693741	1491	85	5.9	932	5	BQ889757	AGENCOURT
1419	85	5.9	758	5	BU930058	AGENCOURT	1492	85	5.9	933	8	BZ555013	pacsl-60
1420	85	5.9	759	4	BG911876	602809466	1493	85	5.9	939	4	BI821988	603040015
1421	85	5.9	760	7	CN137328	OX1_56_C1	1494	85	5.9	941	5	BQ921058	AGENCOURT
1422	85	5.9	762	7	CN137341	OX1_56_E0	1495	85	5.9	941	5	BQ957968	AGENCOURT
1423	85	5.9	767	7	CK775713	966847_MA	1496	85	5.9	950	2	BE791304	601582866
1424	85	5.9	773	4	BG036563	602326338	1497	85	5.9	953	4	BG172978	602335452
1425	85	5.9	774	5	BG232963	60232963	1498	85	5.9	954	4	BZ523835	603051956
1426	85	5.9	778	8	BZ564855	pacsl-164	1499	85	5.9	970	9	CG251027	OGWJF51TH
1427	85	5.9	780	7	CO888647	BovGen_16	1500	85	5.9	977	5	BQ929937	AGENCOURT
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## ALIGNMENTS

RESULT 1	AKO34144	3688 bp	linear	HTC 03-APR-2004
AKO34144	Mus musculus adult male diencephalon cDNA, RIKEN full-length			
LOCUS	enriched library, clone:9330159116			
DEFINITION	product:hypothetical protein,			
	full insert sequence.			
ACCESSION	AKO34144			
VERSION	AKO34144.1	GI:26329732		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1			
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Math. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,			
	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to			
	prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,			
	Konno, H., Akiyama, J., Nishi, K., Kutsuna, T., Tashiro, H., Itoh, M.,			
	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,			
	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,			
	Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,			
	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,			
	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format			
	Genome Res. 10 (11), 1757-1771 (2000)			
JOURNAL				



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AUTHORS
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Functional annotation of a full-length mouse cDNA collection
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6 (bases 1 to 3688)
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Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/translation="EDLFLFEDGQVDFAFEVTTTASHEGLDSVPVVDQQLLYTCFCFYIG
ELRLKLSWSGSGRSGFVRKITPTTSLGALPLOTSGLOLAQLAEAFHNPQPS
LRRVTFVAERIGNCVGHIKATLVDLVOAESLLQOLVARGQEGDPAQLLESIC
SQLCPHGAQLTQCEPCORSPPTAVRALLEETPAVLSEAENIAGLATEKACSWL
SANTALIRRVKAAVSMRLRAQPEPTARVERRCGRACSHHAPLSHLISLKVLI
SLAAGPRDFEGVSPHEHRLMLLSLWDDFQGFVPLQLLSLPRNGLADTRPREW
IPILGPTQFEGHARLLMLLSLWDDFQGFVPLQLLSLPRNGLADTRPREW
DLLFLRLRELKDLMLGHLETEACGLRINEAQWPCDFSEELSTLFLRFLAPHLLEPQ
LRACELMQPNRGTVLAQS"
ORIGIN
Alignment Scores:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Rutheria; Rodentia; Sciurognathi; Muridae; Mus.

Pred. No.: 9,22e-103 Length: 3688
Score: 1168.00 Matches: 231
Percent Similarity: 93.00% Conservatives: 8
Best Local Similarity: 89.88% Mismatches: 18
Query Match: 81.56% Indels: 0
DB: 3 Gaps: 0
US-10-015-388a-54 (1-280) x AK034144 (1-3688)
QY 24 GluAspLeuPhePheLeuGluGluGlyProSerTyrAlaPheGluValAspThrValAla 43
Db 2 CAGGACTTATTCTTTCTAGAAAGATGGTCAGGTAGATGCTTTTGAGGTGACTACAACTGCT 61
QY 44 ProGluHisGlyLeuAspAsnAlaProValValAlaPheGlnGlnLeuLeuTyrThrCysCys 63
Db 62 TCAGAGCATGGTTTGGACAGTGTACCTGTTGTGACACAGCAGCTGTATATACCTGTGTC 121
QY 64 ProTyrIleGlyGluLeuArgLysLeuLeuAlaSerTrpValSerGlySerSerGlyArg 83
Db 122 CCTTACATTGGAGAGCTCCGGAAGCTGCTTCTCTCTGGGTTTCAGGAAGCAGTGGGCGG 181
QY 84 SerGlyGlyPheMetArgLysIleThrProThrThrThrThrThrSerLeuGlyAlaGlnPro 103
Db 182 AGTGAGGCTTTGTGAGGAAATCACTCCCACTACCAACAGCAGCTGGGAGCCCTGCT 241
QY 104 SerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAlaGlnAlaPhePheHisAsnGlnPro 123
Db 242 CTCAGACACACAGGGGCTCAGGCTCACTGTGAGGCTTTTTCACCAACAGGCA 301
QY 124 ProSerLeuArgArgThrValGluPheValAlaGluArgIleGlySerAspCysVallys 143
Db 302 CCTCCCTGGCAGAGCTGTAGAAATTTGTGCAGAGAAGAAATTTGGATCAAACTGTGTCAA 361
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Db 362 CACATCAAGGCGACACTGGTAGAGATTGGTGTGATCAAGCAGAGTCACTTCTTTCAGGAG 421
QY 164 GlnLeuValThrGlnGlyGluGluGlyCysAspProAlaGlnLeuLeuGluLeuLeuCys 183
Db 422 CAGCTGTGGCAGCGGACAGAGAGGGGAGATTCAGCAGCAGCTTTTGGATCTCTTGTGT 481
QY 184 SerGlnLeuCysProHisGlyAlaGlnAlaLeuAlaLeuGlyArgGluPheCysGlnArg 203
Db 482 TCTCAACTCTGCCCATGGGGCCCAAGCATTTGCCAGGGGGCGGAGTTCTGCCAAAGG 541
QY 204 LysSerProGlyAlaValArgAlaLeuLeuProGluThrProAlaAlaValLeuSer 223
Db 542 AAGAGCCCCACCGCTGTGGGAGCACTGTACAGAGAGACCCAGGCTGTGTCTTAAGC 601
QY 224 SerAlaGluAsnIleAlaValGlyLeuAlaThrGluLysAlaCysAlaTrpLeuSerAla 243
Db 602 AGTCAGAGAACAATTGCTGTGGGCTTGGACAGAGAAGAGCTGCTCTTGTGTTCAGCC 661
QY 244 AsnIleThrAlaLeuIleArgArgGluValLysAlaAlaValSerArgThrLeuArgAla 263
Db 662 AACATCAGCGCTGATTAGAGGGAAGTGAAGCAGCGCTGAGTCGATCTGCTACAGGCC 721
QY 264 GlnGlyProGluProAlaAlaArgGlyGluArgGlyCysSerArgAla 280
Db 722 CAGGGTCTTGAGCAACTGCCCGGTGGAGCGGAGGGGCTGCTCCCGAGCC 772

RESULT 2
BB626090
LOCUS
DEFINITION
BB626090 RIKEN full-length enriched, adult male diencephalon Mus
musculus cDNA clone 9330159116 5', mRNA sequence.
ACCESSION
BB626090
VERSION
BB626090.1
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Rutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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1 (bases 1 to 603)
REFERENCE
AUTHORS Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C.,
Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.
TITLE Transcriptome analysis of mouse stem cells and early embryos
JOURNAL PLoS Biol. 1 (3), 410-419 (2003)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: E0842 row: C column: 03
Seq primer: M13 Reverse
High quality sequence stop: 603
POLYA=No.
FEATURES
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Location/Qualifiers
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/organism="Mus musculus"
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/lab_host="DH10B"
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(Long)"
(note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). The
mRNAs were extracted from a pool of 360 embryos at 4-cell
stage. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer [Invitrogen]:
5'-PCACTAGTCTAGATCGCGAGCGCCCTTTT-3' from
10.8ng of mRNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker L1-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.2Kb. The library was
constructed by Yulan Piao."
ORIGIN
Alignment Scores:
Pred. No.: 3,786-79 Length: 603
Score: 915.00 Matches: 180
Percent Similarity: 93.94% Conservative: 6
Best Local Similarity: 90.91% Mismatches: 12
Query Match: 63.90% Indels: 0
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Qy 56 GlnGlnLeuLeuTyrThrCysCysProTyrIleGlyGluLeuArgLysLeuLeuAlaSer 75

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Qy 116 GlnAlaPhePheHisAsnGlnProProSerLeuArgArgThrValGlnPheValAlaGlu 135
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Qy 156 GlnAlaGluSerLeuGlnGluGlnLeuValThrGlnGlyGluGlnGlyGlyAspPro 175
368 CAGCAGAGTCACCTTTCAGGAGCAGCTGTGTGGCAGCGGACAGGAGGGGAGATCCA 427
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Qy 196 LeuGlyArgGluPheCysGlnArgLysSerProGlyAlaValAlaArgAlaLeuLeuProGlu 215
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Qy 216 GluThrProAlaAlaValLeuSerSerAlaGluAsnIleAlaValGlyLeuAla 233
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DEFINITION musculus cDNA clone NTA:E0757H05 IMAGE:30901528 5', mRNA sequence.
CN718045
VERSION CN718045.1 GI:47487430
SOURCE EST.
ORGANISM Mus musculus (house mouse)
REFERENCE 1 (bases 1 to 576)
AUTHORS Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C.,
Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.
TITLE Transcriptome analysis of mouse stem cells and early embryos
JOURNAL PLoS Biol. 1 (3), 410-419 (2003)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: E0757 row: H column: 05
Seq primer: M13 Reverse
High quality sequence stop: 576
POLYA=No.
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(Long)"
/notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). The
mRNAs were extracted from a pool of 360 embryos at 4-cell
stage. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer [Invitrogen]:
5'-PGACTAGTCTAGATCGGACGCGCCCTTTT-3' from
10.8ng of mRNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lona-linker Lu-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.2Kb. The library was
constructed by Yulan Piao."

```

## ORIGIN

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Alignment Scores:
Pred. No.:      8.94e-75      Length:      576
Score:          870.00      Matches:      170
Percent Similarity: 93.12%      Conservative: 6
Best Local Similarity: 89.95%      Mismatches: 13
Query Match:      60.75%      Indels:      0
DB:              7          Gaps:      0

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US-10-015-388A-54 (1-280) x CN718045 (1-576)

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Qy 56 GlnGlnLeuLeuTyThrCysCysProTyrlleGlyGluLeuArgLysLeuLeuAlaSer 75
Db 68 CAGCAGCTGTTATATACCTGTGTGCCCCCTACATTGGAGAGCTCCGAAACTGCTTGTCC 127
Qy 76 TrpValSerGlySerSerGlyArgSerGlyPheMetArgLysIleThrProThrThr 95
Db 128 TGGGTTTCAGAGACAGTGGCGGAGTGGAGCTTTGTGAGGAAATCACTCCCACTACC 187
Qy 96 ThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAla 115
Db 188 ACCAGCAGCTGGGAGCCCTGCTCTCCAGACCAAGCCAGGGGCTCGAGGCTCAACTTGCT 247
Qy 116 GlnAlaPhePheHisAsnGlnProProSerLeuArgArgThrValGluPheValAlaGlu 135
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Db 368 CAAGCAGAGTCACTTCTTCAGGAGCAGCTGGTGGCAGCGGGACAGGAGGGAGATCCA 427
Qy 176 AlaGlnLeuLeuGluLeuLeuCysSerClnLeuCysProHisGlyAlaGlnAlaLeuAla 195
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ACCESSION  BF075771
VERSION     BF075771.1 GI:10869282
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1 (bases 1 to 528)
AUTHORS     Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
Quackenbush,J. and Keele,J.W.
TITLE       Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
JOURNAL     Mamm. Genome 13 (8), 475-478 (2002)
MEDLINE     22213789
PUBMED      12226715
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -mismatch 12 options.
            PCR Primers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTCCTCCAGTCACGACG
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                    endometrium, hypothalamus, pituitary, and placenta."
ORIGIN
Alignment Scores:
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Score:          845.00      Matches:      164
Percent Similarity: 97.14%      Conservative: 6
Best Local Similarity: 93.71%      Mismatches: 5
Query Match:      59.01%      Indels:      0
DB:              2          Gaps:      0
US-10-015-388A-54 (1-280) x BF075771 (1-528)
Qy 59 LeuTyThrCysCysProTyrlleGlyGluLeuArgLysLeuLeuAlaSerTrpValSer 78
Db 2 CTCTACACCTGCTGCCCTATATTGGAGAGCTCCGAAACTGCTGGTTCATGGGTATCA 61
Qy 79 GlySerSerGlyArgSerGlyGlyPheMetArgLysIleThrProThrThrThrSer 98
Db 62 GGCAGCAGTGGCGGAGTGGGGGCTTCTGTAGGAAATTCACCCCAACCACTGGG 121

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QY 99 LeuGlyAlaGlnProSerGlnThrSerGlnGlnGlnAlaGlnLeuAlaGlnAlaPhe 118  
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 Db 362 TTGGAGATCTTGTGTTCAGCTGTGCCCCCAGCGGGCCCATGCTGACCTGGGGCGG 421  
 QY 199 GluPheCysGlnArgLysSerProGlyAlaValAlaGlnAlaLeuLeuProGluThrPro 218  
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 Db 482 GCAGCGCTTCGAGCAGTGCAGATATATTGCCGTGGGGCTTGCA 526

## RESULT 6

BQ082104

LOCUS

DEFINITION

K-BST0054026 S7SNU71981 Homo sapiens cDNA clone S7SNU71981-14-C09

5', mRNA sequence.

ACCESSION

BQ082104

VERSION

BQ082104.1

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 541)

Oh,K.N., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience &amp; Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 14 row: C column: 09

High quality sequence stop: 541.

Location/Qualifiers

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Site 2: NotI; The poly (A)+ RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then decapped

with tobacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including EcoR

I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-tailed mRNA by priming with dt-tailed vector. The dt-tailed vector was designed to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10F' with electroporation method."

## ORIGIN

Alignment Scores: 1.42e-67 Length: 541  
 Pred. No.: 796.00 Matches: 163  
 Score: 796.00 Conservative: 0  
 Percent Similarity: 98.79% Mismatches: 2  
 Best Local Similarity: 98.79% Indels: 1  
 Query Match: 55.59% Gaps: 0  
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US-10-015-388A-54 (1-280) x BQ082104 (1-541)

QY 116 GlnAlaPhePheHisAsnGlnProSerLeuArgArgThrValGlnPheValAlaGlu 135  
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 VERSION BI344908.1 GI:15038197  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 1 (bases 1 to 589)  
 Fahnenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J.,  
 Vallet, J., Wise, T., Rohrer, G.A., Perteau, G., Sultana, R.,  
 Quackenbush, J., and Keele, J.W.  
 Porcine gene discovery by normalized cDNA-library sequencing and  
 EST cluster assembly  
 Mamm. Genome 13 (8), 475-478 (2002)  
 2213789  
 12226715  
 CONTACT: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel.: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@mail.marc.usda.gov  
 Single pass sequencing. Bases called and alt trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -minscore 18  
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Db 245 TCCCTGGCGCAGGACTGGAGTTTGTGGCAGAGAAATTGGCTTAATCTGTGTCAAGCAT 304  
 Qy 145 IleLysAlaThrLeuValAlaAspLeuValArgGlnAlaGluSerLeuLeuGlnGln 164  
 Db 305 ATCAAGGCCACACTGGTAGCAGATCTGGTGGCCAGGACAGAGTGGCTTCTTCAGGAGCAG 364  
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 Db 365 CTGGTGCAGCAGGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 424  
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 Db 425 CAGTGTGCCCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 469  
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 VERSION CD578927  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 727)  
 NTH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Dr. Jim Lin, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at  
 http://genome.uiowa.edu/distribution/mousefl.html  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)  
 Seq primer: pYX-5.  
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 /note="Organ: Brain; Vector: pYX-Asc; Site\_1: EcoR I;  
 Site\_2: Not I; The library was constructed according  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. Denatured RNA was size fractionated on a 1% agarose  
 gel. First strand cDNA synthesis was primed with oligo-dT  
 primer containing a Not I site. Double strand cDNA was  
 size selected according to mRNA size fraction, ligated  
 with EcoR I adaptor, digested with NotI and then cloned  
 directionally into pYX-Asc vector. The library tag  
 sequence located between the Not I site and the polyA tail  
 is AGCGAGCAG. This library was created for the University  
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
 Developing Mouse Nervous System', supported by National  
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
 program coordinator."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 5.09e-59 Length: 727  
 Score: 710.50 Matches: 154







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Db      641 AACGAGCACCCTCCCTCGCGGAGGACTGTAGATTGTGNGCAGAGAAGATTGGATCAACTG 700
Qy      141 CysValLysHisIleLysAlaThrLeuValAlaLeuVal 154
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Db      701 TGT---CAACACATCAAGCGCACACTGTTAGCAGATTGGTG 739

RESULT 10
CR375103 661 bp mRNA linear EST 22-APR-2004
LOCUS    CR375103 AGENAE Rainbow trout normalized testis library (tcbl)
DEFINITION
Oncorhynchus mykiss cdna clone tcbl0027c.n.03 5prim, mRNA sequence.
ACCESSION
CR375103
VERSION  CR375103.1 GI:46500668
KEYWORDS EST.
SOURCE   Oncorhynchus mykiss (rainbow trout)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE
1 (bases 1 to 661)
Gavoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cdna
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
Contact: Guiguen Y
INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenassupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0027 row: n column: 3
Seq primer: M13R.
FEATURES
source
1. .661
Location/Qualifiers
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:9022"
/clone="tcbl0027c.n.03"
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/lab_host="DH10B"
/clone_lib="AGENAE Rainbow trout normalized testis library
(tcbl)"
/note="Vector: pT7T3D-pac; Clone distribution : AGENAE
Resource centre: Francois PIUMI.
Francois.PIUMI@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (IUREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN
Alignment Scores:
Pred. No.: 2.54e-50 Length: 661
Score: 621.00 Matches: 123
Percent Similarity: 72.48% Conservative: 35
Best Local Similarity: 56.42% Mismatches: 56
Query Match: 43.37% Indels: 4
DB: 7 Gaps: 2

US-10-015-388A-54 (1-280) x CR375103 (1-661)
Qy      47 GlyLeuAspAsnAlaProValValAspGlnGlnLeuLeuThrCysCysProTyrIle 66
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Db      17 GGACTTGACTCTCCCTCGCTGGTGGACCAAGCTCTCTACACTGCTGCTTCCTG 76
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Qy      67 GlyGluLeuArgLysLeuLeuAlaSerTrpValSerGlySerSerGlyArgSerGlyGly 86
      ::::|||||
Db      77 GGTGAGTTCCGTAAGCTCTCGCTGCTTTGTGCGCGGTAGCTCTGCCAGGGGTGGAGGC 136
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Qy      87 PheMetArgLysIleThrProThrThrThrSerLeuGlyAla---GlnProSerGln 105
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Db      137 CTCATCGTAAAGTACACCCCTACCTCTGTGAGCTAAGAGGTACCCCAACACACCCAGG 196
Qy      106 ThrSerGlnGlyLeuGlnAlaGlnLeuAlaGlnAlaPhePheHisAsnGlnProProSer 125
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Db      197 TCACAGCAAAATACAGGTGGATTGTGGAGCAAGCCTTCTTCCATAACCAAGCCTCCATCT 256
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Qy      126 LeuArgArgThrValGluPheValAlaGluArgIleGlySerAsnCysValLysHisIle 145
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Db      257 CTCAGACGAACGGTGGAGTTTGTAGCTGAGAGGGTGGATCCAACTGTGTGTCAACATATG 316
      ::::|||||
Qy      146 LysAlaThrLeuValAlaAspLeuValArgGlnAlaGluSerLeuLeuGlnGlnLeu 165
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Db      317 AAGTCAAGCTGGTGTGTGAGTGTCCGTGGTGGAGAGGTGCTGGAGAGGGGCTG 376
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Qy      166 ValThrGlnGlyGluGluGlyGlyAspProAlaGlnLeuGluIleLeuCysSerGln 185
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Db      377 ATCTCA-----CCAGGGGCCCAACCTCTGATACTCAACGACTCCATCTGTGCTCAA 427
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Qy      186 LeuCysProHisGlyAlaGlnAlaLeuAlaLeuGlyArgGluPheCysGlnArgLysSer 205
      ::::|||||
Db      428 CTCTGTGACGGGGGCCAGGAGGCTCTAGAGAGACTACCAAGGTTTTCAGTGAAGAGGGT 487
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Qy      206 ProGlyAlaValArgAlaLeuLeuProGluGluThrProAlaAlaValLeuSerSerAla 225
      ::::|||||
Db      488 CCAGAAGCCATCCGGGTTCTTCTCTGACGAGAGCTCCCGCTGTCTCAGTACGCT 547
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Qy      226 GluAsnIleAlaValGlyLeuAlaThrGluLysAlaCysAlaTrpLeuSerSerAlaAsnIle 245
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Qy      246 ThrAlaLeuLeuArgArgGluValLysAlaAlaValSerArgThrLeuArgAla 263
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RESULT 11
LOCUS    BI541289
DEFINITION BI541289 MARC 1BOV Bos taurus cdna 5', mRNA sequence.
ACCESSION BI541289
VERSION    BI541289.1 GI:15382401
KEYWORDS  EST.
SOURCE    Bos taurus (cow)
ORGANISM  Bos taurus
REFERENCE
1 (bases 1 to 567)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cdna
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
JOURNAL   21180013
MEDLINE   11282978
PUBMED
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGACG
Plate: 120 row: N column: 12
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
1. .567
FEATURES
source

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[illegible]

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 3100 and 3700 capillary sequencers. Raw sequence data was batch  
 processed analyzed, groomed and submitted by the Animal  
 Biotechnology Center (URL:  
<http://primer.ansci.umn.edu/software.html>), University of  
 Minnesota. Trace files have been submitted to the NCBI trace  
 archive (<http://www.ncbi.nlm.nih.gov/Traces/trace.cgi>).  
 Chromatograms were analyzed with Phred version: 0.00925.c . Vector  
 (pCMV SPORT6, Invitrogen). Sus scrofa mitochondrion  
 (gi|5835862|ref|NC\_000845.1|, Escherichia coli K12 (gi|5835862|  
 ref|NC\_000913.1|), Porcine reproductive and respiratory syndrome  
 virus (gi|11878202|gb|AF303357.1|AF303357), Altheromonas sp.16S rRNA  
 gene (gi|4218471|emb|Y15322.1|Y15322), Sus scrofa 28S ribosomal  
 RNA (gi|3388170|gb|AF080393.1|AF080393), and Sus scrofa 18S ribosomal  
 RNA (gi|3885982|gb|AF102857.1|AF102857). Sequences were identified  
 and masked by Crossmatch -minscore=20, -mismatch=12, -penalty=-8.  
 SWAR alignment scores were set to match score=1, gap initial  
 penalty=-3 and gap extension penalty=-2. A continuous stretch of at  
 least 50 bases of a PHRED quality 20 were required for  
 submission. 5' and 3' TERNINI were defined by a continuous stretch  
 of 10 nucleotides with a PHRED quality not less than 20. A terminal  
 stretch of at most 40 un-masked bases were automatically trimmed  
 when flanking masked sequence. Sequences with an INTERNAL continuous  
 stretch of at most 20 bases with PHRED quality less than 20 were  
 automatically prepared for submission. HIQUAL\_START and HIQUAL\_STOP  
 refer to the coordinates on CLIP\_QUALITY and CLIP\_VECTOR at the  
 NCBI trace archive.  
 Plate: 24 row: G column: 03  
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 High quality sequence start: 67  
 High quality sequence stop: 417.  
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 /db\_xref="taxon:9823"  
 /clone="PPSUBLIB.24G03"  
 /tissue\_type="Peyer's patch"  
 /clone\_lib="UNMPPM3"  
 /notes="Organ: small intestine, jejunum; Vector:  
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 patches were isolated from healthy, 4-6 week old  
 cross-bred pigs. RNA was extracted either immediately or  
 after 3 hours stimulation in an Using chamber with one of  
 the following treatments: 1) no treatment, 2) Salmonella  
 choleraesuis vaccine strain SC-54, 3) phorbol myristate  
 acetate, concanavalin A, and 8-bromo-cyclic AMP, and 4)  
 lipopolysaccharide and cholera toxin. Each treatment was  
 performed in the presence and absence of cycloheximide.  
 Purified poly A+ RNA from each of the treated tissues  
 (2-4) was combined together, reverse transcribed, and  
 cloned in to pCMVSPORT6 to make a library of approximately

530,000 recombinant clones with an average insert size of  
 1.0 kbp. Poly A+ RNA from freshly isolated and non-treated  
 tissue from an Using chamber (treatment 1) was cloned in  
 the same manner to produce an unstimulated cDNA library of  
 approximately 900,000 clones with an average insert size  
 of 1.5 kbp. Equal portions of the two libraries were  
 pooled and then subtracted with porcine St fibroblast RNA  
 to create a subtracted porcine Peyer's patch library of  
 approximately 6,000 clones with an average insert size of  
 1.0 kbp."

## ORIGIN

Alignment Scores:  
 Pred. No.: 5.7e-35 Length: 476  
 Score: 462.00 Matches: 96  
 Percent Similarity: 95.15% Conservative: 2  
 Best Local Similarity: 93.20% Mismatches: 5  
 Query Match: 32.26% Indels: 1  
 DB: 6 Gaps: 0

US-10-015-388A-54 (1-280) x CB286548 (1-476)

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 Db 3 ACTGGCTGGGGGCCAGCCCTCCCGGACACCCAGGCGCTGCAGGCACAGCTGGCCCAA 62  
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 Qy 117 AlaPhePheHisAsnGlnProProSerLeuArgThrValGluPheValAlaGluArg 136  
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 Db 63 GCCTTCTTCCC-AACCCAGCGCCATCTCCGCGAGGACTGTGGAGTTTGTGCAGAGAGA 121  
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 Qy 137 IleGlySerAsnGlyValLysHisIleLysAlaThrLeuValAlaAspLeuValArgGln 156  
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 Db 122 ATTGGCTTAACCTGTGTCAAGCATATCAAGGCCACACTGGTAGCAGATCTGTGGCCAG 181  
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 Qy 157 AlaGluSerLeuLeuGlnGlnLeuValThrGlnGlyGluGlyGlyAspProhla 176  
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 Db 182 GCAGAGTCGCTTCTTCAGGAGCAGCTGTGACGAGGACGAGAGGGGGAGACCCAGCC 241  
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 Qy 177 GlnLeuLeuGluIleLeuLeuGlySerGlnLeuGlyProHisGlyAlaGlnAlaLeuAlaLeu 196  
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 Qy 197 GlyArgGlu 199  
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 Db 302 GGGCGGGAG 310

## RESULT 14

AW478789 288 bp mRNA linear EST 25-APR-2001  
 LOCUS 21675 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.  
 DEFINITION  
 ACCESSION AW478789  
 VERSION AW478789.1 GI:7048895  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 288)  
 AUTHORS Smith, R.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,  
 Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,  
 Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,  
 Chitko-McKown, C.G., Perte, G., Holt, I., Kazamychewa, S., Liang, F.,  
 Quackenbush, J. and Keele, J.W.  
 TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA  
 libraries and construction of a gene index for cattle  
 JOURNAL Genome Res. 11 (4), 626-630 (2001)  
 MEDLINE 21180013  
 PUBMED 11282978  
 COMMENT Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366



Qy 96 ThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAla 115  
Db 189 ACCAGCAGCCTGGGAGCCCTGCCTCTCCAGACCCAGCCAGGGGCTGAGGCTCAACTTGCT 248  
Qy 116 GlnAlaPhePheHisAsnGlnProProSerLeuArgArgThrValGlu 131  
Db 249 GAGGCTTTTTCACACACAGCCACCTCCCTGCGCAGGACTGTAGAA 296

Search completed: March 29, 2005, 10:59:04  
Job time : 3276 secs

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C 95	58	1.6	1164	6	AX098194	Sequence	C 168	57	1.6	1464	6	BD270355	50 human
C 96	58	1.6	1204	6	AX040958	Sequence	C 169	57	1.6	1485	6	AR177965	Sequence
C 97	58	1.6	1229	9	BC073962	Homo sapi	C 170	57	1.6	1576	9	HSM801341	Sequence
C 98	58	1.6	1314	6	AX098191	Sequence	C 171	57	1.6	1621	6	BD107842	36 human
C 99	58	1.6	1329	6	BD107881	36 human	C 172	57	1.6	1734	6	BD275139	48 Human
C 100	58	1.6	1361	6	BD223128	98 human	C 173	57	1.6	2000	6	BD252089	47 secret
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C 104	58	1.6	1376	6	BD223130	98 human	C 177	57	1.6	2581	6	AR339790	Sequence
C 105	58	1.6	1376	6	AR243828	Sequence	C 178	57	1.6	2581	6	BD131136	45 human
C 106	58	1.6	1388	6	BD260628	49 human	C 179	57	1.6	2584	6	BD140660	36 human
C 107	58	1.6	1390	6	BD260732	50 human	C 180	57	1.6	2584	6	AR409315	Sequence
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C 109	58	1.6	1411	6	AR340578	Sequence	C 182	57	1.6	2853	6	AX086566	Sequence
C 110	58	1.6	1480	6	AX780118	Sequence	C 183	57	1.6	3566	9	HSM803611	Sequence
C 111	58	1.6	1480	6	AX780119	Sequence	C 184	57	1.6	65016	2	AC090620	Homo sapi
C 112	58	1.6	1554	8	AB107693	Nicotiana	C 185	57	1.6	78000	9	AC115676	Homo sapi
C 113	58	1.6	1618	6	AR374729	Sequence	C 186	57	1.6	136417	9	AC007254	Homo sapi
C 114	58	1.6	1733	6	BD062047	Novel tum	C 187	57	1.6	156788	2	AC150449	Pan trogl
C 115	58	1.6	1733	6	CQ838245	Sequence	C 188	57	1.6	240864	2	AC006510	Homo sapi
C 116	58	1.6	1772	6	BD130999	67 Human	C 189	56	1.6	72	6	AX381283	Sequence
C 117	58	1.6	1772	6	AX251708	Sequence	C 190	56	1.6	73	6	AX381604	Sequence
C 118	58	1.6	1779	6	AR339750	Sequence	C 191	56	1.6	74	6	AX381324	Sequence
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C 120	58	1.6	1815	6	AX098200	Sequence	C 193	56	1.6	77	6	AX381197	Sequence
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C 122	58	1.6	1834	6	AX350867	Sequence	C 195	56	1.6	81	6	AX381811	Sequence
C 123	58	1.6	1834	6	AX074222	Sequence	C 196	56	1.6	82	6	AX381282	Sequence
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C 137	58	1.6	2242	6	CQ496562	Sequence	C 210	56	1.6	931	6	BD218549	71 human
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C 139	58	1.6	2259	6	BD260167	50 human	C 212	56	1.6	980	6	BD078436	101 human
C 140	58	1.6	2325	10	RNU30290	U30290 Rattus norv	C 213	56	1.6	1058	6	BD275398	50 Human
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C 142	58	1.6	2369	6	AR438050	Sequence	C 215	56	1.6	1261	6	BD194910	86 human
C 143	58	1.6	2391	6	CQ489398	Sequence	C 216	56	1.6	1261	6	CQ855238	Sequence
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C 145	58	1.6	2614	6	AX098201	Sequence	C 218	56	1.6	1367	6	BD074331	50 human
C 146	58	1.6	2713	6	AX474240	Sequence	C 219	56	1.6	1407	6	AX127526	Sequence
C 147	58	1.6	2713	6	AX474270	Sequence	C 220	56	1.6	1421	6	BD074318	50 human
C 148	58	1.6	2713	6	AX474271	Sequence	C 221	56	1.6	1722	6	BD218620	71 human
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C 151	58	1.6	2719	6	AR117332	Sequence	C 224	56	1.6	4773	6	CQ412935	Sequence
C 152	58	1.6	2719	6	AR411439	Sequence	C 225	56	1.6	128899	9	AC391139	Human DNA
C 153	58	1.6	2738	6	AX127525	Sequence	C 226	56	1.6	136901	2	AC041036	Homo sapi
C 154	58	1.6	2875	6	AX247632	Sequence	C 227	56	1.6	166173	2	AC023060	Homo sapi
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C 156	58	1.6	3021	6	BD275441	50 Human	C 229	56	1.6	169247	9	AL669970	Human DNA
C 157	58	1.6	3196	6	BD232172	Novel sec	C 230	56	1.6	174210	2	EX005241	Homo sapi
C 158	58	1.6	3354	6	BD249815	33 human	C 231	56	1.6	220000	2	AC108707	Homo sapi
C 159	58	1.6	5109	6	AX643010	Sequence	C 232	56	1.6	243558	9	AC010310	Sequence
C 160	58	1.6	87424	9	AC006077	Homo sapi	C 233	56	1.6	283951	2	AC109383	Rattus no
C 161	58	1.6	126034	9	AC008670	Homo sapi	C 234	56	1.6	291762	2	AC125887	Rattus no
C 162	58	1.6	174793	2	CNS051E5	Human chr	C 235	56	1.6	343504	2	AL158031	Homo sapi
C 163	58	1.6	240200	9	AC122075	Rattus no	C 236	55	1.5	129	6	AX901537	Sequence
C 164	57	1.6	1069	6	AR177949	Sequence	C 237	55	1.5	129	6	BD037070	Sequence
C 165	57	1.6	1315	6	AR162252	Sequence	C 238	55	1.5	131	6	AX902861	Sequence

C 239	55	1.5	131	6	BD038394	Sequence	BD038394	Sequence	C 312	54	1.5	2386	8	BNA9608	Brassica
C 240	55	1.5	172	6	AX261854	Sequence	AX261854	Sequence	C 313	54	1.5	2436	5	BC080972	BC080972 Xenopus t
C 241	55	1.5	432	9	BC040830	Homo sapi	BC040830	Homo sapi	C 314	54	1.5	2455	10	BC061762	BC061762 Rattus no
C 242	55	1.5	604	6	BD072953	70 human	BD072953	70 human	C 315	54	1.5	2530	10	BC052848	BC052848 Mus muscu
C 243	55	1.5	809	6	BD260752	Sequence	BD260752	Sequence	C 316	54	1.5	2649	9	BC063539	BC063539 Homo sapi
C 244	55	1.5	974	6	CQ493762	Sequence	CQ493762	Sequence	C 317	54	1.5	3006	6	AX497163	AX497163 Sequence
C 245	55	1.5	1001	6	BD276420	143 Human	BD276420	143 Human	C 318	54	1.5	3214	6	I32738	I32738 Sequence 17
C 246	55	1.5	3069	9	BC010058	Homo sapi	BC010058	Homo sapi	C 319	54	1.5	3214	6	I38714	I38714 Sequence 17
C 247	55	1.5	3451	6	EI3998	Cyanidium c	EI3998	Cyanidium c	C 320	54	1.5	3273	9	BC030532	BC030532 Homo sapi
C 248	55	1.5	36942	9	AC093782	Sequence	AC093782	Sequence	C 321	54	1.5	3552	6	CQ412820	CQ412820 Sequence
C 249	55	1.5	38486	9	AC083880	Homo sapi	AC083880	Homo sapi	C 322	54	1.5	3552	6	CQ489581	CQ489581 Sequence
C 250	55	1.5	38852	9	AC006261	Sequence	AC006261	Sequence	C 323	54	1.5	3552	6	CQ495422	CQ495422 Sequence
C 251	55	1.5	64557	2	AC130386	Homo sapi	AC130386	Homo sapi	C 324	54	1.5	5962	5	BC070852	BC070852 Xenopus l
C 252	55	1.5	75698	9	AP000228	Homo sapi	AP000228	Homo sapi	C 325	54	1.5	67024	9	AP001494	AP001494 Homo sapi
C 253	55	1.5	80878	9	AC011480	Homo sapi	AC011480	Homo sapi	C 326	54	1.5	85538	9	AC127904	AC127904 Homo sapi
C 254	55	1.5	100000	9	AP000140	Homo sapi	AP000140	Homo sapi	C 327	54	1.5	119569	9	AC020929	AC020929 Homo sapi
C 255	55	1.5	123722	9	AC018515	Sequence	AC018515	Sequence	C 328	54	1.5	123101	9	HS108713	HS108713 Homo sapi
C 256	55	1.5	132832	9	AC091934	Sequence	AC091934	Sequence	C 329	54	1.5	143045	9	AC008750	AC008750 Homo sapi
C 257	55	1.5	148290	9	AL359199	Human DNA	AL359199	Human DNA	C 330	54	1.5	164508	2	AC104130	AC104130 Homo sapi
C 258	55	1.5	150236	2	AC023292	Homo sapi	AC023292	Homo sapi	C 331	54	1.5	164652	2	AC021625	AC021625 Homo sapi
C 259	55	1.5	161014	9	AP000088	Homo sapi	AP000088	Homo sapi	C 332	54	1.5	172024	2	AC078971	AC078971 Homo sapi
C 260	55	1.5	168658	9	AC019278	Homo sapi	AC019278	Homo sapi	C 333	54	1.5	174695	2	AC149448	AC149448 Papio anu
C 261	55	1.5	169118	2	AC073313	Sequence	AC073313	Sequence	C 334	54	1.5	183946	2	AC009164	AC009164 Homo sapi
C 262	55	1.5	172274	9	AP000924	Homo sapi	AP000924	Homo sapi	C 335	54	1.5	184264	2	AC118233	AC118233 Mus muscu
C 263	55	1.5	172482	9	AC022309	Homo sapi	AC022309	Homo sapi	C 336	54	1.5	195993	2	AC134953	AC134953 Pan trogl
C 264	55	1.5	172985	2	AC087695	Sequence	AC087695	Sequence	C 337	54	1.5	212011	2	AC129932	AC129932 Mus muscu
C 265	55	1.5	174084	2	AC084395	Homo sapi	AC084395	Homo sapi	C 338	54	1.5	220173	9	AC012183	AC012183 Homo sapi
C 266	55	1.5	174311	9	AP002788	Homo sapi	AP002788	Homo sapi	C 339	53	1.5	58	6	AX381765	AX381765 Sequence
C 267	55	1.5	175645	9	AC073114	Sequence	AC073114	Sequence	C 340	53	1.5	60	6	AX381481	AX381481 Sequence
C 268	55	1.5	177163	9	AC100786	Homo sapi	AC100786	Homo sapi	C 341	53	1.5	69	6	E82858	E82858 Secretary p
C 269	55	1.5	178704	2	AC023180	Homo sapi	AC023180	Homo sapi	C 342	53	1.5	85	6	BD003061	BD003061 Polynucle
C 270	55	1.5	182557	2	AC091942	Sequence	AC091942	Sequence	C 343	53	1.5	90	6	AX381279	AX381279 Sequence
C 271	55	1.5	188992	9	AL157834	Human DNA	AL157834	Human DNA	C 344	53	1.5	125	6	AX494464	AX494464 Sequence
C 272	55	1.5	190394	9	AL157834	Human DNA	AL157834	Human DNA	C 345	53	1.5	127	9	IROEST143	IROEST143 Sequence
C 273	55	1.5	190592	2	AC015806	Homo sapi	AC015806	Homo sapi	C 346	53	1.5	144	6	BD138840	BD138840 Homo sapi
C 274	55	1.5	198146	2	AC023499	Homo sapi	AC023499	Homo sapi	C 347	53	1.5	144	6	BD138840	BD138840 Secreted
C 275	55	1.5	198764	9	AC103809	Homo sapi	AC103809	Homo sapi	C 348	53	1.5	144	6	BD005387	BD005387 Secreted
C 276	55	1.5	202418	2	AC150815	Sequence	AC150815	Sequence	C 349	53	1.5	160	6	AX494504	AX494504 Sequence
C 277	55	1.5	203521	9	BS000205	Callithrix	BS000205	Callithrix	C 350	53	1.5	173	6	AX185626	AX185626 Sequence
C 278	55	1.5	340000	9	AP001694	Homo sapi	AP001694	Homo sapi	C 351	53	1.5	204	6	CQ487345	CQ487345 Sequence
C 279	54	1.5	93	93	CQ832576	Sequence	CQ832576	Sequence	C 352	53	1.5	211	6	CQ483120	CQ483120 Sequence
C 280	54	1.5	221	6	CQ527278	Sequence	CQ527278	Sequence	C 353	53	1.5	214	6	CQ670912	CQ670912 Sequence
C 281	54	1.5	351	6	AR506477	Sequence	AR506477	Sequence	C 354	53	1.5	219	6	CQ528993	CQ528993 Sequence
C 282	54	1.5	510	6	CQ411734	Sequence	CQ411734	Sequence	C 355	53	1.5	222	6	CQ411279	CQ411279 Sequence
C 283	54	1.5	625	8	AF049925	Petunia x	AF049925	Petunia x	C 356	53	1.5	225	6	CQ701286	CQ701286 Sequence
C 284	54	1.5	763	10	BC028541	Mus muscu	BC028541	Mus muscu	C 357	53	1.5	226	6	CQ473951	CQ473951 Sequence
C 285	54	1.5	796	6	AX364304	Sequence	AX364304	Sequence	C 358	53	1.5	234	6	CQ397739	CQ397739 Sequence
C 286	54	1.5	854	6	AX430945	Sequence	AX430945	Sequence	C 359	53	1.5	234	6	CQ404036	CQ404036 Sequence
C 287	54	1.5	873	8	BT009024	Triticum	BT009024	Triticum	C 360	53	1.5	235	6	CQ529081	CQ529081 Sequence
C 288	54	1.5	911	8	AF083749	Arabidops	AF083749	Arabidops	C 361	53	1.5	240	6	CQ405709	CQ405709 Sequence
C 289	54	1.5	970	9	BC035850	Homo sapi	BC035850	Homo sapi	C 362	53	1.5	241	6	CQ398756	CQ398756 Sequence
C 290	54	1.5	1118	8	AF305075	Nicotiana	AF305075	Nicotiana	C 363	53	1.5	248	6	CQ529028	CQ529028 Sequence
C 291	54	1.5	1150	3	AF332209	Caenorhab	AF332209	Caenorhab	C 364	53	1.5	264	6	CQ467407	CQ467407 Sequence
C 292	54	1.5	1194	6	AX105295	Sequence	AX105295	Sequence	C 365	53	1.5	269	6	CQ475616	CQ475616 Sequence
C 293	54	1.5	1418	10	AF361490	Rattus no	AF361490	Rattus no	C 366	53	1.5	275	6	AX381137	AX381137 Sequence
C 294	54	1.5	1532	9	BC053733	Homo sapi	BC053733	Homo sapi	C 367	53	1.5	281	6	CQ410312	CQ410312 Sequence
C 295	54	1.5	1640	10	BC062007	Rattus no	BC062007	Rattus no	C 368	53	1.5	281	6	CQ504127	CQ504127 Sequence
C 296	54	1.5	1723	6	BD223494	94 human	BD223494	94 human	C 369	53	1.5	283	6	CQ529455	CQ529455 Sequence
C 297	54	1.5	1723	6	AR243128	Sequence	AR243128	Sequence	C 370	53	1.5	289	6	CQ423504	CQ423504 Sequence
C 298	54	1.5	1723	6	AR404309	Sequence	AR404309	Sequence	C 371	53	1.5	293	6	CQ432641	CQ432641 Sequence
C 299	54	1.5	1821	9	BC003056	Homo sapi	BC003056	Homo sapi	C 372	53	1.5	296	6	CQ398869	CQ398869 Sequence
C 300	54	1.5	1931	6	CQ382665	Sequence	CQ382665	Sequence	C 373	53	1.5	296	6	CQ405149	CQ405149 Sequence
C 301	54	1.5	1931	6	BD131019	67 Human	BD131019	67 Human	C 374	53	1.5	300	6	AX185628	AX185628 Sequence
C 302	54	1.5	1932	6	CQ383199	Sequence	CQ383199	Sequence	C 375	53	1.5	317	6	CQ483299	CQ483299 Sequence
C 303	54	1.5	1932	6	BD130953	67 Human	BD130953	67 Human	C 376	53	1.5	318	6	CQ399318	CQ399318 Sequence
C 304	54	1.5	1953	10	BC034135	Mus muscu	BC034135	Mus muscu	C 377	53	1.5	318	6	CQ405595	CQ405595 Sequence
C 305	54	1.5	1985	9	BC006345	Homo sapi	BC006345	Homo sapi	C 378	53	1.5	323	6	CQ529148	CQ529148 Sequence
C 306	54	1.5	2030	10	BC051019	Mus muscu	BC051019	Mus muscu	C 379	53	1.5	328	6	CQ410507	CQ410507 Sequence
C 307	54	1.5	2073	9	HSW801468	Sequence	HSW801468	Sequence	C 380	53	1.5	332	6	CQ398523	CQ398523 Sequence
C 308	54	1.5	2093	5	BC074543	Homo sapi	BC074543	Homo sapi	C 381	53	1.5	332	6	CQ404810	CQ404810 Sequence
C 309	54	1.5	2240	5	BC066420	Danio rer	BC066420	Danio rer	C 382	53	1.5	336	6	CQ397671	CQ397671 Sequence
C 310	54	1.5	2261	10	BC043710	Mus muscu	BC043710	Mus muscu	C 383	53	1.5	337	6	CQ403968	CQ403968 Sequence
C 311	54	1.5	2269	6	AX280370	Sequence	AX280370	Sequence	C 384	53	1.5	337	6	CQ529025	CQ529025 Sequence

c 385	53	1.5	338	6	CQ517148	Sequence	458	53	1.5	524	6	CQ528859	Sequence	CQ528859
386	53	1.5	343	6	CQ529095	Sequence	459	53	1.5	531	6	CQ394991	Sequence	CQ394991
387	53	1.5	346	6	CQ410605	Sequence	460	53	1.5	531	6	CQ401337	Sequence	CQ401337
388	53	1.5	350	6	CQ398682	Sequence	c 461	53	1.5	531	6	CQ524679	Sequence	CQ524679
389	53	1.5	350	6	CQ404965	Sequence	462	53	1.5	535	6	CQ471891	Sequence	CQ471891
390	53	1.5	351	6	CQ397828	Sequence	463	53	1.5	536	6	CQ505690	Sequence	CQ505690
391	53	1.5	351	6	CQ404123	Sequence	464	53	1.5	539	6	CQ410791	Sequence	CQ410791
c 392	53	1.5	352	6	CQ525050	Sequence	c 465	53	1.5	553	8	AY080594	Arabidops	AY080594
393	53	1.5	352	6	CQ529009	Sequence	466	53	1.5	554	6	CQ417692	Sequence	CQ417692
394	53	1.5	358	6	CQ399231	Sequence	467	53	1.5	567	6	CQ525234	Sequence	CQ525234
395	53	1.5	358	6	CQ405509	Sequence	468	53	1.5	570	6	CQ398736	Sequence	CQ398736
396	53	1.5	361	6	CQ465788	Sequence	469	53	1.5	570	6	CQ405019	Sequence	CQ405019
c 397	53	1.5	367	6	CQ523125	Sequence	c 470	53	1.5	577	8	BT009563	Triticum	BT009563
398	53	1.5	375	6	CQ411403	Sequence	c 471	53	1.5	587	9	BC070308	Homo sapi	BC070308
399	53	1.5	375	6	CQ513063	Sequence	472	53	1.5	597	6	AX187052	Sequence	AX187052
400	53	1.5	380	6	CQ410420	Sequence	473	53	1.5	612	6	AX187054	Sequence	AX187054
401	53	1.5	383	6	CQ410935	Sequence	474	53	1.5	621	6	AX187131	Sequence	AX187131
402	53	1.5	383	6	CQ502211	Sequence	475	53	1.5	629	6	CQ481104	Sequence	CQ481104
403	53	1.5	383	6	CQ511079	Sequence	476	53	1.5	638	6	CQ398462	Sequence	CQ398462
404	53	1.5	384	6	CQ411533	Sequence	477	53	1.5	638	6	CQ404749	Sequence	CQ404749
405	53	1.5	385	6	CQ411979	Sequence	478	53	1.5	644	6	CQ431087	Sequence	CQ431087
406	53	1.5	386	6	CQ411194	Sequence	c 479	53	1.5	653	10	BC065379	Mus muscu	BC065379
407	53	1.5	386	6	CQ525228	Sequence	c 480	53	1.5	682	9	AK000414	Homo sapi	AK000414
408	53	1.5	388	6	CQ410454	Sequence	c 481	53	1.5	686	10	BC060302	Mus muscu	BC060302
409	53	1.5	388	6	CQ427522	Sequence	482	53	1.5	693	6	CQ422235	Sequence	CQ422235
410	53	1.5	390	6	CQ410737	Sequence	483	53	1.5	705	6	CQ397951	Sequence	CQ397951
411	53	1.5	396	6	AR391187	Sequence	484	53	1.5	705	6	CQ404243	Sequence	CQ404243
412	53	1.5	396	6	AR392892	Sequence	485	53	1.5	722	6	CQ432325	Sequence	CQ432325
413	53	1.5	396	6	AR489622	Sequence	486	53	1.5	723	6	CQ397655	Sequence	CQ397655
414	53	1.5	396	6	AR493863	Sequence	487	53	1.5	723	6	CQ403953	Sequence	CQ403953
415	53	1.5	396	6	AX093192	Sequence	488	53	1.5	731	6	CQ432687	Sequence	CQ432687
416	53	1.5	404	6	CQ524546	Sequence	489	53	1.5	739	6	CQ432333	Sequence	CQ432333
417	53	1.5	406	6	CQ528922	Sequence	490	53	1.5	752	6	CQ411585	Sequence	CQ411585
418	53	1.5	407	6	CQ528868	Sequence	491	53	1.5	755	6	CQ410683	Sequence	CQ410683
419	53	1.5	410	6	CQ397607	Sequence	492	53	1.5	764	6	AX187080	Sequence	AX187080
420	53	1.5	410	6	CQ403906	Sequence	c 493	53	1.5	796	8	AY114140	Apium gra	AY114140
421	53	1.5	414	6	CQ410920	Sequence	c 494	53	1.5	826	6	BD192687	123 human	BD192687
422	53	1.5	420	6	CQ524985	Sequence	c 495	53	1.5	826	6	AR184158	Sequence	AR184158
423	53	1.5	425	6	CQ506214	Sequence	496	53	1.5	830	6	CQ482724	Sequence	CQ482724
424	53	1.5	426	6	CQ507189	Sequence	497	53	1.5	851	6	CQ427278	Sequence	CQ427278
425	53	1.5	426	6	CQ512975	Sequence	c 498	53	1.5	862	8	AF46582282	Allium ce	AF465823
426	53	1.5	428	6	AX286914	Sequence	c 499	53	1.5	884	9	AK026462	Homo sapi	AK026462
427	53	1.5	433	6	CQ397727	Sequence	c 500	53	1.5	892	6	BD269299	33 human	BD269299
428	53	1.5	433	6	CQ404024	Sequence	c 501	53	1.5	933	10	BC048388	Mus muscu	BC048388
429	53	1.5	433	6	CQ411349	Sequence	c 502	53	1.5	951	10	BC039793	Mus muscu	BC039793
430	53	1.5	434	6	CQ410846	Sequence	c 503	53	1.5	951	10	BC060993	Mus muscu	BC060993
431	53	1.5	436	6	CQ503829	Sequence	c 504	53	1.5	961	14	MDU76034	Microplis	U76034
432	53	1.5	436	6	CQ512635	Sequence	c 505	53	1.5	1019	10	BC002004	BC002004	BC002004
433	53	1.5	440	6	CQ396156	Sequence	c 506	53	1.5	1034	6	AR487878	Mus muscu	AR487878
434	53	1.5	440	6	CQ402481	Sequence	c 507	53	1.5	1052	6	BD223087	98 human	BD223087
435	53	1.5	443	6	CQ524852	Sequence	c 508	53	1.5	1052	6	AR243785	Sequence	AR243785
436	53	1.5	445	6	CQ473555	Sequence	c 509	53	1.5	1053	5	BC077790	Xenopus l	BC077790
437	53	1.5	457	6	CQ427379	Sequence	c 510	53	1.5	1064	3	AK174286	Ciona int	AK174286
c 438	53	1.5	457	6	CQ516772	Sequence	c 511	53	1.5	1071	9	BC009727	Homo sapi	BC009727
c 439	53	1.5	459	6	CQ522436	Sequence	c 512	53	1.5	1123	5	BC077523	Xenopus l	BC077523
440	53	1.5	462	6	CQ502253	Sequence	c 513	53	1.5	1124	5	BC084519	Xenopus t	BC084519
441	53	1.5	462	6	CQ511117	Sequence	c 514	53	1.5	1173	3	AY069745	Drosophil	AY069745
442	53	1.5	463	6	CQ407721	Sequence	c 515	53	1.5	1184	9	BC025928	Homo sapi	BC025928
443	53	1.5	463	6	CQ417793	Sequence	c 516	53	1.5	1184	10	BC052699	Mus muscu	BC052699
444	53	1.5	463	6	CQ529157	Sequence	c 517	53	1.5	1184	10	BC061042	Mus muscu	BC061042
445	53	1.5	472	6	CQ483076	Sequence	c 518	53	1.5	1197	9	BC071820	Homo sapi	BC071820
446	53	1.5	474	6	CQ529586	Sequence	c 519	53	1.5	1205	9	BC039058	Homo sapi	BC039058
447	53	1.5	478	6	CQ475731	Sequence	c 520	53	1.5	1223	6	AR282251	Sequence	AR282251
448	53	1.5	479	6	CQ524663	Sequence	c 521	53	1.5	1223	6	AR399207	Sequence	AR399207
449	53	1.5	486	6	CQ507231	Sequence	c 522	53	1.5	1248	9	BC041457	Homo sapi	BC041457
450	53	1.5	491	6	CQ410290	Sequence	c 523	53	1.5	1264	10	BC024097	Mus muscu	BC024097
451	53	1.5	496	6	CQ524816	Sequence	c 524	53	1.5	1279	5	BC061954	Danio rer	BC061954
452	53	1.5	498	6	CQ481059	Sequence	c 525	53	1.5	1282	9	BC017745	Homo sapi	BC017745
453	53	1.5	504	6	CQ524846	Sequence	c 526	53	1.5	1288	3	TBBDPWSYN	Z54162 T.brucei	BT009194
c 454	53	1.5	508	10	AF352782	Mus muscu	c 527	53	1.5	1291	8	BT009194	Triticum	BT009194
455	53	1.5	516	6	CQ525238	Sequence	c 528	53	1.5	1298	9	BC004945	Homo sapi	BC004945
456	53	1.5	522	6	CQ411909	Sequence	c 529	53	1.5	1300	6	AX244569	Sequence	AX244569
457	53	1.5	524	6	CQ408865	Sequence	c 530	53	1.5	1300	8	AF141642	Vitis ber	AF141642

C 531	1.5	1301	8	BT009271	Triticum	C 604	53	1.5	1845	5	XLCYCE	Z13966 Xenopus lae
C 532	1.5	1305	8	PCDIALDHA	Z19568 P.deltoides	C 605	53	1.5	1851	9	AK026744	AK026744 Homo sapi
C 533	1.5	1310	8	AF464902	Oryza sat	C 606	53	1.5	1862	10	BC060687	BC060687 Mus muscu
C 534	1.5	1310	10	BC019402	BC019402 Mus muscu	C 607	53	1.5	1866	8	AB042956	AB042956 Nicotiana
C 535	1.5	1320	8	AF061570	Arabidops	C 608	53	1.5	1910	9	BSM801106	AL117416 Homo sapi
C 536	1.5	1334	3	AY360135	Dictyoste	C 609	53	1.5	1921	10	BC005597	BC005597 Mus muscu
C 537	1.5	1355	6	AR527700	Sequence	C 610	53	1.5	1929	8	AB025714	AB025714 Nicotiana
C 538	1.5	1355	6	AX074159	Sequence	C 611	53	1.5	1941	5	BC077766	BC077766 Xenopus l
C 539	1.5	1376	6	BD194853	86 human	C 612	53	1.5	1951	5	BC078039	BC078039 Xenopus l
C 540	1.5	1376	6	CQ855181	Sequence	C 613	53	1.5	1975	5	BC067563	BC067563 Danio rer
C 541	1.5	1400	5	BC071084	Xenopus l	C 614	53	1.5	1977	6	BD192668	BD192668 123 human
C 542	1.5	1403	10	BC024509	Mus muscu	C 615	53	1.5	1977	6	AR184139	AR184139 Sequence
C 543	1.5	1407	3	AF344172	Ciona int	C 616	53	1.5	1988	10	BC029720	BC029720 Mus muscu
C 544	1.5	1407	10	BC013450	BC013450 Mus muscu	C 617	53	1.5	1993	10	BC062202	BC062202 Mus muscu
C 545	1.5	1410	9	BC008364	Homo sapi	C 618	53	1.5	2009	3	AK116580	AK116580 Ciona int
C 546	1.5	1410	10	BC083136	BC083136 Mus muscu	C 619	53	1.5	2073	9	BSM802983	AL713655 Homo sapi
C 547	1.5	1414	10	BC010336	BC010336 Mus muscu	C 620	53	1.5	2085	5	BC077186	BC077186 Xenopus l
C 548	1.5	1443	10	BC061219	BC061219 Mus muscu	C 621	53	1.5	2102	5	BC056790	BC056790 Danio rer
C 549	1.5	1445	6	AX052751	Sequence	C 622	53	1.5	2102	10	BC039217	BC039217 Mus muscu
C 550	1.5	1473	10	BC013520	BC013520 Mus muscu	C 623	53	1.5	2103	6	BD223104	BD223104 98 human
C 551	1.5	1481	10	BC034714	BC034714 Mus muscu	C 624	53	1.5	2103	6	AR243802	AR243802 Sequence
C 552	1.5	1494	5	BC063335	BC063335 Xenopus t	C 625	53	1.5	2134	10	BC024712	BC024712 Mus muscu
C 553	1.5	1495	5	BC046652	BC046652 Xenopus l	C 626	53	1.5	2155	9	BC015749	BC015749 Homo sapi
C 554	1.5	1505	9	BC015812	BC015812 Homo sapi	C 627	53	1.5	2174	10	BC036173	BC036173 Mus muscu
C 555	1.5	1518	9	BC008591	BC008591 Homo sapi	C 628	53	1.5	2175	5	AB056480	AB056480 Rana cate
C 556	1.5	1521	9	BC014584	BC014584 Homo sapi	C 629	53	1.5	2181	10	BC026983	BC026983 Mus muscu
C 557	1.5	1526	5	BC084319	BC084319 Xenopus l	C 630	53	1.5	2187	10	BC052181	BC052181 Mus muscu
C 558	1.5	1534	5	BC076027	Danio rer	C 631	53	1.5	2191	9	BC034703	BC034703 Homo sapi
C 559	1.5	1550	6	CQ795868	CQ795868 Sequence	C 632	53	1.5	2193	9	AB070198	AB070198 Macaca fa
C 560	1.5	1550	8	AF486650	AF486650 Citrus x	C 633	53	1.5	2198	9	BC031550	BC031550 Homo sapi
C 561	1.5	1582	6	A77033	A77033 Sequence 10	C 634	53	1.5	2208	9	BC016137	BC016137 Homo sapi
C 562	1.5	1582	6	A77035	A77035 Sequence 12	C 635	53	1.5	2230	9	BC053996	BC053996 Homo sapi
C 563	1.5	1582	6	AR100218	AR100218 Sequence	C 636	53	1.5	2329	5	BC074616	BC074616 Xenopus t
C 564	1.5	1582	6	AR100220	AR100220 Sequence	C 637	53	1.5	2384	6	AX780522	AX780522 Sequence
C 565	1.5	1585	5	BC083224	BC083224 Danio rer	C 638	53	1.5	2384	6	AX780523	AX780523 Sequence
C 566	1.5	1591	9	BSM801261	BSM801261 Homo sapi	C 639	53	1.5	2430	9	BSM805511	AL834423 Homo sapi
C 567	1.5	1591	10	AF087943	AF087943 Rattus no	C 640	53	1.5	2444	8	AF401636	AF401636 Rehmannia
C 568	1.5	1602	9	AF111801	BC024516 Mus muscu	C 641	53	1.5	2444	10	BC051679	BC051679 Mus muscu
C 569	1.5	1603	10	BC024516	BC024516 Mus muscu	C 642	53	1.5	2463	10	BC005449	BC005449 Mus muscu
C 570	1.5	1605	8	BT009414	Triticum	C 643	53	1.5	2492	5	BC074549	BC074549 Xenopus t
C 571	1.5	1612	10	BC079028	BC079028 Rattus no	C 644	53	1.5	2515	10	BC081769	BC081769 Rattus no
C 572	1.5	1615	5	BC044158	BC044158 Danio rer	C 645	53	1.5	2516	9	BC020965	BC020965 Homo sapi
C 573	1.5	1616	9	BC013416	BC013416 Homo sapi	C 646	53	1.5	2578	10	BC026526	BC026526 Mus muscu
C 574	1.5	1617	10	BC043453	BC043453 Mus muscu	C 647	53	1.5	2609	10	BC034658	BC034658 Mus muscu
C 575	1.5	1621	9	BSM803093	AL713720 Homo sapi	C 648	53	1.5	2635	5	BC067384	BC067384 Danio rer
C 576	1.5	1623	9	BC030572	BC030572 Homo sapi	C 649	53	1.5	2645	3	AY118446	AY118446 Drosophil
C 577	1.5	1632	5	BC045260	BC045260 Xenopus l	C 650	53	1.5	2678	9	BSM802267	AL137533 Homo sapi
C 578	1.5	1638	5	BC049298	BC049298 Danio rer	C 651	53	1.5	2712	6	AX686742	AX686742 Sequence
C 579	1.5	1640	9	BC050738	BC050738 Homo sapi	C 652	53	1.5	2712	6	AX780361	AX780361 Sequence
C 580	1.5	1656	5	BC064161	BC064161 Xenopus t	C 653	53	1.5	2712	9	BC001199	BC001199 Homo sapi
C 581	1.5	1656	5	BC068336	BC068336 Danio rer	C 654	53	1.5	2722	10	BC075615	BC075615 Mus muscu
C 582	1.5	1665	3	AB025584	AB025584 Dictyoste	C 655	53	1.5	2756	5	BC063896	BC063896 Xenopus t
C 583	1.5	1667	10	BC019215	BC019215 Mus muscu	C 656	53	1.5	2767	10	BC066791	BC066791 Mus muscu
C 584	1.5	1678	9	BSM802263	AL137530 Homo sapi	C 657	53	1.5	2780	5	BC056280	BC056280 Danio rer
C 585	1.5	1694	6	BD132536	BD132536 Secreted	C 658	53	1.5	2780	5	BC023021	BC023021 Homo sapi
C 586	1.5	1707	6	AR487851	AR487851 Sequence	C 659	53	1.5	2819	5	AF267849	AF267849 Xenopus l
C 587	1.5	1707	10	BC026570	BC026570 Mus muscu	C 660	53	1.5	2838	6	AX249742	AX249742 Sequence
C 588	1.5	1719	10	BC056192	BC056192 Mus muscu	C 661	53	1.5	2914	10	BC050274	BC050274 Mus muscu
C 589	1.5	1724	9	BC003101	BC003101 Homo sapi	C 662	53	1.5	3016	10	BC083896	BC083896 Rattus no
C 590	1.5	1744	8	ATPYK10	X89413 Arabidopsis	C 663	53	1.5	3038	9	BSM806221	BSM806221 Homo sapi
C 591	1.5	1760	9	BC035407	BC035407 Homo sapi	C 664	53	1.5	3285	9	AK130342	AK130342 Homo sapi
C 592	1.5	1779	5	BC068210	BC068210 Homo sapi	C 665	53	1.5	3353	9	BSM807301	BSM807301 Homo sapi
C 593	1.5	1782	5	BC080059	BC080059 Xenopus l	C 666	53	1.5	3370	9	BC036689	BC036689 Homo sapi
C 594	1.5	1784	9	BC018906	BC018906 Homo sapi	C 667	53	1.5	3390	10	BC010727	BC010727 Mus muscu
C 595	1.5	1795	9	BC009439	BC009439 Homo sapi	C 668	53	1.5	3396	5	BC070774	BC070774 Xenopus l
C 596	1.5	1802	3	AK112634	AK112634 Ciona int	C 669	53	1.5	3440	9	BC013609	BC013609 Homo sapi
C 597	1.5	1806	6	BC045509	BC045509 Danio rer	C 670	53	1.5	3468	10	BC054379	BC054379 Mus muscu
C 598	1.5	1812	6	BD227271	BD227271 Secreted	C 671	53	1.5	3473	9	BC030601	BC030601 Homo sapi
C 599	1.5	1817	9	BC038370	BC038370 Homo sapi	C 672	53	1.5	3478	10	BC068301	BC068301 Mus muscu
C 600	1.5	1820	5	BC056518	BC056518 Danio rer	C 673	53	1.5	3501	6	AS28471	AS28471 Sequence
C 601	1.5	1827	6	AX556899	AX556899 Sequence	C 674	53	1.5	3501	6	AX463904	AX463904 Sequence
C 602	1.5	1838	9	BC039122	BC039122 Homo sapi	C 675	53	1.5	3581	6	AR034821	AR034821 Sequence
C 603	1.5	1840	3	DDU73686	U73686 Dictyostell	C 676	53	1.5	3581	6	E07381	E07381 cdNA encodi

C 677	53	1.5	3724	10	BC044902	BC044902 Mus muscu	C 750	53	1.5	191728	2	AL512269	AL512269 Homo sapi
C 678	53	1.5	3734	9	HS806342	BX538141 Homo sapi	751	53	1.5	193072	2	AC110986	AC110986 Rattus no
C 679	53	1.5	3815	9	BC025777	BC025777 Homo sapi	752	53	1.5	193894	2	AC114730	AC114730 Homo sapi
C 680	53	1.5	3859	10	MM0289242	AJ289242 Mus muscu	C 753	53	1.5	197817	2	AP001185	AP001185 Homo sapi
C 681	53	1.5	3922	9	HS804163	AL832852 Homo sapi	C 754	53	1.5	197915	2	BX927328	BX927328 Danio rer
C 682	53	1.5	4325	10	BC060196	BC060196 Mus muscu	755	53	1.5	197925	2	AC091308	AC091308 Mus muscu
C 683	53	1.5	4329	9	BC071579	BC071579 Homo sapi	756	53	1.5	198466	2	AC150006	AC150006 Pan trogl
C 684	53	1.5	4435	5	XLMTLZ	Z97214 Xenopus lae	C 757	53	1.5	200711	2	AC133960	AC133960 Homo sapi
C 685	53	1.5	4533	3	BC030221	BC030221 Homo sapi	758	53	1.5	201400	2	AL929539	AL929539 Homo sapi
C 686	53	1.5	4875	3	AB009080	AB009080 Dictyoste	C 759	53	1.5	203120	2	AC148499	AC148499 Callithri
C 687	53	1.5	6163	10	BC052150	BC052150 Mus muscu	C 760	53	1.5	205102	2	AC148500	AC148500 Callithri
C 688	53	1.5	6182	5	BC073527	BC073527 Dictyoste	761	53	1.5	209387	2	AC127401	AC127401 Rattus no
C 689	53	1.5	7801	3	AY160101	AY160101 Dictyoste	762	53	1.5	209387	2	AC096448	AC096448 Rattus no
C 690	53	1.5	10008	9	HS807741	BX647595 Homo sapi	763	53	1.5	221265	2	AC106345	AC106345 Rattus no
C 691	53	1.5	21526	9	AP001618	AP001618 Homo sapi	764	53	1.5	221897	2	AC106320	AC106320 Rattus no
C 692	53	1.5	23499	2	AC149322	AC149322 Phakopsor	765	53	1.5	222685	2	AC140971	AC140971 Canis fam
C 693	53	1.5	30439	2	AC145658	AC145658 Homo sapi	766	53	1.5	223958	2	AC127401	AC127401 Rattus no
C 694	53	1.5	38692	3	AC116919	AC116919 Dictyoste	767	53	1.5	237615	2	AC138257	AC138257 Mus muscu
C 695	53	1.5	40116	6	AX5733409	AX5733409 Sequence	C 768	53	1.5	238604	2	AC115164	AC115164 Rattus no
C 696	53	1.5	40116	6	AX573386	AX573386 Sequence	769	53	1.5	252989	2	AC126984	AC126984 Rattus no
C 697	53	1.5	40611	3	AC116987	AC116987 Dictyoste	C 770	53	1.5	264232	2	AC151602	AC151602 Mus muscu
C 698	53	1.5	40661	8	BX842617	BX842617 Neurospor	C 771	53	1.5	296096	2	AC110522	AC110522 Mus muscu
C 699	53	1.5	49999	6	AX015915	AX015915 Sequence	772	53	1.5	331039	3	AC116979	AC116979 Dictyoste
C 700	53	1.5	54865	9	AC126124	AC126124 Homo sapi	773	53	1.5	336578	9	AP001745	AP001745 Homo sapi
C 701	53	1.5	64707	3	AC115607	AC115607 Dictyoste	C 774	53	1.5	342743	2	AC103119	AC103119 Rattus no
C 702	53	1.5	82139	3	AC115684	AC115684 Dictyoste	775	52	1.5	56	6	AX381739	AX381739 Sequence
C 703	53	1.5	84550	3	PFWAL1P2_3	Continuation (4 of	776	52	1.5	72	6	AX381405	AX381405 Sequence
C 704	53	1.5	85165	8	NC99H12	AL451018 Neurospor	777	52	1.5	193	6	CQ411913	CQ411913 Sequence
C 705	53	1.5	94636	2	BX997739	BX997739 Danio rer	778	52	1.5	226	6	AX184991	AX184991 Sequence
C 706	53	1.5	97790	2	AC101676_3	Continuation (4 of	C 779	52	1.5	258	6	AX423856	AX423856 Sequence
C 707	53	1.5	102370	9	HSJ976013	AL117354 Human DNA	C 780	52	1.5	258	6	AX984550	AX984550 Sequence
C 708	53	1.5	110000	2	AC140833_1	Continuation (2 of	C 781	52	1.5	258	6	BD119409	BD119409 EST and e
C 709	53	1.5	110000	3	AC116305_3	Continuation (4 of	C 782	52	1.5	267	6	CQ524749	CQ524749 Sequence
C 710	53	1.5	111882	3	AC115612	AC115612 Dictyoste	783	52	1.5	271	6	CQ423793	CQ423793 Sequence
C 711	53	1.5	119219	8	BX842631	BX842631 Neurospor	C 784	52	1.5	276	6	CQ526564	CQ526564 Sequence
C 712	53	1.5	120379	9	AC073885	AC073885 Homo sapi	C 785	52	1.5	276	6	AX426832	AX426832 Sequence
C 713	53	1.5	125958	3	AC115592	AC115592 Dictyoste	C 786	52	1.5	276	6	AX987526	AX987526 Sequence
C 714	53	1.5	132644	9	AC104801	AC104801 Homo sapi	C 787	52	1.5	282	6	BD122385	BD122385 EST and e
C 715	53	1.5	138403	9	BS000131	BS000131 Pan trogl	788	52	1.5	290	8	CNS010XQ	AL116946 Botrytis
C 716	53	1.5	142916	9	AL928921	AL928921 Human DNA	789	52	1.5	294	6	CQ398035	CQ398035 Sequence
C 717	53	1.5	147201	2	AC053469	AC053469 Homo sapi	790	52	1.5	294	6	CQ404327	CQ404327 Sequence
C 718	53	1.5	151700	9	AC133528	AC133528 Homo sapi	791	52	1.5	294	6	CQ524533	CQ524533 Sequence
C 719	53	1.5	151759	2	AC149967	AC149967 Strongylo	C 792	52	1.5	294	6	CQ488101	CQ488101 Sequence
C 720	53	1.5	152665	2	AC027005	AC027005 Homo sapi	C 793	52	1.5	295	6	CQ517890	CQ517890 Sequence
C 721	53	1.5	153751	3	AC116551	AC116551 Dictyoste	C 794	52	1.5	303	6	CQ517890	CQ517890 Sequence
C 722	53	1.5	153807	2	AC015823	AC015823 Homo sapi	C 795	52	1.5	314	6	CQ472429	CQ472429 Sequence
C 723	53	1.5	156975	2	CR394534	CR394534 Danio rer	C 796	52	1.5	337	6	CQ523858	CQ523858 Sequence
C 724	53	1.5	158198	2	AC012013	AC012013 Homo sapi	C 797	52	1.5	358	6	CQ516500	CQ516500 Sequence
C 725	53	1.5	158408	2	BX927402	BX927402 Danio rer	C 798	52	1.5	373	6	CQ526143	CQ526143 Sequence
C 726	53	1.5	159234	2	AC108397	AC108397 Mus muscu	C 799	52	1.5	380	6	CQ517942	CQ517942 Sequence
C 727	53	1.5	160237	2	AC149093	AC149093 Pan trogl	800	52	1.5	384	6	AX185690	AX185690 Sequence
C 728	53	1.5	160390	2	AC0688186	AC0688186 Homo sapi	C 801	52	1.5	391	6	CQ515943	CQ515943 Sequence
C 729	53	1.5	162771	9	AC138781	AC138781 Homo sapi	C 802	52	1.5	394	6	CQ517396	CQ517396 Sequence
C 730	53	1.5	163494	2	AP002391	AP002391 Homo sapi	803	52	1.5	396	6	AR391219	AR391219 Sequence
C 731	53	1.5	163635	2	CR392027	CR392027 Danio rer	804	52	1.5	396	6	AR392924	AR392924 Sequence
C 732	53	1.5	163635	2	CR392027	CR392027 Danio rer	805	52	1.5	396	6	AR489654	AR489654 Sequence
C 733	53	1.5	165415	2	AC016663	AC016663 Homo sapi	806	52	1.5	396	6	AR493895	AR493895 Sequence
C 734	53	1.5	167082	2	AC021472	AC021472 Homo sapi	807	52	1.5	396	6	AR093224	AR093224 Sequence
C 735	53	1.5	167403	2	AC015686	AC015686 Homo sapi	808	52	1.5	399	6	AR085693	AR085693 Sequence
C 736	53	1.5	169032	2	AP0156431	AP0156431 Homo sapi	C 809	52	1.5	399	6	I18358	I18358 Sequence 13
C 737	53	1.5	169124	2	AP001375	AP001375 Homo sapi	C 810	52	1.5	399	6	I21345	I21345 Sequence 12
C 738	53	1.5	169932	9	AC141741	AC141741 Apis mell	811	52	1.5	399	6	I34395	I34395 Sequence 13
C 739	53	1.5	173169	9	AC068538	AC068538 Homo sapi	C 812	52	1.5	402	6	Q427146	Q427146 Sequence
C 740	53	1.5	173232	2	AC009830	AC009830 Homo sapi	813	52	1.5	404	6	CQ517410	CQ517410 Sequence
C 741	53	1.5	180736	2	AC023925	AC023925 Homo sapi	C 814	52	1.5	419	9	BC079477	BC079477 Homo sapi
C 742	53	1.5	182871	3	AC117176	AC117176 Dictyoste	C 815	52	1.5	423	6	CQ669214	CQ669214 Sequence
C 743	53	1.5	183689	2	AC146129	AC146129 Pan trogl	C 816	52	1.5	425	3	AK174345	AK174345 Ciona int
C 744	53	1.5	185571	9	AC133781	AC133781 Homo sapi	C 817	52	1.5	429	6	CQ517247	CQ517247 Sequence
C 745	53	1.5	185666	2	CR405687	CR405687 Mus muscu	C 818	52	1.5	435	8	CA8487043	AJ487043 Cicer ari
C 746	53	1.5	187549	2	AC101747	AC101747 Mus muscu	C 819	52	1.5	436	6	AX186794	AX186794 Sequence
C 747	53	1.5	189072	2	AC113496	AC113496 Mus muscu	C 820	52	1.5	442	6	CQ524625	CQ524625 Sequence
C 748	53	1.5	189445	2	AC018739	AC018739 Homo sapi	C 821	52	1.5	451	6	CQ467469	CQ467469 Sequence
C 749	53	1.5	191154	2	AC132150	AC132150 Homo sapi	822	52	1.5				

C 823	823	52	1.5	467	6	CQ524824	Sequence	C 896	52	1.5	1174	6	CQ827970	Sequence
C 824	824	52	1.5	495	6	CQ409678	Sequence	C 897	52	1.5	1175	9	AB072787	Macaca fa
C 825	825	52	1.5	496	6	CQ525103	Sequence	C 898	52	1.5	1202	3	AY122189	Drosophila
C 826	826	52	1.5	501	5	BC077673	Xenopus t	C 899	52	1.5	1207	9	BC042078	Homo sapi
C 827	827	52	1.5	515	6	CQ399071	Sequence	C 900	52	1.5	1208	5	GSPMADPR	X82397 Gallus sp.
C 828	828	52	1.5	515	6	CQ405350	Sequence	C 901	52	1.5	1220	5	BC065349	Danio rer
C 829	829	52	1.5	534	6	CX284254	Sequence	C 902	52	1.5	1229	10	BC055401	Mus muscu
C 830	830	52	1.5	556	6	CQ508215	Sequence	C 903	52	1.5	1248	9	BC013747	Homo sapi
C 831	831	52	1.5	556	6	CQ508315	Sequence	C 904	52	1.5	1255	9	BC069211	Homo sapi
C 832	832	52	1.5	556	6	CQ510257	Sequence	C 905	52	1.5	1271	9	BC035309	Homo sapi
C 833	833	52	1.5	556	6	CQ511753	Sequence	C 906	52	1.5	1291	6	BD250012	Insect p5
C 834	834	52	1.5	560	3	AF107490	Pasciolla	C 907	52	1.5	1301	3	AK174651	Ciona int
C 835	835	52	1.5	571	10	BC035956	Mus muscu	C 908	52	1.5	1325	9	BC002365	Homo sapi
C 836	836	52	1.5	572	9	BC032439	Homo sapi	C 909	52	1.5	1335	9	AF271350	Homo sapi
C 837	837	52	1.5	574	6	CQ525654	Sequence	C 910	52	1.5	1340	5	BC055268	Xenopus t
C 838	838	52	1.5	605	8	AF079185	Arabidops	C 911	52	1.5	1340	9	AK024992	Homo sapi
C 839	839	52	1.5	605	9	BC016300	Homo sapi	C 912	52	1.5	1345	10	BC048718	Mus muscu
C 840	840	52	1.5	612	6	AR506683	Sequence	C 913	52	1.5	1353	3	AY070501	Drosophila
C 841	841	52	1.5	620	6	AR090422	Sequence	C 914	52	1.5	1370	8	BT009638	Triticum
C 842	842	52	1.5	629	3	AY437139	Amblyomma	C 915	52	1.5	1380	5	BC078271	Danio rer
C 843	843	52	1.5	663	10	BC058460	Rattus no	C 916	52	1.5	1400	5	BC076441	Danio rer
C 844	844	52	1.5	677	5	BC053818	Xenopus t	C 917	52	1.5	1414	9	BC063670	Homo sapi
C 845	845	52	1.5	681	6	CQ487445	Sequence	C 918	52	1.5	1418	3	AK113899	Ciona int
C 846	846	52	1.5	695	6	CQ467211	Sequence	C 919	52	1.5	1426	10	BC078790	Rattus no
C 847	847	52	1.5	739	3	AF466588	Aedes aeg	C 920	52	1.5	1430	3	AK115508	Ciona int
C 848	848	52	1.5	756	3	AK174008	Ciona int	C 921	52	1.5	1445	9	BC040875	Homo sapi
C 849	849	52	1.5	759	8	AF002226	Nicotiana	C 922	52	1.5	1457	6	AX535066	Sequence
C 850	850	52	1.5	768	6	CQ415516	Sequence	C 923	52	1.5	1480	9	BC030516	Homo sapi
C 851	851	52	1.5	783	6	CX406873	Sequence	C 924	52	1.5	1494	6	CQ879142	Sequence
C 852	852	52	1.5	814	6	CQ482030	Sequence	C 925	52	1.5	1497	5	BC067639	Danio rer
C 853	853	52	1.5	834	9	BC063494	Homo sapi	C 926	52	1.5	1514	9	BC050367	Homo sapi
C 854	854	52	1.5	843	6	CQ769391	Sequence	C 927	52	1.5	1517	10	BC083686	Rattus no
C 855	855	52	1.5	879	6	AX482482	Sequence	C 928	52	1.5	1525	8	PBSYN	X79904 Phalaenopsi
C 856	856	52	1.5	896	6	CQ432465	Sequence	C 929	52	1.5	1527	10	BC051428	Mus muscu
C 857	857	52	1.5	912	8	AB061251	Solanum t	C 930	52	1.5	1535	5	BC080491	Xenopus t
C 858	858	52	1.5	912	8	AR061492	Partheniu	C 931	52	1.5	1538	10	BC024943	Mus muscu
C 859	859	52	1.5	913	9	HSM802273	AL137537 Homo sapi	C 932	52	1.5	1547	9	BC071644	Homo sapi
C 860	860	52	1.5	916	3	RP061144	U61144 Rhodnius pr	C 933	52	1.5	1553	3	BT003593	Drosophila
C 861	861	52	1.5	916	6	E12747	E12747 Rhodnius pr	C 934	52	1.5	1566	8	CRO7333	Catharant
C 862	862	52	1.5	916	6	E17385	E17385 cDNA encodi	C 935	52	1.5	1566	9	BC073938	Homo sapi
C 863	863	52	1.5	951	6	BD021498	Novel gen	C 936	52	1.5	1567	9	HSM806640	Homo sapi
C 864	864	52	1.5	951	6	BD101436	Novel gen	C 937	52	1.5	1576	6	BD275146	Human
C 865	865	52	1.5	976	6	AX780238	Sequence	C 938	52	1.5	1579	10	BC078941	Rattus no
C 866	866	52	1.5	979	5	BC082389	Xenopus t	C 939	52	1.5	1589	10	BC014703	Mus muscu
C 867	867	52	1.5	989	8	CPCR7	Y08243 C. pteroides	C 940	52	1.5	1602	5	BC074563	Xenopus t
C 868	868	52	1.5	991	6	AR123139	Sequence	C 941	52	1.5	1606	9	BC065192	Homo sapi
C 869	869	52	1.5	991	6	AR124091	Sequence	C 942	52	1.5	1619	10	BC057862	Mus muscu
C 870	870	52	1.5	991	6	AX100360	Sequence	C 943	52	1.5	1620	5	BC066394	Danio rer
C 871	871	52	1.5	991	8	AF243368	Sequence	C 944	52	1.5	1625	9	BC072433	Homo sapi
C 872	872	52	1.5	1010	5	BC065601	Danio rer	C 945	52	1.5	1634	9	HSM807708	Homo sapi
C 873	873	52	1.5	1013	6	A32826	Synthetic c	C 946	52	1.5	1648	10	BC063167	Rattus no
C 874	874	52	1.5	1013	6	I11571	I11571 Sequence 23	C 947	52	1.5	1661	8	AY299287	Arabidops
C 875	875	52	1.5	1013	6	I24003	Sequence 30	C 948	52	1.5	1666	5	BC077976	Xenopus t
C 876	876	52	1.5	1014	3	AY118285	AY118285 Drosophila	C 949	52	1.5	1673	6	AX772808	Sequence
C 877	877	52	1.5	1014	6	A30330	A30330 Artificial	C 950	52	1.5	1680	10	BC049920	Mus muscu
C 878	878	52	1.5	1015	6	A32827	A32827 Synthetic c	C 951	52	1.5	1708	3	BT006334	Drosophila
C 879	879	52	1.5	1016	6	A30331	A30331 Artificial	C 952	52	1.5	1716	9	AB060897	Macaca fa
C 880	880	52	1.5	1032	6	BD266697	Sequence	C 953	52	1.5	1719	5	BC063347	Xenopus t
C 881	881	52	1.5	1032	6	AR216396	Sequence	C 954	52	1.5	1737	3	AY084201	Drosophila
C 882	882	52	1.5	1049	3	AK174965	AK174965 Ciona int	C 955	52	1.5	1738	6	CQ768038	Sequence
C 883	883	52	1.5	1052	3	AK115940	AK115940 Ciona int	C 956	52	1.5	1738	6	AX538151	Sequence
C 884	884	52	1.5	1061	8	THIGPWR	T11528 T. harzianum	C 957	52	1.5	1739	6	PCU42442	Sequence
C 885	885	52	1.5	1071	3	BT015310	BT015310 Drosophila	C 958	52	1.5	1743	6	CQ767534	Sequence
C 886	886	52	1.5	1095	5	BC061298	BC061298 Xenopus t	C 959	52	1.5	1743	6	AX454788	Sequence
C 887	887	52	1.5	1114	6	AR229215	Sequence	C 960	52	1.5	1743	6	AX470409	Sequence
C 888	888	52	1.5	1114	6	AX810716	AX810716 Sequence	C 961	52	1.5	1743	6	AX491266	Sequence
C 889	889	52	1.5	1114	6	BD084191	BD084191 28 human	C 962	52	1.5	1743	6	AX538144	Sequence
C 890	890	52	1.5	1115	9	BC014240	BC014240 Homo sapi	C 963	52	1.5	1743	5	BC068326	Danio rer
C 891	891	52	1.5	1141	10	BC071255	BC071255 Mus muscu	C 964	52	1.5	1750	9	BC060667	Homo sapi
C 892	892	52	1.5	1162	8	AF275315	AF275315 Lotus jap	C 965	52	1.5	1769	5	BC084179	Xenopus t
C 893	893	52	1.5	1174	6	A92311	A92311 Sequence 1	C 966	52	1.5	1771	9	BC071744	Homo sapi
C 894	894	52	1.5	1174	6	AR075389	AR075389 Sequence	C 967	52	1.5	1772	10	BC058245	Mus muscu
C 895	895	52	1.5	1174	6	AR094310	AR094310 Sequence	C 968	52	1.5	1790	9	BC042674	Homo sapi

c 969 1.5 1797 8 ATTERROCH Y13156 Arabidopsis c1042 1.5 2356 10 BC061208  
 c 970 1.5 1808 9 BC063490 Homo sapi c1043 1.5 2374 5 BC074289  
 c 971 1.5 1810 9 BC035719 Homo sapi c1044 1.5 2384 3 AY069709 Drosophila  
 c 972 1.5 1813 9 BC072674 Homo sapi c1045 1.5 2417 10 BC026514 Mus muscu  
 c 973 1.5 1822 5 BC061285 Xenopus t c1046 1.5 2431 10 BC083598  
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 c 983 1.5 1868 8 BC001652 Homo sapi c1056 1.5 2583 9 BC042500  
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 c 987 1.5 1889 10 BC033439 Mus muscu c1060 1.5 2618 9 BC013971  
 c 988 1.5 1891 3 AY113192 Drosophila c1061 1.5 2620 10 BC070922  
 c 989 1.5 1891 5 AY573378 Xenopus l c1062 1.5 2644 3 AK114253 Ciona int  
 c 990 1.5 1898 3 AK112173 Ciona int c1063 1.5 2655 5 BC073367 Xenopus l  
 c 991 1.5 1899 5 BC064160 Xenopus t c1064 1.5 2714 3 AK115386 Ciona int  
 c 992 1.5 1909 5 BC063365 Xenopus t c1065 1.5 2728 9 BC075803  
 c 993 1.5 1917 5 BC077622 Xenopus l c1066 1.5 2778 5 BC073595 Xenopus l  
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 c 996 1.5 1950 9 BC033818 Homo sapi c1069 1.5 2899 9 BC028198  
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 c 999 1.5 1990 10 BC042668 Mus muscu c1072 1.5 2943 10 BC005526  
 c1000 1.5 1998 9 BC062622 Homo sapi c1073 1.5 2976 5 BC070623 Xenopus l  
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 c1002 1.5 2010 9 BC033812 Homo sapi c1075 1.5 3021 9 BC040265  
 c1003 1.5 2010 9 BC037567 Homo sapi c1076 1.5 3044 9 BC042334 Homo sapi  
 c1004 1.5 2025 9 AF414120 Homo sapi c1077 1.5 3050 10 BC016898  
 c1005 1.5 2035 5 BC076993 Xenopus t c1078 1.5 3062 5 BC076939 Xenopus t  
 c1006 1.5 2052 9 HSM802809 Homo sapi c1079 1.5 3128 9 HSM807508  
 c1007 1.5 2068 9 BC002970 Homo sapi c1080 1.5 3138 6 AX780324 Sequence  
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 c1010 1.5 2086 10 BC031495 Mus muscu c1083 1.5 3143 3 S73271 trahalase l  
 c1011 1.5 2098 10 BC069043 Mus muscu c1084 1.5 3144 10 BC036172 Mus muscu  
 c1012 1.5 2100 8 PSA345045 Pisum sat c1085 1.5 3241 10 BC007178  
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 c1016 1.5 2156 10 BC023141 Sequence c1089 1.5 3355 5 BC068364 Danio rer  
 c1017 1.5 2160 5 BC064874 Xenopus t c1090 1.5 3388 9 BC068238 Homo sapi  
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 c1019 1.5 2200 9 BC036773 Homo sapi c1092 1.5 3470 6 CO493188 Sequence  
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 c1024 1.5 2240 9 BC036449 Homo sapi c1097 1.5 3814 9 BC030701 Homo sapi  
 c1025 1.5 2241 6 BD275430 50 Human c1098 1.5 3893 10 AF116573  
 c1026 1.5 2249 9 BC044942 Homo sapi c1099 1.5 3989 9 BC036764 Homo sapi  
 c1027 1.5 2252 10 AF047716 Mus muscu c1100 1.5 4043 10 BC059904  
 c1028 1.5 2262 10 BC062078 Rattus no c1101 1.5 4075 9 BC021300 Homo sapi  
 c1029 1.5 2273 10 BC058802 Mus muscu c1102 1.5 4108 9 HSM806223  
 c1030 1.5 2274 9 BC003590 Homo sapi c1103 1.5 4387 5 DRE5690  
 c1031 1.5 2275 8 AK100133 Oryza sat c1104 1.5 4408 3 AF474344  
 c1032 1.5 2281 10 BC019164 Mus muscu c1105 1.5 4512 10 BC060621 Mus muscu  
 c1033 1.5 2289 9 BC042537 Homo sapi c1106 1.5 4560 10 BC058654 Mus muscu  
 c1034 1.5 2291 6 AX086931 Sequence c1107 1.5 4733 5 BC080918 Xenopus t  
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 c1036 1.5 2321 6 CO412783 Sequence c1109 1.5 5170 10 BC051426  
 c1037 1.5 2327 5 BC043840 Xenopus l c1110 1.5 5534 3 AF474336  
 c1038 1.5 2328 10 BC057458 Mus muscu c1111 1.5 6200 6 BD232461 Dictyoste  
 c1039 1.5 2338 5 BC067588 Danio rer c1112 1.5 6200 6 AR221284 Sequence  
 c1040 1.5 2339 10 BC034663 Mus muscu c1113 1.5 6200 6 AR338509 Sequence  
 c1041 1.5 2339 10 BC034663 Mus muscu c1114 1.5 6200 6 AR338509 Sequence

BC061208 Mus muscu  
 BC074289 Xenopus l  
 AY069709 Drosophila  
 BC026514 Mus muscu  
 BC083598 Rattus no  
 BC031660 Homo sapi  
 BC041664 Homo sapi  
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 BC076840 Xenopus l  
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 BC072520 Rattus no  
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 BC013971 Homo sapi  
 BC070922 Rattus no  
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 AK115386 Ciona int  
 BC075803 Homo sapi  
 BC073595 Xenopus l  
 BC080596 Homo sapi  
 AB088422 Bombyx mo  
 BC028198 Homo sapi  
 BC039839 Homo sapi  
 AF421187 Neopora  
 BC005526 Mus muscu  
 BC070623 Xenopus l  
 BC074638 Xenopus t  
 BC048935 Mus muscu  
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 BC082460 Xenopus l  
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 BC047564 Homo sapi  
 CO493188 Sequence  
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 BX647580 Homo sapi  
 BC047240 Homo sapi  
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 AF116573 Mus muscu  
 BC036764 Homo sapi  
 BC059904 Mus muscu  
 BC021300 Homo sapi  
 BX538052 Homo sapi  
 AJ005690 Danio rer  
 AF474344 Dictyoste  
 BC060621 Mus muscu  
 BC058654 Mus muscu  
 BC080918 Xenopus t  
 BC043088 Homo sapi  
 BC051426 Mus muscu  
 AF474336 Dictyoste  
 BD232461 Recombina  
 AR221284 Sequence  
 AR338509 Sequence



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cl116	52	1.5	6200	6	AX353687	Sequence	1189	51	1.4	101	6	AX494448	Sequence
cl117	52	1.5	6200	6	AX490847	Sequence	1190	51	1.4	102	6	AX381427	Sequence
cl118	52	1.5	6889	10	BC053522	Mus muscu	cl1191	51	1.4	132	6	AX496057	Sequence
cl119	52	1.5	7084	9	HSB803370	Alu32063 Homo sapi	cl1192	51	1.4	143	6	AX255922	Sequence
cl120	52	1.5	8281	9	HSB801490	Alu33623 Homo sapi	cl1193	51	1.4	179	6	CQ525853	Sequence
cl121	52	1.5	6854	2	AC100175	Alu33623 Homo sapi	cl1194	51	1.4	188	6	CQ527214	Sequence
cl122	52	1.5	105682	3	AC116957_3	Continuation (4 of	cl1195	51	1.4	186	6	CQ525204	Sequence
cl123	52	1.5	110000	2	AC112124_2	Continuation (3 of	cl1196	51	1.4	195	6	CQ525204	Sequence
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cl125	52	1.5	110000	3	AC116984_1	Continuation (2 of	cl1198	51	1.4	195	6	AX984511	Sequence
cl126	52	1.5	125817	2	AC016400	Continuation (2 of	cl1199	51	1.4	195	6	BD119370	EST and e
cl127	52	1.5	132254	3	AC116330	AC016400 Homo sapi	cl1199	51	1.4	196	6	CQ525476	Sequence
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cl130	52	1.5	150864	9	AC096588	AL033375 Human DNA	cl1202	51	1.4	200	6	CQ525905	Sequence
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cl133	52	1.5	153375	2	AC145837	AC116551 Dictyoste	cl1205	51	1.4	203	6	AX384889	Sequence
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cl143	52	1.5	168169	2	AC145953	AC145953 Pan trogl	cl1216	51	1.4	223	6	CQ523534	Sequence
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 3580)  
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vages,A., Vandlen,R., Watanabe,C., Wiand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., and Godowski,P.  
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment  
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)  
PUBMED 12975309  
REFERENCE 2 (bases 1 to 3580)  
AUTHORS Clark,H.F.  
TITLE Direct Submission  
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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1 (bases 1 to 3212)  
Strausberg,R.  
Direct Submission  
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Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTF  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
info@bcgsc.bc.ca  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
Leticia Hsiao, Martin Krzywinski, Reta Kutache, Oliver Lee, Soo  
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven  
Ness, Pawan Pandon, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline  
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,

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George Yang, Scott Zuyderduyn, Marco Marra.  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
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AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REMARK

BC066640 4350 bp mRNA linear PRI 30-MAR-2004  
Homo sapiens congenital dyserythropoietic anemia, type I, mRNA  
(cDNA clone MGC:71365 IMAGE:6577335), complete cds.  
BC066640  
MGC.  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, K.H., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
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Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bonfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 4350)  
Straussberg, R.  
Direct Submission  
Submitted (01-MAR-2004) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>









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ACCESSION AL133019  
VERSION AL133019.1 GI:6453499  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2145)  
AUTHORS Bloecher,H., Boescher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and Wiemann,S.  
TITLE Direct Submission  
JOURNAL Submitted (15-NOV-1999) MIPS, Am Klopferspitz 18a, D-82152 Martinsried, GERMANY  
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.  
This clone (DKFp434G2127) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mips.biochem.mpg.de/proj/cDNA/.  
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ACCESSION AC016400
VERSION AC016400.1 GI:6468793
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 129517)
Ben-Asher, B., Avidan, N., Olender, T., Lancet, D., Salmon, L. and
Tamary, H.
Sequencing of human chromosome 15 D15S488 region
TITLE Sequencing of human chromosome 15 D15S488 region
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 129517)
Ben-Asher, B., Avidan, N., Olender, T., Lancet, D., Salmon, L. and
Tamary, H.
Direct Submission
TITLE Direct Submission
JOURNAL Submitted (26-NOV-1999) Dept. of Molecular Genetics, Weizmann
Institute of Science, P.O.Box 26, Rehovot 76100, Israel
COMMENT center: The Weizmann Institute, Crown Genome Center Web site:
http://bioinfo.weizmann.ac.il/genome_center/sequencing.html
Contact: lgenash@weizmann.ac.il
Statistics Sequencing vector: PUC18 Chemistry: Big Dye
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terminators.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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VERSION AC090510.4 GI:18249987
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 148295)
AUTHORS Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,
Pate,D. and Hood,L.
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TITLE
JOURNAL
REFERENCE
AUTHORS
Sequencing of human chromosome 15 D15S146-D15S117 region
Unpublished
2 (bases 1 to 148295)
Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Madan,A.,
Nesbitt,R., Traicoff,R. and Hood,L.
Direct Submission
Submitted (27-FEB-2001) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
98105, USA
3 (bases 1 to 148295)
Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,
Pate,D. and Hood,L.
Direct Submission
Submitted (19-JAN-2002) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
98105, USA
On Jan 19, 2002 this sequence version replaced gi:17436948.
----- Genome Center
Center: Multimegabase Sequencing Center
Center code: UMWSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: lezowen@systemsbiology.org
----- Summary Statistics
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Assembly: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
Note: data from AC018362 [Drafting center UMWSC] and AC068727
[Drafting center UMWSC] were added for finishing.
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the extent possible."
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misc_feature 100366..148295
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QY	1809	GAAGGAGAGTTGGCTGATTTGGGATATGTCAGAAAGTCCAGAGATGCCAGTCCTGG	1868
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QY	1929	TGTCACACAGAAATTCAGCCCTCATTTGCTATCCAGCATCTCTTAAACCTTTGAGTCT	1988
Db	85215	TGTCACACAGAAATTCAGCCCTCATTTGCTATCCAGCATCTCTTAAACCTTTGAGTCT	85156
QY	1969	TGGAATTCATGACAGAGGCAATGACTCTGCTTAACTATGAAGAAAGTTAAACATGA	2048
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QY	2109	CTAACACAGCGCGGTCTGGTGGCTATGCTATCCAGCATCTCTTAAACCTTTGAGGCTGAG	2168
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ACCESSION AL136332  
VERSION AL136332.5 GI:14572584  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 209157)  
AUTHORS Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,  
Brotier, P., Catcollin, L., Barbe, V., Pelletier, E., Artiguenave, F.,  
Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C.,  
Gyapay, G., Saurin, W. and Weissbach, J.  
Sequencing of the human chromosome 14  
Unpublished

REFERENCE 2 (bases 1 to 209157)  
Genoscope.  
Direct Submission  
Submitted (22-MAY-2002) Genoscope - Centre National de Sequençage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
On Jun 27, 2001 this sequence version replaced gi:12657317.  
----- Genome Center  
Center: Genoscope / Centre National de Sequençage  
Center code: GS  
Web site: http://www.genoscope.cns.fr/  
Contact: SegRef@genoscope.cns.fr  
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The following BAC sequence is oriented from the T7 to the SP6 end.  
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Downstream BAC (overlapping the SP6 end) : R-828K24 -----  
Finishing boundaries  
FINISHED SEGMENT STARTS AT BASE 34450  
FINISHED SEGMENT ENDS AT BASE 103340  
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Assembly program: Phrap; version 2.0  
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Overall quality chart :  
Range : bases  
0 : 35  
1 - 9 : 69  
10 - 19 : 442  
20 - 29 : 1059  
30 - 39 : 3289  
40 - 49 : 12373  
50 - 59 : 16399  
60 - 69 : 12862  
70 - 79 : 21626  
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VERSION AK026092.1 GI:10438830
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE
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AUTHORS Kawabata,A., Hiki,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
TITLE JOURNAL
REFERENCE JOURNAL
AUTHORS
TITLE JOURNAL
SUBMITTED (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail: fcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry for Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing; Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
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VERSION CQ851120.1 GI:51509332
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
REFERENCE 1
AUTHORS Isogai,T., Yamamoto,J., Nishikawa,T., Isono,Y., Sugiyama,T.,
Otsuki,T., Wakamatsu,A., Ishii,S., Nagai,K. and Irie,R.
TITLE Full-length human cDNA
JOURNAL Patent: EP 1447413-A 1589 18-AUG-2004;
Research Association for Biotechnology (JP)
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## ORIGIN

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Scoring table: OLGOW-NUC

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ID	AAC58112	standard; cDNA; 3580 BP.				
DE	Human PRO1295	nucleotide sequence SEQ ID NO:28.				
PN	WO200053750-A1.					
PD	14-SEP-2000.					
PA	(GETH ) GENENTECH INC.					
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Best Local Similarity	100.0%;	Pred. No. 0;				
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ID	AAA37037	standard; cDNA; 3580 BP.				
DE	Human PRO1295	(UNQ664) cDNA sequence SEQ ID NO:53.				
PN	WO200012708-A2.					
PD	09-MAR-2000.					
PA	(GETH ) GENENTECH INC.					
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PN	WO200078961-A1.					
PD	28-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
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PN	US2003073130-A1.					
PD	17-APR-2003.					
PA	(GETH ) GENENTECH INC.					
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PD	06-MAR-2003.					
PA	(GETH ) GENENTECH INC.					
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PD	17-APR-2003.					
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PD	03-APR-2003.					
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PD	29-MAY-2003.					
PA	(GETH ) GENENTECH INC.					
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PD	01-MAY-2003.					
PA	(GETH ) GENENTECH INC.					
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PD	20-MAR-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 10;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 11						
ID	ADD38212	standard; cDNA; 3580 BP.				
DE	Human cDNA encoding secreted/transmembrane protein PRO1295.					
PN	US2003096955-A1.					
PD	22-MAY-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 10;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 12						
ID	ADD39168	standard; cDNA; 3580 BP.				
DE	Human cDNA encoding secreted/transmembrane protein PRO1295.					
PN	US2003096954-A1.					
PD	22-MAY-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 10;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 13						
ID	ADD38691	standard; cDNA; 3580 BP.				
DE	Human cDNA encoding secreted/transmembrane protein PRO1295.					
PN	US2003092061-A1.					
PD	15-MAY-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 10;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 14						
ID	ADD40122	standard; cDNA; 3580 BP.				
DE	Human cDNA encoding secreted/transmembrane protein PRO1295.					
PN	US2003082627-A1.					
PD	01-MAY-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 10;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 15						
ID	ADB50343	standard; cDNA; 3580 BP.				

DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2003069179-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 10; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 16  
ID ADE19955 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2003092883-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 10; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 17  
ID ADE49866 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2003082626-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 10; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 18  
ID ADE21424 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2003082628-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 10; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 19  
ID ADF29849 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2003204053-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 10; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 20  
ID ADF5742 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2003204054-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 10; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 21  
ID ADH99246 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2003065142-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 10; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 22  
ID ADE96426 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 12; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 23  
ID ADF25737 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 12; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 24  
ID ADF24636 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 12; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 25  
ID ADF29372 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 12; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 26  
ID ADE96903 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 12; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 27  
ID ADH02941 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 12; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 28  
ID ADH03895 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 12; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 29  
ID ADH03418 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 12; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 30  
ID ADH04372 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2004005626-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 12; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 31  
ID ADH61373 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 12; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 32  
ID ADL94572 standard; cDNA; 3580 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1295.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3580; DB 12; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 33  
ID ADO05609 standard; DNA; 4725 BP.  
DE Human erythrocyte differentiation factor, Codanin-1 encoding DNA.  
PN WO2004035535-A2.

PD 29-APR-2004.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.  
 Query Match 42.3%; Score 1515; DB 12; Length 4725;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 34  
 ID AA199229 standard; DNA; 4137 BP.  
 DE Human excretory related polynucleotide SEQ ID NO 993.  
 PN WO200155313-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 29.5%; Score 1056; DB 4; Length 4137;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-277;  
 RESULT 35  
 ID AA163579 standard; DNA; 4137 BP.  
 DE Human kidney related polynucleotide SEQ ID NO 894.  
 PN WO200155323-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 29.5%; Score 1056; DB 5; Length 4137;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-277;  
 RESULT 36  
 ID ADM44207 standard; cDNA; 2240 BP.  
 DE Novel human arginine-rich protein cDNA #571.  
 PN US2004053250-A1.  
 PD 18-MAR-2004.  
 PA (TANG/) TANG Y T.  
 PA (XUEA/) XUE A.  
 PA (DRMA/) DRMANAC R T.  
 Query Match 27.8%; Score 995; DB 12; Length 2240;  
 Best Local Similarity 99.9%; Pred. No. 2.9e-260;  
 RESULT 37  
 ID AB211689 standard; cDNA; 1833 BP.  
 DE Human polynucleotide SEQ ID NO 571.  
 PN WO200270539-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 26.3%; Score 941; DB 6; Length 1833;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-245;  
 RESULT 38  
 ID AAK89946 standard; DNA; 32187 BP.  
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3522.  
 PN WO200155314-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 24.3%; Score 871; DB 4; Length 32187;  
 Best Local Similarity 99.9%; Pred. No. 4.3e-227;  
 RESULT 39  
 ID ADP22979 standard; cDNA; 2793 BP.  
 DE PRO polypeptide encoding cDNA SEQ ID NO:73.  
 PN WO2004041170-A2.  
 PD 21-MAY-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 20.3%; Score 725; DB 13; Length 2793;  
 Best Local Similarity 99.9%; Pred. No. 2.8e-187;  
 RESULT 40  
 ID ADR08083 standard; cDNA; 3589 BP.  
 DE Full length human cDNA useful for treating neurological disease Seq 1589.  
 PN EP1447413-A2.  
 PD 18-AUG-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match 20.3%; Score 725; DB 13; Length 3589;  
 Best Local Similarity 99.9%; Pred. No. 2.6e-187;  
 RESULT 41  
 ID AA252877 standard; cDNA; 802 BP.  
 DE Human prostate tumor cDNA library derived EST fragment #20.  
 PN DE19820190-A1.  
 PD 04-NOV-1999.  
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
 Query Match 16.7%; Score 598; DB 2; Length 802;  
 Best Local Similarity 99.8%; Pred. No. 8.8e-153;  
 RESULT 42  
 ID AAF66762 standard; cDNA; 413 BP.  
 DE Novel human polynucleotide, SEQ ID NO: 2518.  
 PN WO200102568-A2.  
 PD 11-JAN-2001.  
 PA (CHIR ) CHIRON CORP.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 9.8%; Score 350; DB 5; Length 413;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-85;  
 RESULT 43  
 ID ADF80502 standard; DNA; 357 BP.  
 DE Leukaemia-related DNA sequence #1058.  
 PN WO2003039443-A2.  
 PD 15-MAY-2003.  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
 PA (HAPE/) HAFERLACH T.  
 PA (SCHO/) SCHOCH C.  
 PA (KERN/) KERN W.  
 Query Match 8.8%; Score 314; DB 10; Length 357;  
 Best Local Similarity 100.0%; Pred. No. 7e-76;  
 RESULT 44  
 ID AAH99000 standard; cDNA; 403 BP.  
 DE Human EST-derived coding sequence SEQ ID NO: 857.  
 PN WO200154477-A2.  
 PD 02-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 8.3%; Score 296; DB 4; Length 403;  
 Best Local Similarity 99.7%; Pred. No. 4.9e-71;  
 RESULT 45  
 ID ACH42160 standard; cDNA; 464 BP.  
 DE Human foetal brain cDNA #3527.  
 PN US2003073623-A1.  
 PD 17-APR-2003.  
 PA (DRMA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 Query Match 7.7%; Score 274; DB 9; Length 464;  
 Best Local Similarity 99.3%; Pred. No. 4.2e-65;  
 RESULT 46  
 ID AB211935 standard; cDNA; 2223 BP.  
 DE Human polynucleotide SEQ ID NO 817.  
 PN WO200270539-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 5.6%; Score 201; DB 6; Length 2223;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-45;  
 RESULT 47  
 ID ADM44453 standard; cDNA; 2223 BP.  
 DE Novel human arginine-rich protein cDNA #817.  
 PN US2004053250-A1.  
 PD 18-MAR-2004.  
 PA (TANG/) TANG Y T.  
 PA (XUEA/) XUE A.  
 PA (DRMA/) DRMANAC R T.  
 Query Match 5.6%; Score 201; DB 12; Length 2223;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-45;  
 RESULT 48  
 ID ABN97391 standard; DNA; 177 BP.  
 DE Gene #3889 used to diagnose liver cancer.  
 PN WO200229103-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 4.8%; Score 173; DB 6; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-37;  
 RESULT 49  
 ID AA198743 standard; cDNA; 441 BP.  
 DE Human excretory related polynucleotide SEQ ID NO 187.  
 PN WO200155313-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.2%; Score 152; DB 4; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-32;



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Query Match
Best Local Similarity 1.6%; Score 58; DB 12; Length 81;
RESULT 68
ID ADT95070 standard; cDNA; 89 BP.
DE Colon cancer associated human cDNA sequence #589.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 89;
RESULT 69
ID ADT95330 standard; cDNA; 92 BP.
DE Colon cancer associated human cDNA sequence #849.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 92;
RESULT 70
ID ABX55117 standard; cDNA; 93 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #5046.
PN US2002137160-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 93;
RESULT 71
ID ADD35066 standard; DNA; 95 BP.
DE Mouse mitochondrial DNA sequence SEQ ID NO:2846.
PN WO2003020220-A2.
PD 13-MAR-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 95;
RESULT 72
ID ADT94820 standard; cDNA; 97 BP.
DE Colon cancer associated human cDNA sequence #339.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 97;
RESULT 73
ID ABX60796 standard; DNA; 102 BP.
DE Arabidopsis thaliana polynucleotide #142.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAM/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 102;
RESULT 74
ID ABX61529 standard; DNA; 103 BP.
DE Arabidopsis thaliana polynucleotide #875.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAM/) HAMILTON C M.

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PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 103;
RESULT 75
ID ABX61191 standard; DNA; 103 BP.
DE Arabidopsis thaliana polynucleotide #537.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAM/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 103;
RESULT 76
ID ADT95788 standard; cDNA; 103 BP.
DE Colon cancer associated human cDNA sequence #1307.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 103;
RESULT 77
ID ABX61368 standard; DNA; 104 BP.
DE Arabidopsis thaliana polynucleotide #714.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAM/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 104;
RESULT 78
ID ADT94949 standard; cDNA; 104 BP.
DE Colon cancer associated human cDNA sequence #468.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 104;
RESULT 79
ID ABX60741 standard; DNA; 105 BP.
DE Arabidopsis thaliana polynucleotide #87.
PN US2002142319-A1.
PD 03-OCT-2002.

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PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 100.0%; DB 10; Length 105;
RESULT 80
ID ADD35198 standard; DNA; 106 BP.
DE Mouse mitochondrial DNA sequence SEQ ID NO:2978.
PN WO2003020220-A2.
PD 13-MAR-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 100.0%; DB 10; Length 106;
RESULT 81
ID ABX61169 standard; DNA; 109 BP.
DE Arabidopsis thaliana polynucleotide #515.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 100.0%; DB 10; Length 109;
RESULT 82
ID ABX61450 standard; DNA; 109 BP.
DE Arabidopsis thaliana polynucleotide #796.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 100.0%; DB 10; Length 109;
RESULT 83
ID ABX42131 standard; cDNA; 111 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #7296.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 100.0%; DB 10; Length 111;
RESULT 84
ID ABX61125 standard; DNA; 112 BP.
DE Arabidopsis thaliana polynucleotide #471.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 100.0%; DB 10; Length 112;
RESULT 85
ID ADT94947 standard; cDNA; 112 BP.
DE Colon cancer associated human cDNA sequence #466.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 100.0%; DB 11; Length 112;
RESULT 86
ID ABX61189 standard; DNA; 113 BP.
DE Arabidopsis thaliana polynucleotide #535.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 100.0%; DB 10; Length 113;
RESULT 87
ID ABX61401 standard; DNA; 114 BP.
DE Arabidopsis thaliana polynucleotide #747.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 100.0%; DB 10; Length 114;
RESULT 88
ID ADT95198 standard; cDNA; 114 BP.
DE Colon cancer associated human cDNA sequence #717.
PN US2003087818-A1.
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PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match  
 Best Local Similarity 1.6%; Score 58; DB 11; Length 114;  
 RESULT 89  
 ID ABX60912 standard; DNA; 115 BP.  
 DE Arabidopsis thaliana polynucleotide #258.  
 PN US2002142319-A1.  
 PD 03-OCT-2002.  
 PA (GORL/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAM/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (HARG/) HARGISS T R.  
 PA (YUY/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHAW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 Query Match  
 Best Local Similarity 1.6%; Score 58; DB 10; Length 115;  
 RESULT 90  
 ID ABX61120 standard; DNA; 116 BP.  
 DE Arabidopsis thaliana polynucleotide #466.  
 PN US2002142319-A1.  
 PD 03-OCT-2002.  
 PA (GORL/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAM/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (HARG/) HARGISS T R.  
 PA (YUY/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHAW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 Query Match  
 Best Local Similarity 1.6%; Score 58; DB 10; Length 116;  
 RESULT 91  
 ID ADT95242 standard; cDNA; 116 BP.  
 DE Colon cancer associated human cDNA sequence #761.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match  
 Best Local Similarity 1.6%; Score 58; DB 11; Length 116;  
 RESULT 92  
 ID ADT95224 standard; cDNA; 117 BP.  
 DE Colon cancer associated human cDNA sequence #743.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match  
 Best Local Similarity 1.6%; Score 58; DB 11; Length 117;  
 RESULT 93  
 ID ABX61196 standard; DNA; 118 BP.  
 DE Arabidopsis thaliana polynucleotide #542.  
 PN US2002142319-A1.  
 PD 03-OCT-2002.  
 PA (GORL/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAM/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (HARG/) HARGISS T R.  
 PA (YUY/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.

PA (MATH/) MATHAW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 Query Match  
 Best Local Similarity 1.6%; Score 58; DB 10; Length 118;  
 RESULT 94  
 ID ADT95578 standard; cDNA; 118 BP.  
 DE Colon cancer associated human cDNA sequence #1097.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match  
 Best Local Similarity 1.6%; Score 58; DB 11; Length 118;  
 RESULT 95  
 ID ABX35904 standard; cDNA; 119 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #1069.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match  
 Best Local Similarity 1.6%; Score 58; DB 8; Length 119;  
 RESULT 96  
 ID ADT95794 standard; cDNA; 119 BP.  
 DE Colon cancer associated human cDNA sequence #1313.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match  
 Best Local Similarity 1.6%; Score 58; DB 11; Length 119;  
 RESULT 97  
 ID ABX60705 standard; DNA; 121 BP.  
 DE Arabidopsis thaliana polynucleotide #51.  
 PN US2002142319-A1.  
 PD 03-OCT-2002.  
 PA (GORL/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAM/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (HARG/) HARGISS T R.  
 PA (YUY/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHAW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 Query Match  
 Best Local Similarity 1.6%; Score 58; DB 10; Length 121;  
 RESULT 98  
 ID ADT95271 standard; cDNA; 121 BP.  
 DE Colon cancer associated human cDNA sequence #790.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match  
 Best Local Similarity 1.6%; Score 58; DB 11; Length 121;  
 RESULT 99  
 ID ADT94786 standard; cDNA; 122 BP.  
 DE Colon cancer associated human cDNA sequence #305.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match  
 Best Local Similarity 1.6%; Score 58; DB 11; Length 122;  
 RESULT 100  
 ID ADT95288 standard; cDNA; 122 BP.  
 DE Colon cancer associated human cDNA sequence #807.

PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.6%; Score 58; DB 11; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
 RESULT 101  
 ID ADT95241 standard; cDNA; 123 BP.  
 DE Colon cancer associated human cDNA sequence #760.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.6%; Score 58; DB 11; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
 RESULT 102  
 ID ABX0896 standard; DNA; 124 BP.  
 DE Arabidopsis thaliana polynucleotide #242.  
 PN US2002142319-A1.  
 PD 03-OCT-2002.  
 PA (GORG/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAM/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (HARG/) HARGISS T R.  
 PA (YUY/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 Query Match 1.6%; Score 58; DB 10; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
 RESULT 103  
 ID ADT95479 standard; cDNA; 126 BP.  
 DE Colon cancer associated human cDNA sequence #998.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.6%; Score 58; DB 11; Length 126;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
 RESULT 104  
 ID ABX61459 standard; DNA; 128 BP.  
 DE Arabidopsis thaliana polynucleotide #805.  
 PN US2002142319-A1.  
 PD 03-OCT-2002.  
 PA (GORG/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAM/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (HARG/) HARGISS T R.  
 PA (YUY/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 Query Match 1.6%; Score 58; DB 10; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
 RESULT 105  
 ID ADT95260 standard; cDNA; 133 BP.  
 DE Colon cancer associated human cDNA sequence #779.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.6%; Score 58; DB 11; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
 RESULT 106  
 ID ADT95694 standard; cDNA; 135 BP.  
 DE Colon cancer associated human cDNA sequence #1213.  
 PN US2003087818-A1.

PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.6%; Score 58; DB 11; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
 RESULT 107  
 ID ABX42392 standard; cDNA; 136 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #7557.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 1.6%; Score 58; DB 8; Length 136;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
 RESULT 108  
 ID ADT95450 standard; cDNA; 141 BP.  
 DE Colon cancer associated human cDNA sequence #969.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.6%; Score 58; DB 11; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
 RESULT 109  
 ID ADT95577 standard; cDNA; 145 BP.  
 DE Colon cancer associated human cDNA sequence #1096.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.6%; Score 58; DB 11; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
 RESULT 110  
 ID ADT95485 standard; cDNA; 145 BP.  
 DE Colon cancer associated human cDNA sequence #1004.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.6%; Score 58; DB 11; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
 RESULT 111  
 ID ABX41830 standard; cDNA; 152 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #6995.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 1.6%; Score 58; DB 8; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
 RESULT 112  
 ID AAI84674 standard; cDNA; 165 BP.  
 DE Human polynucleotide SEQ ID NO 4734.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 1.6%; Score 58; DB 4; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
 RESULT 113  
 ID ABX35959 standard; cDNA; 181 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #1124.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 1.6%; Score 58; DB 8; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
 RESULT 114  
 ID ABX36136 standard; cDNA; 181 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #1301.  
 PN US2002137139-A1.

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PD 26-SEP-2002...
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 181;
RESULT 115
ID ABX61443 standard; DNA; 186 BP.
DE Arabidopsis thaliana polynucleotide #789.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL//) GORLACH J.
PA (ANY//) AN Y.
PA (HAMI//) HAMILTON C M.
PA (PRIC//) PRICE J L.
PA (HARG//) HARGISS T R.
PA (YUY//) YU Y.
PA (RAME//) RAMEAKA J G.
PA (PAGE//) PAGE A.
PA (MATH//) MATHW A V.
PA (LEDF//) LEDFORD B L.
PA (WOES//) WOESSNER J P.
PA (HAAS//) HAAS W D.
PA (GARC//) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 186;
RESULT 116
ID ABX60862 standard; DNA; 196 BP.
DE Arabidopsis thaliana polynucleotide #208.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL//) GORLACH J.
PA (ANY//) AN Y.
PA (HAMI//) HAMILTON C M.
PA (PRIC//) PRICE J L.
PA (HARG//) HARGISS T R.
PA (YUY//) YU Y.
PA (RAME//) RAMEAKA J G.
PA (PAGE//) PAGE A.
PA (MATH//) MATHW A V.
PA (LEDF//) LEDFORD B L.
PA (WOES//) WOESSNER J P.
PA (HAAS//) HAAS W D.
PA (GARC//) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 196;
RESULT 117
ID ABX49827 standard; cDNA; 203 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #14992.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 203;
RESULT 118
ID ABX38577 standard; cDNA; 203 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3742.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 203;
RESULT 119
ID ABX38781 standard; cDNA; 207 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3946.
PN US2002137139-A1.

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PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 207;
RESULT 120
ID ABX41435 standard; cDNA; 208 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6600.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 208;
RESULT 121
ID ABX39781 standard; cDNA; 219 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4946.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 219;
RESULT 122
ID ABX49357 standard; cDNA; 220 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #14522.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 220;
RESULT 123
ID ABX35502 standard; cDNA; 223 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #667.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 223;
RESULT 124
ID ABX45169 standard; cDNA; 228 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #10334.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 228;
RESULT 125
ID ABX47018 standard; cDNA; 236 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12183.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 236;

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RESULT 126  
ID ABX48174 standard; cDNA; 239 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #13339.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 8; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
RESULT 127  
ID ABX47809 standard; cDNA; 241 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #12974.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 8; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
RESULT 128  
ID ABX38052 standard; cDNA; 242 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #3217.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 8; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
RESULT 129  
ID ABX35484 standard; cDNA; 272 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #649.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 8; Length 272;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
RESULT 130  
ID ABX37131 standard; cDNA; 277 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #2296.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 8; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
RESULT 131  
ID ABX46910 standard; cDNA; 283 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #12075.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 8; Length 283;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
RESULT 132  
ID ABX48177 standard; cDNA; 286 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #13342.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 8; Length 286;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
RESULT 133  
ID ABX48174 standard; cDNA; 239 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #13339.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 8; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
RESULT 134  
ID ABX37883 standard; cDNA; 296 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #3048.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 8; Length 296;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
RESULT 135  
ID ABX61005 standard; DNA; 301 BP.  
DE Arabidopsis thaliana polynucleotide #351.  
PN US2002142319-A1.  
PD 03-OCT-2002.  
PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (HARG/) HARGISS T R.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 10; Length 301;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
RESULT 136  
ID ABL87211 standard; cDNA; 310 BP.  
DE Human ovarian cancer related cDNA clone SEQ ID NO:10189.  
PN WO200192581-A2.  
PD 06-DEC-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 6; Length 310;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
RESULT 137  
ID ABX41150 standard; cDNA; 312 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #6315.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 8; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
RESULT 138  
ID ABX37743 standard; cDNA; 316 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #2908.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 8; Length 316;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;

PA (WARR//) WARREN W C.  
 Query Match 1.6%; Score 58; DB 8; Length 316;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 RESULT 139  
 ID ABX43454 standard; cDNA; 325 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #8619.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT//) BYATT J C.  
 PA (MATH//) MATHIALAGAN N.  
 PA (TAON//) TAO N.  
 PA (WARR//) WARREN W C.  
 Query Match 1.6%; Score 58; DB 8; Length 325;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 RESULT 140  
 ID ADQ03196 standard; DNA; 330 BP.  
 DE Arabidopsis homeobox transcription factor seqid 42.  
 PN US2004123339-A1.  
 PD 24-JUN-2004.  
 PA (CONN//) CONNER T W.  
 PA (HECK//) HECK G R.  
 PA (LIUJ//) LIU J.  
 Query Match 1.6%; Score 58; DB 12; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 RESULT 141  
 ID ABX41811 standard; cDNA; 337 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #6976.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT//) BYATT J C.  
 PA (MATH//) MATHIALAGAN N.  
 PA (TAON//) TAO N.  
 PA (WARR//) WARREN W C.  
 Query Match 1.6%; Score 58; DB 8; Length 337;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 RESULT 142  
 ID ABX46565 standard; cDNA; 350 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #11730.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT//) BYATT J C.  
 PA (MATH//) MATHIALAGAN N.  
 PA (TAON//) TAO N.  
 PA (WARR//) WARREN W C.  
 Query Match 1.6%; Score 58; DB 8; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 RESULT 143  
 ID ABX49433 standard; cDNA; 358 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #14598.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT//) BYATT J C.  
 PA (MATH//) MATHIALAGAN N.  
 PA (TAON//) TAO N.  
 PA (WARR//) WARREN W C.  
 Query Match 1.6%; Score 58; DB 8; Length 358;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 RESULT 144  
 ID ACN68453 standard; DNA; 358 BP.  
 DE Breast cancer related marker, seq id 9603.  
 PN US200309974-A1.  
 PD 29-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 11; Length 358;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 RESULT 145  
 ID ABQ85687 standard; DNA; 359 BP.  
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 557.  
 PN US2002062014-A1.  
 PD 23-MAY-2002.  
 PA (GORL//) GORLACH J.  
 PA (ANYI//) AN Y.  
 PA (HAMI//) HAMILTON C M.

PA (PRIC//) PRICE J L.  
 PA (RAIN//) RAINES T M.  
 PA (YUYU//) YU Y.  
 PA (RAME//) RAMEAKA J G.  
 PA (PAGE//) PAGE A.  
 PA (MATH//) MATHW A V.  
 PA (LEDF//) LEDFORD B L.  
 PA (WOES//) WOESSNER J P.  
 PA (HAAS//) HAAS W D.  
 PA (GARC//) GARCIA C A.  
 PA (KRIC//) KRICKER M.  
 PA (SLAT//) SLATER T.  
 PA (DAVI//) DAVIS K R.  
 PA (ALLE//) ALLEN K.  
 PA (HOFF//) HOFFMAN N.  
 PA (HURB//) HURBAN P.  
 Query Match 1.6%; Score 58; DB 6; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 RESULT 146  
 ID ABX41004 standard; cDNA; 370 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #5169.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT//) BYATT J C.  
 PA (MATH//) MATHIALAGAN N.  
 PA (TAON//) TAO N.  
 PA (WARR//) WARREN W C.  
 Query Match 1.6%; Score 58; DB 8; Length 370;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 RESULT 147  
 ID ABX38044 standard; cDNA; 382 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #3209.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT//) BYATT J C.  
 PA (MATH//) MATHIALAGAN N.  
 PA (TAON//) TAO N.  
 PA (WARR//) WARREN W C.  
 Query Match 1.6%; Score 58; DB 8; Length 382;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 RESULT 148  
 ID ABQ85229 standard; DNA; 385 BP.  
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 99.  
 PN US2002062014-A1.  
 PD 23-MAY-2002.  
 PA (GORL//) GORLACH J.  
 PA (ANYI//) AN Y.  
 PA (HAMI//) HAMILTON C M.  
 PA (PRIC//) PRICE J L.  
 PA (RAIN//) RAINES T M.  
 PA (YUYU//) YU Y.  
 PA (RAME//) RAMEAKA J G.  
 PA (PAGE//) PAGE A.  
 PA (MATH//) MATHW A V.  
 PA (LEDF//) LEDFORD B L.  
 PA (WOES//) WOESSNER J P.  
 PA (HAAS//) HAAS W D.  
 PA (GARC//) GARCIA C A.  
 PA (KRIC//) KRICKER M.  
 PA (SLAT//) SLATER T.  
 PA (DAVI//) DAVIS K R.  
 PA (ALLE//) ALLEN K.  
 PA (HOFF//) HOFFMAN N.  
 PA (HURB//) HURBAN P.  
 Query Match 1.6%; Score 58; DB 6; Length 385;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 RESULT 149  
 ID ABX47838 standard; cDNA; 392 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #13003.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT//) BYATT J C.  
 PA (MATH//) MATHIALAGAN N.

PA (TAON/) TAO N.  
PA (WARR/) WARREN W C. 1.6%; Score 58; DB 8; Length 392;  
Query Match 100.0%; Pred. No. 1.1e-06;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 150  
ID AAS44810 standard; DNA; 394 BP.  
DE Human contig polynucleotide sequence #63.  
PN WO200164834-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.6%; Score 58; DB 4; Length 394;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 151  
ID ABX42549 standard; cDNA; 394 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #7714.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.6%; Score 58; DB 8; Length 394;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 152  
ID ABX53255 standard; cDNA; 401 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #3184.  
PN US2002137160-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.6%; Score 58; DB 8; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 153  
ID ABX42327 standard; cDNA; 410 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #7492.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.6%; Score 58; DB 8; Length 410;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 154  
ID ABX39273 standard; cDNA; 410 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #4438.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.6%; Score 58; DB 8; Length 410;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 155  
ID ABX43996 standard; cDNA; 414 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #9161.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.6%; Score 58; DB 8; Length 414;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 156  
ID ABX41704 standard; cDNA; 415 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #6869.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.

PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C. 1.6%; Score 58; DB 8; Length 415;  
Query Match 100.0%; Pred. No. 1.1e-06;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 157  
ID ABX39702 standard; cDNA; 418 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #4867.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.6%; Score 58; DB 8; Length 418;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 158  
ID ABX47983 standard; cDNA; 420 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #13148.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.6%; Score 58; DB 8; Length 420;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 159  
ID ABX40752 standard; cDNA; 432 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #5917.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.6%; Score 58; DB 8; Length 432;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 160  
ID AAI93088 standard; cDNA; 438 BP.  
DE Human polynucleotide SEQ ID NO 13148.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.6%; Score 58; DB 4; Length 438;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 161  
ID ABL94042 standard; cDNA; 445 BP.  
DE Arabidopsis thaliana nucleic acid sequence Ref:2027807 SEQ ID NO:807.  
PN US200203280-A1.  
PD 21-FEB-2002.  
PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
Query Match 1.6%; Score 58; DB 6; Length 445;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 162

PD 26-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 3; Length 594;  
Best Local Similarity 100.0%; Pred. No. 9.8e-07;  
RESULT 169  
ID ACN87667 standard; DNA; 617 BP.  
DE Breast cancer related marker, seq id 8917.  
FN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.6%; Score 58; DB 11; Length 617;  
Best Local Similarity 100.0%; Pred. No. 9.7e-07;  
RESULT 170  
ID ACN81732 standard; DNA; 631 BP.  
DE Breast cancer related marker, seq id 2882.  
FN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.6%; Score 58; DB 11; Length 631;  
Best Local Similarity 100.0%; Pred. No. 9.7e-07;  
RESULT 171  
ID AAH33423 standard; cDNA; 637 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:479.  
FN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 4; Length 637;  
Best Local Similarity 100.0%; Pred. No. 9.6e-07;  
RESULT 172  
ID ABQ66000 standard; DNA; 646 BP.  
DE Arabidopsis thaliana polynucleotide SEQ ID NO 577.  
FN US2002059663-A1.  
PD 16-MAY-2002.  
PA (GORL/) GORLACH J.  
PA (ANYI/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUYU/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHEW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
Query Match 1.6%; Score 58; DB 6; Length 646;  
Best Local Similarity 100.0%; Pred. No. 9.6e-07;  
RESULT 173  
ID AAC87363 standard; cDNA; 703 BP.  
DE Human developmentally-regulated hippocampus EST, SEQ ID NO:6.  
FN WO200070036-A2.  
PD 23-NOV-2000.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.6%; Score 58; DB 4; Length 703;  
Best Local Similarity 100.0%; Pred. No. 9.3e-07;  
RESULT 174  
ID ABL89582 standard; cDNA; 722 BP.  
DE Human polynucleotide SEQ ID NO 144.  
FN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 6; Length 722;  
Best Local Similarity 100.0%; Pred. No. 9.3e-07;  
RESULT 175  
ID ABL87202 standard; cDNA; 735 BP.  
DE Human ovarian cancer related cDNA clone SEQ ID NO:10180.



PN WO200192581-A2.  
PD 06-DEC-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 58; DB 6; Length 735;  
Best Local Similarity 100.0%; Pred. No. 9.2e-07;  
RESULT 176  
ID AAF18114 standard; DNA; 786 BP.  
DE Lung cancer associated polynucleotide sequence SEQ ID 133.  
PN WO200055180-A2.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match 1.6%; Score 58; DB 3; Length 786;  
Best Local Similarity 100.0%; Pred. No. 9e-07;  
RESULT 177  
ID AAC59594 standard; cDNA; 820 BP.  
DE Human secreted protein gene 29 SEQ ID NO:39.  
PN WO200056883-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 3; Length 820;  
Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
RESULT 178  
ID ABN98845 standard; DNA; 856 BP.  
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 613.  
PN US2002023281-A1.  
PD 21-FEB-2002.  
PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHAW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOPE/) HOFFMAN N.  
PA (HURE/) HUREAN P.  
Query Match 1.6%; Score 58; DB 6; Length 856;  
Best Local Similarity 100.0%; Pred. No. 8.8e-07;  
RESULT 179  
ID ADJ57936 standard; cDNA; 863 BP.  
DE Rat NARC 14A cDNA.  
PN US2004009553-A1.  
PD 15-JAN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.6%; Score 58; DB 12; Length 863;  
Best Local Similarity 100.0%; Pred. No. 8.8e-07;  
RESULT 180  
ID ACC48070 standard; cDNA; 905 BP.  
DE Nucleotide sequence of cDNA pPC86-Clone 28R.  
PN WO2003000273-A1.  
PD 03-JAN-2003.  
PA (AUTO-) AUTOGEN RES PTY LTD.  
Query Match 1.6%; Score 58; DB 10; Length 905;  
Best Local Similarity 100.0%; Pred. No. 8.6e-07;  
RESULT 181  
ID ADI42584 standard; DNA; 923 BP.  
DE Plant transcription factor polynucleotide #673.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER/) SHERMAN B K.  
PA (RIEC/) RIECHMANN J L.  
PA (JIAN/) JIANG C.  
PA (HEAR/) HEARD J E.

PA (HAAK/) HAAKE V.  
PA (CREE/) CREELMAN R A.  
PA (RATC/) RATCLIFFE O.  
PA (ADAM/) ADAM L J.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J.  
PA (BROU/) BROUN P E.  
PA (PILG/) PILGRIM M L.  
PA (DUBE/) DUBELL A N.  
PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
Query Match 1.6%; Score 58; DB 12; Length 923;  
Best Local Similarity 100.0%; Pred. No. 8.6e-07;  
RESULT 182  
ID ADO02885 standard; cDNA; 923 BP.  
DE Soybean orthologue of Thalecress transcription factor, cDNA #154.  
PN US2004045049-A1.  
PD 04-MAR-2004.  
PA (ZHAN/) ZHANG J.  
PA (FROM/) FROMM M E.  
PA (HEAR/) HEARD J E.  
PA (RIEC/) RIECHMANN J L.  
PA (ADAM/) ADAM L J.  
PA (BROU/) BROUN P E.  
PA (PINE/) PINEDA O.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J S.  
PA (YUGG/) YU G.  
PA (JIAN/) JIANG C.  
PA (SAMA/) SAMAHA R S.  
PA (PILG/) PILGRIM M L.  
PA (CREE/) CREELMAN R A.  
PA (DUBE/) DUBELL A N.  
PA (RATC/) RATCLIFFE O.  
PA (KUMI/) KUMIMOTO R.  
PA (SHER/) SHERMAN B K.  
Query Match 1.6%; Score 58; DB 12; Length 923;  
Best Local Similarity 100.0%; Pred. No. 8.6e-07;  
RESULT 183  
ID AAS04268 standard; cDNA; 932 BP.  
DE Murine secreted protein TANGO 269 cDNA sequence.  
PN WO200130831-A1.  
PD 03-MAY-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.6%; Score 58; DB 4; Length 932;  
Best Local Similarity 100.0%; Pred. No. 8.6e-07;  
RESULT 184  
ID AAD07722 standard; cDNA; 938 BP.  
DE Human secreted protein-encoding gene 18 cDNA clone HLYDU43, SEQ ID NO:28.  
PN WO200134800-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 5; Length 938;  
Best Local Similarity 100.0%; Pred. No. 8.6e-07;  
RESULT 185  
ID AAF98707 standard; DNA; 950 BP.  
DE Human ovarian cancer cell expressed sequence 10807.  
PN WO200118542-A2.  
PD 15-MAR-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.6%; Score 58; DB 5; Length 950;  
Best Local Similarity 100.0%; Pred. No. 8.5e-07;  
RESULT 186  
ID AAD07796 standard; cDNA; 1023 BP.  
DE Mouse fibroblast growth factor (zFGF5) cDNA.  
PN WO200139788-A2.  
PD 07-JUN-2001.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 1.6%; Score 58; DB 4; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 8.3e-07;  
RESULT 187  
ID ADF17709 standard; cDNA; 1023 BP.  
DE cDNA encoding mouse fibroblast growth factor zFGF5.

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PN US2003152568-A1.
PD 14-AUG-2003.
PA (WEST/) WEST J W.
Query Match 1.6%; Score 58; DB 10; Length 1023;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
RESULT 188
ID AAD64162 standard; cDNA; 1023 BP.
DE Mouse zFGF5 cDNA.
PN US2003199443-A1.
PD 23-OCT-2003.
PA (DEIS/) DEISHER T A.
PA (CONK/) CONKLIN D C.
Query Match 1.6%; Score 58; DB 10; Length 1023;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
RESULT 189
ID AAC93426 standard; cDNA; 1030 BP.
DE Human secreted protein gene 5 SEQ ID NO:15.
PN WO200061625-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 1.6%; Score 58; DB 3; Length 1030;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
RESULT 190
ID AA26373 standard; cDNA; 1048 BP.
DE Human secreted protein gene 28 SEQ ID NO:38.
PN WO200006698-A1.
PD 10-FEB-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 3; Length 1048;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
RESULT 191
ID ADL71434 standard; cDNA; 1048 BP.
DE Novel human secreted protein cDNA seqid 38.
PN US2004034196-A1.
PD 19-FEB-2004.
PA (KOMA/) KOMATSUULIS G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAPLEUR D W.
PA (WEIY/) WEI Y.
Query Match 1.6%; Score 58; DB 12; Length 1048;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
RESULT 192
ID AA210645 standard; cDNA; 1057 BP.
DE cDNA encoding a human secreted protein.
PN WO9943693-A1.
PD 02-SEP-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 2; Length 1057;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 193
ID ADA39739 standard; cDNA; 1057 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 8; Length 1057;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 194
ID ACC50402 standard; cDNA; 1057 BP.
DE Human secreted protein coding sequence, SEQ ID 69.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 8; Length 1057;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 195
ID AB271222 standard; cDNA; 1057 BP.
DE Human secreted protein-encoding gene 33 cDNA clone HDPFP29, SEQ ID NO:43.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 8; Length 1057;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 196
ID ADC73455 standard; DNA; 1057 BP.
DE Human secreted protein-related DNA - SEQ ID 88.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 10; Length 1057;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 197
ID AAX85048 standard; DNA; 1064 BP.
DE Human secreted protein gene No. 116.
PN WO9924836-A1.
PD 20-MAY-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 2; Length 1064;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 198
ID ACD18972 standard; cDNA; 1064 BP.
DE Novel human secreted protein cDNA #114.
PN US2003028003-A1.
PD 06-FEB-2003.
PA (ROSE/) ROSEN C A.
PA (FENG/) FENG P.
PA (RUBE/) RUBEN S M.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (NIJJ/) NI J.
PA (WEIY/) WEI Y.
PA (SOPP/) SOPPET D R.
PA (MOOR/) MOORE P A.
PA (KYAW/) KYAW H.
PA (LAPL/) LAPLEUR D W.
PA (SHIY/) SHI Y.
PA (JANA/) JANAT F.
PA (ENDR/) ENDRESS G A.
PA (CART/) CARTER K C.
PA (BIRS/) BIRSE C E.
Query Match 1.6%; Score 58; DB 8; Length 1064;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 199
ID ADC73543 standard; DNA; 1064 BP.
DE Human secreted protein-related DNA - SEQ ID 176.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 10; Length 1064;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 200
ID ADD37606 standard; cDNA; 1064 BP.
DE Human secreted protein encoding sequence #88.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 10; Length 1064;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 201
ID ADA56073 standard; DNA; 1064 BP.
DE Gene encoding human secreted protein #252.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 10; Length 1064;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 202
ID ADG78365 standard; cDNA; 1064 BP.
DE Human secreted protein cDNA #116.
PN US2003211472-A1.
PD 13-NOV-2003.
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PA (FENG/) FENG P.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (EENE/) EBER R.  
PA (OLSE/) OLSEN H S.  
PA (NIJU/) NI J.  
PA (WEIY/) WEI Y.  
PA (SOPP/) SOPPET D R.  
PA (MOOR/) MOORE P A.  
PA (KYAW/) KYAW H.  
PA (LAF/) LAFLEUR D W.  
PA (SHIY/) SHI Y.  
PA (JANA/) JANAT F.  
PA (ENDR/) ENDRESS G A.  
PA (CART/) CARTER K C.  
Query Match 1.6%; Score 58; DB 12; Length 1064;  
Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
RESULT 203  
ID ADN60654 standard; cDNA; 1064 BP.  
DE Human secreted polynucleotide #114.  
PN US2004038277-A1.  
PD 26-FEB-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 12; Length 1064;  
Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
RESULT 204  
ID ABT31935 standard; DNA; 1070 BP.  
DE Human breast cancer / ovarian cancer related coding sequence #42.  
PN WO2003000012-A2.  
PD 03-JAN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.6%; Score 58; DB 10; Length 1070;  
Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
RESULT 205  
ID AAS28837 standard; cDNA; 1083 BP.  
DE Human immunoglobulin encoding cDNA SEQ ID NO 83.  
PN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 4; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
RESULT 206  
ID AAS28771 standard; cDNA; 1083 BP.  
DE Human immunoglobulin encoding cDNA SEQ ID NO 17.  
PN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 4; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
RESULT 207  
ID ABA06707 standard; cDNA; 1083 BP.  
DE Human cDNA SEQ ID NO: 373.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 4; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
RESULT 208  
ID ABV84044 standard; cDNA; 1083 BP.  
DE Human polynucleotide SEQ ID NO 373.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 1.6%; Score 58; DB 6; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
RESULT 209  
ID ADB31562 standard; cDNA; 1083 BP.  
DE Human cDNA encoding a novel protein SEQ ID NO 83.  
PN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 4; Length 1172;  
Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
RESULT 210  
ID ADB31496 standard; cDNA; 1083 BP.  
DE Human cDNA encoding a novel protein SEQ ID NO 17.  
PN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 10; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
RESULT 211  
ID ADO62876 standard; DNA; 1091 BP.  
DE Transcription factor G3055 orthologous sequence, SEQ ID 1343.  
PN WO2004031349-A2.  
PD 15-APR-2004.  
PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
Query Match 1.6%; Score 58; DB 12; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
RESULT 212  
ID AAC59409 standard; cDNA; 1126 BP.  
DE Human secreted protein cDNA #18.  
PN WO200056765-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 3; Length 1126;  
Best Local Similarity 100.0%; Pred. No. 8.1e-07;  
RESULT 213  
ID AAC98004 standard; cDNA; 1140 BP.  
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:14.  
PN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 3; Length 1140;  
Best Local Similarity 100.0%; Pred. No. 8.1e-07;  
RESULT 214  
ID AAC81030 standard; cDNA; 1149 BP.  
DE Human secreted protein cDNA sequence #3.  
PN WO200063230-A2.  
PD 26-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 3; Length 1149;  
Best Local Similarity 100.0%; Pred. No. 8e-07;  
RESULT 215  
ID ABQ54664 standard; cDNA; 1156 BP.  
DE Human ovarian antigen HVVCF30 cDNA, SEQ ID NO:544.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 6; Length 1156;  
Best Local Similarity 100.0%; Pred. No. 8e-07;  
RESULT 216  
ID AAP98699 standard; DNA; 1164 BP.  
DE Human ovarian cancer cell expressed sequence 10799.  
PN WO200118542-A2.  
PD 15-MAR-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.6%; Score 58; DB 5; Length 1164;  
Best Local Similarity 100.0%; Pred. No. 8e-07;  
RESULT 217  
ID AAC98117 standard; cDNA; 1172 BP.  
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:127.  
PN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 3; Length 1172;  
Best Local Similarity 100.0%; Pred. No. 8e-07;  
RESULT 218  
ID AAH33220 standard; cDNA; 1172 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:276.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 4; Length 1172;

DE Human polynucleotide SEQ ID NO 638.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 6; Length 1334;  
Best Local Similarity 100.0%; Pred. No. 7.7e-07;  
RESULT 228  
ID AAA26399 standard; cDNA; 1361 BP.  
DE Human secreted protein gene 54 SEQ ID NO:64.  
PN WO200006698-A1.  
PD 10-FEB-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 3; Length 1361;  
Best Local Similarity 100.0%; Pred. No. 7.6e-07;  
RESULT 229  
ID ADL71460 standard; cDNA; 1361 BP.  
DE Novel human secreted protein cDNA seqid 64.  
PN US2004034196-A1.  
PD 19-FEB-2004.  
PA (KOMA/) KOMATSOULIS G A.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (DUAN/) DUAN D R.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAF/) LAFLEUR D W.  
PA (WEIY/) WEI Y.  
Query Match 1.6%; Score 58; DB 12; Length 1361;  
Best Local Similarity 100.0%; Pred. No. 7.6e-07;  
RESULT 230  
ID AAA26453 standard; cDNA; 1375 BP.  
DE Human secreted protein gene 56 SEQ ID NO:118.  
PN WO200006698-A1.  
PD 10-FEB-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 3; Length 1375;  
Best Local Similarity 100.0%; Pred. No. 7.6e-07;  
RESULT 231  
ID ADL71516 standard; cDNA; 1375 BP.  
DE Novel human secreted protein cDNA seqid 120.  
PN US2004034196-A1.  
PD 19-FEB-2004.  
PA (KOMA/) KOMATSOULIS G A.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (DUAN/) DUAN D R.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAF/) LAFLEUR D W.  
PA (WEIY/) WEI Y.  
Query Match 1.6%; Score 58; DB 12; Length 1375;  
Best Local Similarity 100.0%; Pred. No. 7.6e-07;  
RESULT 232  
ID AAA26401 standard; cDNA; 1376 BP.  
DE Human secreted protein gene 56 SEQ ID NO:66.  
PN WO200006698-A1.  
PD 10-FEB-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 3; Length 1376;  
Best Local Similarity 100.0%; Pred. No. 7.6e-07;  
RESULT 233  
ID ADL71462 standard; cDNA; 1376 BP.  
DE Novel human secreted protein cDNA seqid 66.  
PN US2004034196-A1.  
PD 19-FEB-2004.  
PA (KOMA/) KOMATSOULIS G A.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (DUAN/) DUAN D R.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAF/) LAFLEUR D W.  
PA (WEIY/) WEI Y.

Query Match  
Best Local Similarity 1.6%; Score 58; DB 12; Length 1376;  
Pred. No. 7.6e-07;  
RESULT 234  
ID AAC59295 standard; cDNA; 1388 BP.  
DE Human secreted protein cDNA #19.  
PN WO200056753-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 3; Length 1388;  
Pred. No. 7.6e-07;  
RESULT 235  
ID AAC79804 standard; cDNA; 1390 BP.  
DE Human secreted protein gene 6 SEQ ID NO:16.  
PN WO200056336-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 3; Length 1390;  
Pred. No. 7.6e-07;  
RESULT 236  
ID AAX58673 standard; cDNA; 1411 BP.  
DE Rat organic cation transporter OCT-3 cDNA.  
PN WO9924610-A1.  
PD 20-MAY-1999.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 2; Length 1411;  
Pred. No. 7.5e-07;  
RESULT 237  
ID ABL90182 standard; cDNA; 1459 BP.  
DE Human polynucleotide SEQ ID NO 744.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 6; Length 1459;  
Pred. No. 7.5e-07;  
RESULT 238  
ID ADF81719 standard; DNA; 1480 BP.  
DE Leukaemia-related DNA sequence #2275.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE-) HAERLACH T.  
PA (SCHO-) SCHOCH C.  
PA (KERN-) KERN W.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 10; Length 1480;  
Pred. No. 7.4e-07;  
RESULT 239  
ID ADF81720 standard; DNA; 1480 BP.  
DE Leukaemia-related DNA sequence #2276.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE-) HAERLACH T.  
PA (SCHO-) SCHOCH C.  
PA (KERN-) KERN W.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 10; Length 1480;  
Pred. No. 7.4e-07;  
RESULT 240  
ID ADM47744 standard; DNA; 1494 BP.  
DE Polynucleotide sequence #162 useful in producing transgenic plants.  
PN US2003233670-A1.  
PD 18-DEC-2003.  
PA (EDGE-) EDGERTON M D.  
PA (CHOM-) CHOMET P S.  
PA (LACC-) LACCETTI L B.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 12; Length 1494;  
Pred. No. 7.4e-07;  
RESULT 241  
ID AAX4921 standard; cDNA; 1549 BP.  
DE Guman ras carboxy-terminal processing protein cDNA.  
PN WO9914343-A1.  
PD 25-MAR-1999.

PA (ORTH) ORTHO-MCNEIL PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 2; Length 1549;  
Pred. No. 7.3e-07;  
RESULT 242  
ID ABQ54972 standard; cDNA; 1551 BP.  
DE Human ovarian antigen HNOAH83 cDNA, SEQ ID NO:852.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 6; Length 1551;  
Pred. No. 7.3e-07;  
RESULT 243  
ID ADI42788 standard; DNA; 1574 BP.  
DE Plant transcription factor polynucleotide #798.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER-) SHERMAN B K.  
PA (RIEC-) RIECHMANN J L.  
PA (JIAN-) JIANG C.  
PA (HEAR-) HEARD J E.  
PA (HAKE-) HAAKE V.  
PA (CREE-) CREELMAN R A.  
PA (RATC-) RATCLIFFE O.  
PA (ADAM-) ADAM L J.  
PA (REUB-) REUBER T L.  
PA (KEDD-) KEDDIE J.  
PA (BROU-) BROUN P E.  
PA (PILG-) PILGRIM M L.  
PA (DUBE-) DUBELL A N.  
PA (PINE-) PINEDA O.  
PA (YUGG-) YU G.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 12; Length 1574;  
Pred. No. 7.3e-07;  
RESULT 244  
ID ADW57939 standard; cDNA; 1596 BP.  
DE Rat NARC 19 cDNA.  
PN US2004009553-A1.  
PD 15-JAN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 12; Length 1596;  
Pred. No. 7.3e-07;  
RESULT 245  
ID AAF97902 standard; cDNA; 1618 BP.  
DE Human secreted protein cDNA, SEQ ID NO: 29.  
PN WO200121658-A1.  
PD 29-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 4; Length 1618;  
Pred. No. 7.2e-07;  
RESULT 246  
ID ADI42377 standard; DNA; 1637 BP.  
DE Plant transcription factor polynucleotide #512.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER-) SHERMAN B K.  
PA (RIEC-) RIECHMANN J L.  
PA (JIAN-) JIANG C.  
PA (HEAR-) HEARD J E.  
PA (HAKE-) HAAKE V.  
PA (CREE-) CREELMAN R A.  
PA (RATC-) RATCLIFFE O.  
PA (ADAM-) ADAM L J.  
PA (REUB-) REUBER T L.  
PA (KEDD-) KEDDIE J.  
PA (BROU-) BROUN P E.  
PA (PILG-) PILGRIM M L.  
PA (DUBE-) DUBELL A N.  
PA (PINE-) PINEDA O.  
PA (YUGG-) YU G.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 13; Length 1637;  
Pred. No. 7.2e-07;  
RESULT 247  
ID AAV81394 standard; DNA; 1733 BP.

DE Human tumour antigen zsig15 coding sequence.  
 PN W0950552-A1.  
 PD 12-NOV-1998.  
 PA (ZYNO) ZYMOGENETICS INC.  
 Query Match 1.6%; Score 58; DB 2; Length 1733;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-07;  
 RESULT 248  
 ID AAD17173 standard; cDNA; 1779 BP.  
 DE Human ion channel-31d6 (ion31d6) cDNA.  
 PN W020016849-A2.  
 PD 20-SEP-2001.  
 PA (PHAA) PHARMACIA & UPJOHN CO.  
 Query Match 1.6%; Score 58; DB 4; Length 1779;  
 Best Local Similarity 100.0%; Pred. No. 7e-07;  
 RESULT 249  
 ID ACD01559 standard; cDNA; 1779 BP.  
 DE cDNA clone Ion31c4 encoding human ion channel.  
 PN W02003023014-A2.  
 PD 20-MAR-2003.  
 PA (PHAA) PHARMACIA & UPJOHN CO.  
 Query Match 1.6%; Score 58; DB 8; Length 1779;  
 Best Local Similarity 100.0%; Pred. No. 7e-07;  
 RESULT 250  
 ID ADE29300 standard; cDNA; 1779 BP.  
 DE Novel human ion channel ion-31d6 cDNA.  
 PN US2003190714-A1.  
 PD 09-OCT-2003.  
 PA (ROBE) ROBERTS S L.  
 PA (BENJ) BENJAMIN C W.  
 PA (KARN) KARNOVSKY A M.  
 PA (RUBL) RUBLE C L.  
 PA (LINS) LINSKE-O'CONNELL L I.  
 PA (WANG) WANG.  
 PA (LIUD) LIU D.  
 Query Match 1.6%; Score 58; DB 10; Length 1779;  
 Best Local Similarity 100.0%; Pred. No. 7e-07;  
 RESULT 251  
 ID AAZ00802 standard; cDNA; 1810 BP.  
 DE Human secreted protein cDNA encoding gene 1.  
 PN W09940100-A1.  
 PD 12-AUG-1999.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.6%; Score 58; DB 2; Length 1810;  
 Best Local Similarity 100.0%; Pred. No. 7e-07;  
 RESULT 252  
 ID AAF98705 standard; DNA; 1815 BP.  
 DE Human ovarian cancer cell expressed sequence 10805.  
 PN W0200118542-A2.  
 PD 15-MAR-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 1.6%; Score 58; DB 5; Length 1815;  
 Best Local Similarity 100.0%; Pred. No. 7e-07;  
 RESULT 253  
 ID AA294198 standard; cDNA; 1834 BP.  
 DE Membrane-bound herpesvirus entry mediator-2 (mhVEM2) cDNA.  
 PN W0200014230-A1.  
 PD 16-MAR-2000.  
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 Query Match 1.6%; Score 58; DB 3; Length 1834;  
 Best Local Similarity 100.0%; Pred. No. 7e-07;  
 RESULT 254  
 ID ABX90577 standard; cDNA; 1834 BP.  
 DE Human membrane-bound Herpesvirus Entry Mediator-2 (mhVEM-2) cDNA.  
 PN US2002132297-A1.  
 PD 19-SEP-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 10; Length 1834;  
 Best Local Similarity 100.0%; Pred. No. 7e-07;  
 RESULT 255  
 ID ABL90541 standard; cDNA; 1857 BP.  
 DE Human polynucleotide SEQ ID NO 1103.  
 PN W0200190304-A2.  
 PD 29-NOV-2001.

PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.6%; Score 58; DB 6; Length 1857;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;  
 RESULT 256  
 ID ACD01569 standard; DNA; 1865 BP.  
 DE DNA clone 5HT-3C encoding human ion channel.  
 PN W02003023014-A2.  
 PD 20-MAR-2003.  
 PA (PHAA) PHARMACIA & UPJOHN CO.  
 Query Match 1.6%; Score 58; DB 8; Length 1865;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;  
 RESULT 257  
 ID ADI42386 standard; DNA; 1885 BP.  
 DE Plant transcription factor polynucleotide #521.  
 PN US2004019927-A1.  
 PD 29-JAN-2004.  
 PA (SHER) SHERMAN B K.  
 PA (RIEC) RIECHMANN J L.  
 PA (JIAN) JIANG C.  
 PA (HEAR) HEARD J E.  
 PA (HAAR) HAAKE V.  
 PA (CREE) CREELMAN R A.  
 PA (RATC) RATCLIFFE O.  
 PA (ADAM) ADAM L J.  
 PA (REUB) REUBER T L.  
 PA (KEDD) KEDDIE J.  
 PA (BROU) BROUN P E.  
 PA (PILG) PILGRIM M L.  
 PA (DUBE) DUBELL A N.  
 PA (PINE) PINEDA O.  
 PA (YUGG) YU G.  
 Query Match 1.6%; Score 58; DB 12; Length 1885;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;  
 RESULT 258  
 ID ABA96106 standard; cDNA; 1902 BP.  
 DE Human muT dGTPase 26493 cDNA.  
 PN W0200190374-A2.  
 PD 29-NOV-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 6; Length 1902;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;  
 RESULT 259  
 ID ADM47642 standard; DNA; 1920 BP.  
 DE Polynucleotide sequence #60 useful in producing transgenic plants.  
 PN US2003233670-A1.  
 PD 18-DEC-2003.  
 PA (EDGE) EDGERTON M D.  
 PA (CHOM) CHOMET P S.  
 PA (LACC) LACCETTI L B.  
 Query Match 1.6%; Score 58; DB 12; Length 1920;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;  
 RESULT 260  
 ID AAF24994 standard; DNA; 1928 BP.  
 DE Nucleotide sequence of an inositol polyphosphate phosphatase.  
 PN W0200104147-A2.  
 PD 18-JAN-2001.  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 Query Match 1.6%; Score 58; DB 4; Length 1928;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;  
 RESULT 261  
 ID AAC83106 standard; DNA; 1980 BP.  
 DE DNA encoding a protein involved in the cell cycle SEQ ID 21.  
 PN W0200065040-A2.  
 PD 02-NOV-2000.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 1.6%; Score 58; DB 3; Length 1980;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-07;  
 RESULT 262  
 ID AAF21635 standard; DNA; 2022 BP.  
 DE Human breast and ovarian cancer associated antigen gene SEQ ID 22.  
 PN W0200055173-A1.  
 PD 21-SEP-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match  
Best Local Similarity 1.6%; Score 58; DB 3; Length 2022;  
RESULT 263  
ID AAC84241 standard; cDNA; 2029 BP.  
DE Human secreted protein encoding cDNA.  
PN WO200070059-A2.  
PD 23-NOV-2000.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 4; Length 2029;  
RESULT 264  
ID AAC39965 standard; cDNA; 2030 BP.  
DE Murine TANGO 185 cDNA.  
PN WO200018904-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 3; Length 2030;  
RESULT 265  
ID AAC55227 standard; cDNA; 2031 BP.  
DE Human secreted protein gene 8 SEQ ID NO:48.  
PN WO200047602-A1.  
PD 17-AUG-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 3; Length 2031;  
RESULT 266  
ID AAC55226 standard; cDNA; 2031 BP.  
DE Human secreted protein gene 8 SEQ ID NO:47.  
PN WO200047602-A1.  
PD 17-AUG-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 3; Length 2031;  
RESULT 267  
ID AAD06011 standard; DNA; 2034 BP.  
DE Human neuronal apoptosis regulated candidate (NARC) 10C DNA.  
PN WO200131007-A2.  
PD 03-MAY-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 4; Length 2034;  
RESULT 268  
ID ABS56722 standard; cDNA; 2034 BP.  
DE Human NARC10 cDNA.  
PN WO200281516-A2.  
PD 17-OCT-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 8; Length 2034;  
RESULT 269  
ID ADJ57918 standard; cDNA; 2034 BP.  
DE Human NARC 10C cDNA.  
PN US2004009553-A1.  
PD 15-JAN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 12; Length 2034;  
RESULT 270  
ID ABS53034 standard; DNA; 2038 BP.  
DE Arabidopsis thaliana squalene epoxidase polynucleotide #4.  
PN WO200261072-A2.  
PD 08-AUG-2002.  
PA (MONS) MONSANTO TECHNOLOGY LLC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 6; Length 2038;  
RESULT 271  
ID AAH33367 standard; cDNA; 2073 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:423.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 4; Length 2073;  
RESULT 272  
ID AAC99923 standard; cDNA; 2076 BP.  
DE Human secreted protein gene 106 SEQ ID NO:116.  
PN WO200070042-A1.  
PD 23-NOV-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 3; Length 2076;  
RESULT 273  
ID AAC84404 standard; cDNA; 2093 BP.  
DE Mouse TANGO 206 variant 1 cDNA.  
PN WO200069885-A2.  
PD 23-NOV-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 4; Length 2093;  
RESULT 274  
ID AAC84406 standard; cDNA; 2093 BP.  
DE Mouse TANGO 206 variant 3 cDNA.  
PN WO200069885-A2.  
PD 23-NOV-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 4; Length 2093;  
RESULT 275  
ID AAC84405 standard; cDNA; 2093 BP.  
DE Mouse TANGO 206 variant 2 cDNA.  
PN WO200069885-A2.  
PD 23-NOV-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 4; Length 2093;  
RESULT 276  
ID AAC84387 standard; cDNA; 2093 BP.  
DE Mouse TANGO 206 polypeptide encoding cDNA.  
PN WO200069885-A2.  
PD 23-NOV-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 4; Length 2093;  
RESULT 277  
ID AAC81061 standard; cDNA; 2110 BP.  
DE Human secreted protein cDNA sequence #34.  
PN WO200063230-A2.  
PD 26-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 3; Length 2110;  
RESULT 278  
ID ABA06584 standard; cDNA; 2140 BP.  
DE Human cDNA SEQ ID NO: 250.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 4; Length 2140;  
RESULT 279  
ID ABV83921 standard; cDNA; 2140 BP.  
DE Human polynucleotide SEQ ID NO 250.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 6; Length 2140;  
RESULT 280  
ID AAF98703 standard; DNA; 2156 BP.  
DE Human ovarian cancer cell expressed sequence 10803.  
PN WO200118542-A2.  
PD 15-MAR-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.



PA (KEDD)/ KEDDIE J. 1.6%; Score 58; DB 12; Length 2252;  
PA (BROU)/ BROUN P E. 100.0%; Pred. No. 6.5e-07;  
PA (PILG)/ PILGRIM M L.  
PA (DUBE)/ DUBELL A N.  
PA (PINE)/ PINEDA O.  
PA (YUGG)/ YU G. 1.6%; Score 58; DB 12; Length 2252;  
Query Match 100.0%; Pred. No. 6.5e-07;  
Best Local Similarity 100.0%; Pred. No. 6.5e-07;  
RESULT 289  
ID ADO03163 standard; cDNA; 2252 BP.  
DE Corn orthologue of Thalecress transcription factor, cDNA #167.  
PN US2004045049-A1.  
PD 04-MAR-2004.  
PA (ZHAN)/ ZHANG J.  
PA (FROM)/ FROMM M E.  
PA (HEAR)/ HEARD J E.  
PA (RIEC)/ RIECHMANN J L.  
PA (ADAM)/ ADAM L J.  
PA (BROU)/ BROUN P E.  
PA (PINE)/ PINEDA O.  
PA (REUB)/ REUBER T L.  
PA (KEDD)/ KEDDIE J S.  
PA (YUGG)/ YU G.  
PA (JIANG)/ JIANG C.  
PA (SAMA)/ SAMAHA R S.  
PA (PILG)/ PILGRIM M L.  
PA (CREE)/ CREELMAN R A.  
PA (DUBE)/ DUBELL A N.  
PA (RATC)/ RATCLIFFE O.  
PA (KOMI)/ KOMIMOTO R.  
PA (SHER)/ SHERMAN B K.  
Query Match 1.6%; Score 58; DB 12; Length 2252;  
Best Local Similarity 100.0%; Pred. No. 6.5e-07;  
RESULT 290  
ID AAC84274 standard; cDNA; 2257 BP.  
DE Signal transduction protein encoding cDNA.  
PN WO200070059-A2.  
PD 23-NOV-2000.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 1.6%; Score 58; DB 4; Length 2257;  
Best Local Similarity 100.0%; Pred. No. 6.5e-07;  
RESULT 291  
ID AAC74401 standard; cDNA; 2259 BP.  
DE Human secreted protein gene 6 SEQ ID NO:16.  
PN WO200058496-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 3; Length 2259;  
Best Local Similarity 100.0%; Pred. No. 6.5e-07;  
RESULT 292  
ID ABO54591 standard; cDNA; 2266 BP.  
DE Human ovarian antigen HVVER10 cDNA, SEQ ID NO:471.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 6; Length 2266;  
Best Local Similarity 100.0%; Pred. No. 6.5e-07;  
RESULT 293  
ID ADA1585 standard; DNA; 2274 BP.  
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 113.  
PN US2003055236-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 9; Length 2274;  
Best Local Similarity 100.0%; Pred. No. 6.5e-07;  
RESULT 294  
ID AAF22390 standard; cDNA; 2287 BP.  
DE Human secreted protein gene 18 SEQ ID NO:28.  
PN WO200061629-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 3; Length 2287;  
Best Local Similarity 100.0%; Pred. No. 6.5e-07;  
RESULT 295  
ID AAF22390 standard; cDNA; 2287 BP.  
DE Human secreted protein gene 18 SEQ ID NO:28.  
PN WO200061629-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 58; DB 3; Length 2287;  
Best Local Similarity 100.0%; Pred. No. 6.5e-07;

Best Local Similarity 100.0%; Pred. No. 6.5e-07;  
RESULT 295  
ID ABK43731 standard; cDNA; 2292 BP.  
DE DNA encoding novel central nervous system protein #311.  
PN WO200155318-A2.  
PD 02-AUG-2001.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.5e-07;  
RESULT 296  
ID AD154118 standard; cDNA; 2292 BP.  
DE cDNA encoding novel human protein seq id 321.  
PN US2004018969-A1.  
PD 29-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.5e-07;  
RESULT 297  
ID ABQ54938 standard; cDNA; 2294 BP.  
DE Human ovarian antigen HOPKL18 cDNA, SEQ ID NO:818.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.5e-07;  
RESULT 298  
ID AAD33824 standard; cDNA; 2339 BP.  
DE Human secreted protein-encoding gene 13 cDNA clone HNTBN41, SEQ ID NO:23.  
PN WO200224719-A1.  
PD 28-MAR-2002.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.5e-07;  
RESULT 299  
ID AAH34945 standard; cDNA; 2357 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:2027.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.4e-07;  
RESULT 300  
ID ADMA47733 standard; DNA; 2419 BP.  
DE Polynucleotide sequence #151 useful in producing transgenic plants.  
PN US2003333670-A1.  
PD 18-DEC-2003.  
PA (EDGE/) EDGERTON M D.  
PA (CHOM/) CHOMET P S.  
PA (LACC/) LACCETTI L B.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.4e-07;  
RESULT 301  
ID ABV21274 standard; cDNA; 2591 BP.  
DE Human prostate expression marker cDNA 21265.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.3e-07;  
RESULT 302  
ID ABV27093 standard; cDNA; 2591 BP.  
DE Human prostate expression marker cDNA 27084.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.3e-07;  
RESULT 303  
ID AAF98706 standard; DNA; 2614 BP.  
DE Human ovarian cancer cell expressed sequence 10806.  
PN WO200118542-A2.

PD 15-MAR-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 5; Length 2614;  
RESULT 304  
ID AAD43556 standard; cDNA; 2713 BP.  
DE Human CD2000 cDNA.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 6; Length 2713;  
RESULT 305  
ID AAD43566 standard; DNA; 2713 BP.  
DE Human CD2000 DNA #3.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 6; Length 2713;  
RESULT 306  
ID AAD43565 standard; DNA; 2713 BP.  
DE Human CD2000 DNA #2.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 6; Length 2713;  
RESULT 307  
ID AAD43564 standard; DNA; 2713 BP.  
DE Human CD2000 DNA #1.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 6; Length 2713;  
RESULT 308  
ID AAD43567 standard; DNA; 2713 BP.  
DE Human CD2000 DNA #4.  
PN EP1223218-A1.  
PD 17-JUL-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 6; Length 2713;  
RESULT 309  
ID AAD63369 standard; cDNA; 2713 BP.  
DE Human CD2000 cDNA #1.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 10; Length 2713;  
RESULT 310  
ID AAD63378 standard; cDNA; 2713 BP.  
DE Human CD2000 cDNA #4.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 10; Length 2713;  
RESULT 311  
ID AAD63379 standard; cDNA; 2713 BP.  
DE Human CD2000 cDNA #5.  
PN US2003180888-A1.  
PD 25-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 58; DB 10; Length 2713;  
RESULT 312  
ID AAD63376 standard; cDNA; 2713 BP.  
DE Human CD2000 cDNA #2.  
PN US2003180888-A1.  
PD 25-SEP-2003.

PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 10; Length 2713;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;  
 RESULT 313  
 ID AAD63377 standard; cDNA; 2713 BP.  
 DE Human CD2000 cDNA #3.  
 PN US2003180888-A1.  
 PD 25-SEP-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 10; Length 2713;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;  
 RESULT 314  
 ID AAC68661 standard; cDNA; 2719 BP.  
 DE Human APO4 cDNA.  
 PN US6140098-A.  
 PD 31-OCT-2000.  
 PA (SCHE) SCHERING CORP.  
 Query Match 1.6%; Score 58; DB 4; Length 2719;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;  
 RESULT 315  
 ID ADJ63968 standard; DNA; 2719 BP.  
 DE DNA sequence encoding human APO4 protease.  
 PN US6638507-B1.  
 PD 28-OCT-2003.  
 PA (SCHE) SCHERING CORP.  
 Query Match 1.6%; Score 58; DB 10; Length 2719;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;  
 RESULT 316  
 ID AAD06007 standard; DNA; 2738 BP.  
 DE Human neuronal apoptosis regulated candidate (NARC) 9B DNA.  
 PN WO200131007-A2.  
 PD 03-MAY-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 4; Length 2738;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;  
 RESULT 317  
 ID ADJ57931 standard; cDNA; 2738 BP.  
 DE Human NARC 9 cDNA.  
 PN US2004009553-A1.  
 PD 15-JAN-2004.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 12; Length 2738;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;  
 RESULT 318  
 ID ABT31931 standard; DNA; 2778 BP.  
 DE Human breast cancer / ovarian cancer related coding sequence #38.  
 PN WO200300012-A2.  
 PD 03-JAN-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 10; Length 2778;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-07;  
 RESULT 319  
 ID AAD17208 standard; cDNA; 2875 BP.  
 DE Human carnitine acyltransferase, 26886 cDNA.  
 PN WO200166759-A2.  
 PD 13-SEP-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 4; Length 2875;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-07;  
 RESULT 320  
 ID AAF45127 standard; cDNA; 2964 BP.  
 DE Human TANGO 273 cDNA.  
 PN WO20007239-A2.  
 PD 21-DEC-2000.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 5; Length 2964;  
 Best Local Similarity 100.0%; Pred. No. 6e-07;  
 RESULT 321  
 ID ABX94104 standard; cDNA; 2964 BP.  
 DE cDNA encoding human TANGO 273.  
 PN US2002182675-A1.  
 PD 05-DEC-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.

Query Match 1.6%; Score 58; DB 8; Length 2964;  
 Best Local Similarity 100.0%; Pred. No. 6e-07;  
 RESULT 322  
 ID ADM42009 standard; cDNA; 2964 BP.  
 DE Human TANGO 273 cDNA.  
 PN US2003170621-A1.  
 PD 11-SEP-2003.  
 PA (MCCA) MCCARTHY S A.  
 PA (FRAS) FRASER C C.  
 PA (SHAR) SHARP J D.  
 PA (BARN) BARNES T M.  
 PA (KIRS) KIRST S J.  
 PA (MYER) MYERS P S.  
 PA (WRIG) WRIGHTON N.  
 PA (GOOD) GOODEARL A D J.  
 PA (HOLT) HOLTZMAN D A.  
 PA (KHOD) KHODADOUST M.  
 Query Match 1.6%; Score 58; DB 11; Length 2964;  
 Best Local Similarity 100.0%; Pred. No. 6e-07;  
 RESULT 323  
 ID ADO98245 standard; cDNA; 2964 BP.  
 DE Human polynucleotide #7.  
 PN US6764677-B1.  
 PD 20-JUL-2004.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 12; Length 2964;  
 Best Local Similarity 100.0%; Pred. No. 6e-07;  
 RESULT 324  
 ID AAC80579 standard; cDNA; 3021 BP.  
 DE Human secreted protein gene 49 SEQ ID NO:59.  
 PN WO200058467-A1.  
 PD 05-OCT-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.6%; Score 58; DB 3; Length 3021;  
 Best Local Similarity 100.0%; Pred. No. 6e-07;  
 RESULT 325  
 ID ABZ24009 standard; cDNA; 3102 BP.  
 DE Mouse adipose abundant protein (AAP) encoding cDNA.  
 PN WO200296355-A2.  
 PD 05-DEC-2002.  
 PA (GETH) GENENTECH INC.  
 Query Match 1.6%; Score 58; DB 8; Length 3102;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;  
 RESULT 326  
 ID ABZ24027 standard; cDNA; 3102 BP.  
 DE Mouse adipose abundant protein (AAP) encoding cDNA.  
 PN WO200297036-A2.  
 PD 05-DEC-2002.  
 PA (GETH) GENENTECH INC.  
 Query Match 1.6%; Score 58; DB 8; Length 3102;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;  
 RESULT 327  
 ID AAF15989 standard; cDNA; 3118 BP.  
 DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:424.  
 PN WO200055174-A1.  
 PD 21-SEP-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE) ROSEN C A.  
 Query Match 1.6%; Score 58; DB 3; Length 3118;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;  
 RESULT 328  
 ID AAF27781 standard; cDNA; 3169 BP.  
 DE Human MANGO 003 coding sequence SEQ ID NO: 4.  
 PN WO200100673-A1.  
 PD 04-JAN-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 4; Length 3169;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;  
 RESULT 329  
 ID AAZ36812 standard; DNA; 3196 BP.  
 DE DNA encoding a brain-derived signalling factor polypeptide.  
 PN WO9961463-A1.  
 PD 02-DEC-1999.

PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 Query Match 1.6%; Score 58; DB 3; Length 3196;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;  
 RESULT 330  
 ID ABS63368 standard; cDNA; 3196 BP.  
 DE Mouse brain-derived signalling factor (BDSF-1) DNA sequence #1.  
 PN US2002072089-A1.  
 PD 13-JUN-2002.  
 PA (HOLT/) HOLTZMAN D A.  
 PA (MCCA/) MCCARTHY S A.  
 PA (MACB/) MACBETH K J.  
 PA (BUSF/) BUSFIELD S J.  
 PA (PANY/) PAN Y.  
 PA (WHIT/) WHITE D.  
 PA (KHOD/) KHODADOUST M M.  
 PA (GUWW/) GU W.  
 Query Match 1.6%; Score 58; DB 6; Length 3196;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;  
 RESULT 331  
 ID ADR45578 standard; cDNA; 3196 BP.  
 DE Mouse cDNA encoding brain-derived signalling factor, BDSF-1, #1.  
 PN US2004176296-A1.  
 PD 09-SEP-2004.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 13; Length 3196;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;  
 RESULT 332  
 ID AAF22384 standard; cDNA; 3268 BP.  
 DE Human secreted protein gene 12 SEQ ID NO:22.  
 PN WO200061629-A1.  
 PD 19-OCT-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE/) ROSEN C A.  
 Query Match 1.6%; Score 58; DB 3; Length 3268;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-07;  
 RESULT 333  
 ID AAQ80228 standard; DNA; 3344 BP.  
 DE Rat NDF clone 22 DNA.  
 PN WO9428133-A1.  
 PD 08-DEC-1994.  
 PA (AMGE-) AMGEN INC.  
 Query Match 1.6%; Score 58; DB 2; Length 3344;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-07;  
 RESULT 334  
 ID AAC55197 standard; cDNA; 3354 BP.  
 DE Human secreted protein gene 8 SEQ ID NO:18.  
 PN WO200047602-A1.  
 PD 17-AUG-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.6%; Score 58; DB 3; Length 3354;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-07;  
 RESULT 335  
 ID ABK43741 standard; cDNA; 3747 BP.  
 DE DNA encoding novel central nervous system protein #321.  
 PN WO200155318-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.6%; Score 58; DB 4; Length 3747;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-07;  
 RESULT 336  
 ID ADI54128 standard; cDNA; 3747 BP.  
 DE cDNA encoding novel human protein seq id 331.  
 PN US2004018969-A1.  
 PD 29-JAN-2004.  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 Query Match 1.6%; Score 58; DB 12; Length 3747;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-07;  
 RESULT 337  
 ID AAD08362 standard; cDNA; 3953 BP.  
 DE Human secreted protein-encoding gene 18 cDNA clone HJMBB20, SEQ ID NO:28.  
 PN WO200077022-A1.

PD 21-DEC-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.6%; Score 58; DB 4; Length 3953;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-07;  
 RESULT 338  
 ID AAF32707 standard; cDNA; 3953 BP.  
 DE Human secreted protein gene 9 SEQ ID NO:19.  
 PN WO200077255-A1.  
 PD 21-DEC-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.6%; Score 58; DB 4; Length 3953;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-07;  
 RESULT 339  
 ID AAH73308 standard; cDNA; 3974 BP.  
 DE Human cervical cancer marker nucleic acid 4582.  
 PN WO2000142467-A2.  
 PD 14-JUN-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 1.6%; Score 58; DB 4; Length 3974;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-07;  
 RESULT 340  
 ID AAD56522 standard; DNA; 4897 BP.  
 DE Human KIAA1382, 17921 DNA.  
 PN WO20003039341-A2.  
 PD 15-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 8; Length 4897;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;  
 RESULT 341  
 ID ABZ70664 standard; cDNA; 5109 BP.  
 DE Human phospholipid transporter 67108 cDNA.  
 PN EP1266907-A1.  
 PD 18-DEC-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 10; Length 5109;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;  
 RESULT 342  
 ID ADC29731 standard; cDNA; 5502 BP.  
 DE cDNA encoding human aminopeptidase 55304.  
 PN US2002151696-A1.  
 PD 17-OCT-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.6%; Score 58; DB 10; Length 5502;  
 Best Local Similarity 100.0%; Pred. No. 5e-07;  
 RESULT 343  
 ID ADT95109 standard; cDNA; 87 BP.  
 DE Colon cancer associated human cDNA sequence #628.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.6%; Score 57; DB 11; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
 RESULT 344  
 ID ADT94951 standard; cDNA; 108 BP.  
 DE Colon cancer associated human cDNA sequence #470.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.6%; Score 57; DB 11; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
 RESULT 345  
 ID AAH33326 standard; cDNA; 131 BP.  
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:382.  
 PN WO200122920-A2.  
 PD 05-APR-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.6%; Score 57; DB 4; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
 RESULT 346  
 ID AAS29047 standard; cDNA; 155 BP.  
 DE cDNA encoding for human DNA-binding protein #18.  
 PN WO200155162-A1.  
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 57; DB 5; Length 155;  
Best Local Similarity 100.0%; Pred. No. 2.8e-06;  
RESULT 347  
ID ABS68187 standard; cDNA; 155 BP.  
DE cDNA encoding human DNA-binding protein #18.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 1.6%; Score 57; DB 6; Length 155;  
Best Local Similarity 100.0%; Pred. No. 2.8e-06;  
RESULT 348  
ID ADC25181 standard; cDNA; 155 BP.  
DE Human cDNA from extracellular matrix gene 18.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 57; DB 10; Length 155;  
Best Local Similarity 100.0%; Pred. No. 2.8e-06;  
RESULT 349  
ID ABX49026 standard; cDNA; 179 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #14191.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.6%; Score 57; DB 8; Length 179;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
RESULT 350  
ID ABZ08680 standard; cDNA; 226 BP.  
DE Human leukocyte derived cDNA SEQ ID NO 8671.  
PN WO200257414-A2.  
PD 25-JUL-2002.  
PA (BIOC-) BIOCARDIA INC.  
Query Match 1.6%; Score 57; DB 6; Length 226;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 351  
ID AAS29084 standard; cDNA; 237 BP.  
DE cDNA encoding for human DNA-binding protein #55.  
PN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 57; DB 5; Length 237;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
RESULT 352  
ID ABS68224 standard; cDNA; 237 BP.  
DE cDNA encoding human DNA-binding protein #55.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 1.6%; Score 57; DB 6; Length 237;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
RESULT 353  
ID ADC25218 standard; cDNA; 237 BP.  
DE Human cDNA from extracellular matrix gene 55.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 57; DB 10; Length 237;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
RESULT 354  
ID AAH33643 standard; cDNA; 303 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:699.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 57; DB 4; Length 303;

Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
RESULT 355  
ID ABX37863 standard; cDNA; 369 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #3028.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.6%; Score 57; DB 8; Length 369;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
RESULT 356  
ID AA190395 standard; cDNA; 410 BP.  
DE Human polynucleotide SEQ ID NO 10455.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.6%; Score 57; DB 4; Length 410;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
RESULT 357  
ID ABX62372 standard; DNA; 415 BP.  
DE Arabidopsis thaliana expressed sequence related polynucleotide #487.  
PN US2002040490-A1.  
PD 04-APR-2002.  
PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHEN A V.  
PA (LEDF/) LEDFORD B L.  
PA (WORS/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
Query Match 1.6%; Score 57; DB 8; Length 415;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
RESULT 358  
ID ABX60904 standard; DNA; 417 BP.  
DE Arabidopsis thaliana polynucleotide #250.  
PN US2002142319-A1.  
PD 03-OCT-2002.  
PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (HARG/) HARGISS T R.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHEN A V.  
PA (LEDF/) LEDFORD B L.  
PA (WORS/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
Query Match 1.6%; Score 57; DB 10; Length 417;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
RESULT 359  
ID ABL93801 standard; cDNA; 455 BP.  
DE Arabidopsis thaliana nucleic acid sequence Ref:2027566 SEQ ID NO:566.  
PN US2002023280-A1.  
PD 21-FEB-2002.  
PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.

PA (HAMI/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (RAIN/) RAINES T M.  
 PA (YUYI/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHAW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 PA (KRIC/) KRICKER M.  
 PA (SLAT/) SLATER T.  
 PA (DAVI/) DAVIS K R.  
 PA (ALLE/) ALLEN K.  
 PA (HOFF/) HOFFMAN N.  
 PA (HURB/) HURBAN P.

Query Match  
 Best Local Similarity 1.6%; Score 57; DB 6; Length 455;  
 100.0%; Pred. No. 2e-06;

RESULT 360  
 ID ABX60882 standard; DNA; 457 BP.  
 DE Arabidopsis thaliana polynucleotide #228.

PN US2002142319-A1.  
 PD 03-OCT-2002.  
 PA (GORL/) GORLACH J.  
 PA (ANYI/) AN Y.  
 PA (HAMI/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (HARG/) HARGISS T R.  
 PA (YUYI/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHAW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.

Query Match  
 Best Local Similarity 1.6%; Score 57; DB 10; Length 457;  
 100.0%; Pred. No. 2e-06;

RESULT 361  
 ID ADK11877 standard; DNA; 495 BP.  
 DE Breast cancer differentially expressed gene product #283.

PN WO2003057926-A1.  
 PD 17-JUL-2003.

PA (CHIR) CHIRON CORP.  
 Best Local Similarity 1.6%; Score 57; DB 10; Length 495;  
 100.0%; Pred. No. 1.9e-06;

RESULT 362  
 ID AAF16171 standard; cDNA; 738 BP.  
 DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:606.

PN WO200055174-A1.  
 PD 21-SEP-2000.

PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE/) ROSEN C A.  
 Best Local Similarity 1.6%; Score 57; DB 3; Length 738;  
 100.0%; Pred. No. 1.7e-06;

RESULT 363  
 ID AAS41669 standard; cDNA; 819 BP.  
 DE cDNA encoding novel human enzyme polypeptide #885.

PN WO200155301-A2.  
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity 1.6%; Score 57; DB 4; Length 819;  
 100.0%; Pred. No. 1.7e-06;

RESULT 364  
 ID AAF26575 standard; DNA; 893 BP.  
 DE DNA encoding human secreted protein #29.

PN WO200076531-A1.  
 PD 21-DEC-2000.

PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 1.6%; Score 57; DB 4; Length 893;  
 100.0%; Pred. No. 1.6e-06;

RESULT 365

ID AAS40950 standard; cDNA; 900 BP.  
 DE cDNA encoding novel human enzyme polypeptide #166.

PN WO200155301-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 1.6%; Score 57; DB 4; Length 900;  
 100.0%; Pred. No. 1.6e-06;

RESULT 366  
 ID AD142854 standard; DNA; 1023 BP.  
 DE Plant transcription factor polynucleotide #848.

PN US2004019927-A1.  
 PD 29-JAN-2004.

PA (SHER/) SHERMAN B K.  
 PA (RIEC/) RIECHMANN J L.  
 PA (JIAN/) JIANG C.  
 PA (HEAR/) HEARD J E.  
 PA (HAAK/) HAAKE V.  
 PA (CREE/) CREELMAN R A.  
 PA (RATC/) RATCLIFFE O.  
 PA (ADAM/) ADAM L J.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J.  
 PA (BROU/) BROUN P E.  
 PA (PIIG/) PILGRIM M L.  
 PA (DUBE/) DUBELL A N.  
 PA (PINE/) PINEDA O.  
 PA (YUGG/) YU G.

Query Match  
 Best Local Similarity 1.6%; Score 57; DB 12; Length 1023;  
 100.0%; Pred. No. 1.6e-06;

RESULT 367  
 ID AD03052 standard; cDNA; 1023 BP.

DE Soybean orthologue of Thalecress transcription factor, cDNA #214.

PN US2004045049-A1.  
 PD 04-MAR-2004.

PA (ZHAN/) ZHANG J.  
 PA (FROM/) FROMM M E.  
 PA (HEAR/) HEARD J E.  
 PA (RIEC/) RIECHMANN J L.  
 PA (ADAM/) ADAM L J.  
 PA (BROU/) BROUN P E.  
 PA (PINE/) PINEDA O.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J S.  
 PA (YUGG/) YU G.  
 PA (JIAN/) JIANG C.  
 PA (SAMA/) SAMARA R S.  
 PA (PIIG/) PILGRIM M L.  
 PA (CREE/) CREELMAN R A.  
 PA (DUBE/) DUBELL A N.  
 PA (RATC/) RATCLIFFE O.  
 PA (KUMI/) KUMIMOTO R.  
 PA (SHER/) SHERMAN B K.

Query Match  
 Best Local Similarity 1.6%; Score 57; DB 12; Length 1023;  
 100.0%; Pred. No. 1.6e-06;

RESULT 368  
 ID AAC99079 standard; cDNA; 1046 BP.

DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:307.

PN WO200055320-A1.  
 PD 21-SEP-2000.

PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 1.6%; Score 57; DB 3; Length 1046;  
 100.0%; Pred. No. 1.5e-06;

RESULT 369  
 ID AAC60044 standard; cDNA; 1108 BP.  
 DE Human secreted protein gene 20 SEQ ID NO:30.

PN WO200056766-A1.  
 PD 28-SEP-2000.

PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 1.6%; Score 57; DB 3; Length 1108;  
 100.0%; Pred. No. 1.5e-06;

RESULT 370  
 ID ABK43573 standard; cDNA; 1162 BP.

DE DNA encoding novel central nervous system protein #153.

PN WO200155318-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 4; Length 1162;  
RESULT 371  
ID ADI53960 standard; cDNA; 1162 BP.  
DE cDNA encoding novel human protein seq id 163.  
PN US2004018969-A1.  
PD 29-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 12; Length 1162;  
RESULT 372  
ID AAH34600 standard; cDNA; 1194 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1682.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 4; Length 1194;  
RESULT 373  
ID AAF91866 standard; cDNA; 1198 BP.  
DE Human secreted protein-encoding gene 9 cDNA clone HOEK12, SEQ ID NO:19.  
PN WO200118022-A1.  
PD 15-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 4; Length 1198;  
RESULT 374  
ID AAA09025 standard; DNA; 1315 BP.  
DE Human CSAPTE-1 coding sequence.  
PN WO200018890-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 3; Length 1315;  
RESULT 375  
ID AAC59772 standard; cDNA; 1464 BP.  
DE Human secreted protein gene 35 SEQ ID NO:45.  
PN WO200056751-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 3; Length 1464;  
RESULT 376  
ID AA206222 standard; DNA; 1621 BP.  
DE Human secreted protein gene No. 4.  
PN WO9935158-A1.  
PD 15-JUL-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 2; Length 1621;  
RESULT 377  
ID AAC59400 standard; cDNA; 1734 BP.  
DE Human secreted protein cDNA #9.  
PN WO200056765-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 3; Length 1734;  
RESULT 378  
ID AAC68120 standard; cDNA; 2000 BP.  
DE Human secreted protein cDNA sequence #40.  
PN WO200058335-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 3; Length 2000;  
RESULT 379

ID ABZ73487 standard; cDNA; 2000 BP.  
DE Secreted protein-encoding gene 207 cDNA clone HMUAE26, SEQ ID NO:217.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 8; Length 2000;  
RESULT 380  
ID ADA98032 standard; cDNA; 2000 BP.  
DE Human secreted protein cDNA sequence #136.  
PN WO2003004623-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 8; Length 2000;  
RESULT 381  
ID ABZ67096 standard; cDNA; 2000 BP.  
DE Human secreted protein encoding cDNA SEQ ID NO 216.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 10; Length 2000;  
RESULT 382  
ID AAC84351 standard; DNA; 2235 BP.  
DE Corn clone CPR951 FL cDNA sequence.  
PN WO200070069-A1.  
PD 23-NOV-2000.  
PA (MONS-) MONSANTO CO.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 4; Length 2235;  
RESULT 383  
ID AAD13360 standard; cDNA; 2346 BP.  
DE Human secreted protein-encoding gene 16 cDNA clone HCUHQ40, SEQ ID NO:36.  
PN WO200154708-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 4; Length 2346;  
RESULT 384  
ID ABA93749 standard; cDNA; 2389 BP.  
DE Human testis derived cDNA clone tes3\_15n14.  
PN WO200198454-A2.  
PD 27-DEC-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 6; Length 2389;  
RESULT 385  
ID AAL60541 standard; cDNA; 2564 BP.  
DE Human organelle-associated protein (ORGA)-1 cDNA.  
PN WO2003044171-A2.  
PD 30-MAY-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 9; Length 2564;  
RESULT 386  
ID AAZ00842 standard; cDNA; 2581 BP.  
DE Human secreted protein cDNA encoding gene 41.  
PN WO9940100-A1.  
PD 12-AUG-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 2; Length 2581;  
RESULT 387  
ID AAZ10676 standard; cDNA; 2584 BP.  
DE cDNA encoding a human secreted protein.  
PN WO9943693-A1.  
PD 02-SEP-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 57; DB 2; Length 2584;  
RESULT 388  
ID AD116404 standard; DNA; 2720 BP.



DE Human protein modification and maintenance molecule (PMM) gene #37.  
PN WO2003100016-A2.  
PD 04-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 1.6%; Score 57; DB 12; Length 2720;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 389  
ID AAG15081 standard; cDNA; 2748 BP.  
DE Human SECP-53 cDNA.  
PN WO2003087300-A2.  
PD 23-OCT-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 1.6%; Score 57; DB 10; Length 2748;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 390  
ID ABX71352 standard; cDNA; 2853 BP.  
DE Intracellular trafficking-associated cDNA from clone DKFZphtes3\_17n18.  
PN WO200112659-A2.  
PD 22-FEB-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 1.6%; Score 57; DB 5; Length 2853;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 391  
ID AAI58066 standard; cDNA; 3160 BP.  
DE Human polynucleotide SEQ ID NO 269.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.6%; Score 57; DB 4; Length 3160;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
RESULT 392  
ID ABK54751 standard; cDNA; 72 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 221.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 56; DB 6; Length 72;  
Best Local Similarity 100.0%; Pred. No. 6.5e-06;  
RESULT 393  
ID ABK55072 standard; cDNA; 73 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 542.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 56; DB 6; Length 73;  
Best Local Similarity 100.0%; Pred. No. 6.5e-06;  
RESULT 394  
ID ABK54792 standard; cDNA; 74 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 262.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 56; DB 6; Length 74;  
Best Local Similarity 100.0%; Pred. No. 6.5e-06;  
RESULT 395  
ID ABK54924 standard; cDNA; 74 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 394.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 56; DB 6; Length 74;  
Best Local Similarity 100.0%; Pred. No. 6.5e-06;  
RESULT 396  
ID ACN34476 standard; cDNA; 74 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-K6-D12, SEQ:9257.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.6%; Score 56; DB 13; Length 74;  
Best Local Similarity 100.0%; Pred. No. 6.5e-06;

RESULT 397  
ID ABK54665 standard; cDNA; 77 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 135.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 56; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 6.4e-06;  
RESULT 398  
ID ABK54736 standard; cDNA; 79 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 206.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 56; DB 6; Length 79;  
Best Local Similarity 100.0%; Pred. No. 6.4e-06;  
RESULT 399  
ID ABK55279 standard; cDNA; 81 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 749.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 56; DB 6; Length 81;  
Best Local Similarity 100.0%; Pred. No. 6.3e-06;  
RESULT 400  
ID ABK54750 standard; cDNA; 82 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 220.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 56; DB 6; Length 82;  
Best Local Similarity 100.0%; Pred. No. 6.3e-06;  
RESULT 401  
ID ABK54808 standard; cDNA; 82 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 278.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 56; DB 6; Length 82;  
Best Local Similarity 100.0%; Pred. No. 6.3e-06;  
RESULT 402  
ID ABK54687 standard; cDNA; 90 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 157.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 56; DB 6; Length 90;  
Best Local Similarity 100.0%; Pred. No. 6.1e-06;  
RESULT 403  
ID ABK54776 standard; cDNA; 95 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 246.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 56; DB 6; Length 95;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
RESULT 404  
ID ABK54958 standard; cDNA; 100 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 428.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 56; DB 6; Length 100;  
Best Local Similarity 100.0%; Pred. No. 5.9e-06;  
RESULT 405  
ID ADR95353 standard; cDNA; 105 BP.  
DE Colon cancer associated human cDNA sequence #872.  
PN US2003087818-A1.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.6%; Score 56; DB 11; Length 105;  
Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
RESULT 406

ID ABX54764 standard; cDNA; 113 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #4693.  
PN US2002137160-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 8; Length 113;  
Best Local Similarity 100.0%; Pred. No. 5.7e-06;  
RESULT 407  
ID ABA82937 standard; DNA; 115 BP.  
DE Human protective DNA sequence CNI-00749 fragment #36.  
PN WO200176457-A2.  
PD 18-OCT-2001.  
PA (COGE-) COGENT NEUROSCIENCE INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 115;  
Best Local Similarity 100.0%; Pred. No. 5.7e-06;  
RESULT 408  
ID AAS63020 standard; cDNA; 116 BP.  
DE Cell death protective sequence CNI-00725, ORF #11.  
PN WO200176532-A2.  
PD 18-OCT-2001.  
PA (COGE-) COGENT NEUROSCIENCE INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 116;  
Best Local Similarity 100.0%; Pred. No. 5.6e-06;  
RESULT 409  
ID ABK55292 standard; cDNA; 117 BP.  
DE Human colon cancer-associated cDNA, SEQ ID No 762.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 117;  
Best Local Similarity 100.0%; Pred. No. 5.6e-06;  
RESULT 410  
ID ADT95697 standard; cDNA; 128 BP.  
DE Colon cancer associated human cDNA sequence #1216.  
PN US2003087818-A1.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 11; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
RESULT 411  
ID AAS63092 standard; cDNA; 139 BP.  
DE Cell death protective sequence CNI-00728, ORF #24.  
PN WO200176532-A2.  
PD 18-OCT-2001.  
PA (COGE-) COGENT NEUROSCIENCE INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 139;  
Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
RESULT 412  
ID AAS63142 standard; cDNA; 152 BP.  
DE Cell death protective sequence CNI-00732, ORF #8.  
PN WO200176532-A2.  
PD 18-OCT-2001.  
PA (COGE-) COGENT NEUROSCIENCE INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 152;  
Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
RESULT 413  
ID ABK54692 standard; cDNA; 154 BP.  
DE Human colon cancer-associated cDNA, SEQ ID No 152.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 154;  
Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
RESULT 414  
ID AAS41371 standard; cDNA; 159 BP.  
DE cDNA encoding novel human enzyme polypeptide #587.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 4; Length 159;

Best Local Similarity 100.0%; Pred. No. 5.1e-06;  
RESULT 415  
ID ABA82875 standard; DNA; 160 BP.  
DE Human protective DNA sequence CNI-00746 fragment #40.  
PN WO200176457-A2.  
PD 18-OCT-2001.  
PA (COGE-) COGENT NEUROSCIENCE INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 160;  
Best Local Similarity 100.0%; Pred. No. 5.1e-06;  
RESULT 416  
ID ABX45893 standard; cDNA; 160 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #11058.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 8; Length 160;  
Best Local Similarity 100.0%; Pred. No. 5.1e-06;  
RESULT 417  
ID ABK54773 standard; cDNA; 161 BP.  
DE Human colon cancer-associated cDNA, SEQ ID No 243.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 161;  
Best Local Similarity 100.0%; Pred. No. 5.1e-06;  
RESULT 418  
ID ABX42996 standard; cDNA; 286 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #8161.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 8; Length 286;  
Best Local Similarity 100.0%; Pred. No. 4.3e-06;  
RESULT 419  
ID ABX46068 standard; cDNA; 408 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #11233.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 8; Length 408;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
RESULT 420  
ID ABX48319 standard; cDNA; 424 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #13484.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 8; Length 424;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
RESULT 421  
ID ABX60806 standard; DNA; 437 BP.  
DE Arabidopsis thaliana polynucleotide #152.  
PN US2002142319-A1.  
PD 03-OCT-2002.  
PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (HARG/) HARGISS T R.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEKA J G.

PA (PAGE/) PAGE A.  
PA (MATH/) MATHW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 10; Length 437;  
Result 422  
ID AAV55622 standard; cDNA; 485 BP.  
DE Human prostate expression marker cDNA 55613.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 5; Length 485;  
Result 423  
ID AAX30156 standard; DNA; 487 BP.  
DE Human secreted protein gene 12.  
PN WO9910363-A1.  
PD 04-MAR-1999.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 2; Length 487;  
Result 424  
ID ACN50766 standard; cDNA; 554 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-001-Q1-N6-C8, SEQ:5547.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 13; Length 554;  
Result 425  
ID ACN60732 standard; cDNA; 587 BP.  
DE Cotton gymnoecium tissue EST Clone ID: LIB3829-027-Q6-K6-B6, SEQ:15513.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 13; Length 587;  
Result 426  
ID ABZ58160 standard; cDNA; 639 BP.  
DE Human neurotransmitter cDNA.  
PN WO2003005033-A2.  
PD 16-JAN-2003.  
PA (GENE-) GENEPROT INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 8; Length 639;  
Result 427  
ID AAD37774 standard; DNA; 767 BP.  
DE Extended sequence for mouse IMX5\_07.  
PN WO200231116-A2.  
PD 18-APR-2002.  
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 767;  
Result 428  
ID AAX37387 standard; cDNA; 824 BP.  
DE Human secreted protein cDNA fragment containing gene 19.  
PN WO9909155-A1.  
PD 25-FEB-1999.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 2; Length 824;  
Result 429  
ID ACC48069 standard; cDNA; 907 BP.  
DE Nucleotide sequence of cDNA pPC86-Clone 27R.  
PN WO200277188-A2.  
PN WO2003000273-A1.  
PD 03-JAN-2003.  
PA (AUTO-) AUTOGEN RES PTY LTD.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 10; Length 907;  
Result 430  
ID AAS63009 standard; cDNA; 920 BP.  
DE Cell death protective sequence CNI-00725.  
PN WO200176532-A2.  
PD 18-OCT-2001.  
PA (COGE-) COGENT NEUROSCIENCE INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 920;  
Result 431  
ID AAZ98037 standard; cDNA; 931 BP.  
DE Human secreted protein encoding nucleotide sequence SEQ ID NO:31.  
PN WO200004140-A1.  
PD 27-JAN-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 3; Length 931;  
Result 432  
ID AAD11650 standard; cDNA; 931 BP.  
DE Human secreted protein-encoding gene 21 cDNA clone HBAFA02, SEQ ID NO:31.  
PN WO200151504-A1.  
PD 19-JUL-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 4; Length 931;  
Result 433  
ID ABK69746 standard; cDNA; 931 BP.  
DE Human secreted protein gene 21.  
PN WO200226931-A2.  
PD 04-APR-2002.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 931;  
Result 434  
ID AAX37466 standard; cDNA; 980 BP.  
DE Human secreted protein cDNA fragment containing gene 16.  
PN WO9918208-A1.  
PD 15-APR-1999.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 2; Length 980;  
Result 435  
ID AAS63134 standard; cDNA; 1046 BP.  
DE Cell death protective sequence CNI-00732.  
PN WO200176532-A2.  
PD 18-OCT-2001.  
PA (COGE-) COGENT NEUROSCIENCE INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 1046;  
Result 436  
ID AAC80536 standard; cDNA; 1058 BP.  
DE Human secreted protein gene 6 SEQ ID NO:16.  
PN WO200058467-A1.  
PD 05-OCT-2000.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 3; Length 1058;  
Result 437  
ID ADC20162 standard; DNA; 1058 BP.  
DE Human secreted protein coding sequence #101.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 10; Length 1058;  
Result 438  
ID ABT16807 standard; DNA; 1058 BP.  
DE Human secreted protein gene sequence - SEQ ID NO 56.  
PN WO200277188-A2.

PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 10; Length 1058;  
Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
RESULT 439  
ID ABZ67044 standard; cDNA; 1058 BP.  
DE Human secreted protein encoding cDNA SEQ ID NO 164.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 10; Length 1058;  
Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
RESULT 440  
ID ADC78224 standard; cDNA; 1088 BP.  
DE Human secreted protein encoding cDNA SEQ ID NO:31.  
PN WO2003072761-A1.  
PD 04-SEP-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 10; Length 1088;  
Best Local Similarity 100.0%; Pred. No. 2.8e-06;  
RESULT 441  
ID AAF97917 standard; cDNA; 1138 BP.  
DE Human secreted protein cDNA, SEQ ID NO: 44.  
PN WO200121658-A1.  
PD 29-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 4; Length 1138;  
Best Local Similarity 100.0%; Pred. No. 2.8e-06;  
RESULT 442  
ID ADG79383 standard; cDNA; 1233 BP.  
DE Human secreted protein cDNA of the invention SEQ ID NO:189.  
PN WO200268638-A1.  
PD 06-SEP-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 6; Length 1233;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
RESULT 443  
ID AAX04382 standard; DNA; 1261 BP.  
DE Human secreted protein gene 72 clone HCFNN01.  
PN WO9856804-A1.  
PD 17-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 2; Length 1261;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
RESULT 444  
ID ADA39705 standard; cDNA; 1261 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 8; Length 1261;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
RESULT 445  
ID ACC50381 standard; cDNA; 1261 BP.  
DE Human secreted protein coding sequence, SEQ ID 48.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 8; Length 1261;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
RESULT 446  
ID ADA55899 standard; DNA; 1261 BP.  
DE Gene encoding human secreted protein #78.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 10; Length 1261;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
RESULT 447  
ID AAS63048 standard; cDNA; 1293 BP.  
DE Cell death protective sequence CNI-00727.  
PN WO200176532-A2.  
PD 18-OCT-2001.

PA (COGE-) COGENT NEUROSCIENCE INC.  
Query Match 1.6%; Score 56; DB 6; Length 1293;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
RESULT 448  
ID ABA82876 standard; DNA; 1350 BP.  
DE Human protective DNA sequence CNI-00747.  
PN WO200176457-A2.  
PD 18-OCT-2001.  
PA (COGE-) COGENT NEUROSCIENCE INC.  
Query Match 1.6%; Score 56; DB 6; Length 1350;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
RESULT 449  
ID AAO8379 standard; cDNA; 1351 BP.  
DE Human secreted protein-encoding gene 35 cDNA clone HMVDU15, SEQ ID NO:45.  
PN WO200077022-A1.  
PD 21-DEC-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 4; Length 1351;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
RESULT 450  
ID ABZ73488 standard; cDNA; 1351 BP.  
DE Secreted protein-encoding gene 208 cDNA clone HMVDU15, SEQ ID NO:218.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 8; Length 1351;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
RESULT 451  
ID ABZ67097 standard; cDNA; 1351 BP.  
DE Human secreted protein encoding cDNA SEQ ID NO 217.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 10; Length 1351;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
RESULT 452  
ID AAX51714 standard; DNA; 1361 BP.  
DE DNA encoding a human secreted protein.  
PN WO9911293-A1.  
PD 11-MAR-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 2; Length 1361;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
RESULT 453  
ID ABQ92566 standard; cDNA; 1361 BP.  
DE Human secreted protein encoding cDNA SEQ ID NO 24.  
PN WO200257420-A2.  
PD 25-JUL-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 6; Length 1361;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
RESULT 454  
ID ACC50395 standard; cDNA; 1361 BP.  
DE Human secreted protein coding sequence, SEQ ID 62.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 8; Length 1361;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
RESULT 455  
ID AAC69101 standard; DNA; 1362 BP.  
DE Human secreted protein gene 18 clone HKAFH74.  
PN WO200055371-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 3; Length 1362;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 456  
ID AAX51727 standard; DNA; 1367 BP.  
DE DNA encoding a human secreted protein.  
PN WO9911293-A1.  
PD 11-MAR-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.6%; Score 56; DB 2; Length 1367;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 457  
ID ABQ2579 standard; cDNA; 1367 BP.  
DE Human secreted protein encoding cDNA SEQ ID NO 37.  
PN WO200257420-A2.  
PD 25-JUL-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 6; Length 1367;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 458  
ID AAD06008 standard; DNA; 1407 BP.  
DE Human neuronal apoptosis regulated candidate (NARC) 8B DNA.  
PN WO200131007-A2.  
PD 03-MAY-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.6%; Score 56; DB 4; Length 1407;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 459  
ID ADJ57919 standard; cDNA; 1407 BP.  
DE Human NARC 8B cDNA.  
PN US2004009553-A1.  
PD 15-JAN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.6%; Score 56; DB 12; Length 1407;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 460  
ID ADA39727 standard; cDNA; 1421 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 8; Length 1421;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 461  
ID AB271218 standard; cDNA; 1421 BP.  
DE Human secreted protein-encoding gene 29 cDNA clone HDHEB60, SEQ ID NO:39.  
PN WO200276488-A1.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 8; Length 1421;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 462  
ID ADC73447 standard; DNA; 1421 BP.  
DE Human secreted protein-related DNA - SEQ ID 80.  
PN WO2003038053-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 10; Length 1421;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 463  
ID ADD37560 standard; cDNA; 1421 BP.  
DE Human secreted protein encoding sequence #42.  
PN WO200290526-A2.  
PD 14-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 10; Length 1421;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 464  
ID ADA55918 standard; DNA; 1421 BP.  
DE Gene encoding human secreted protein #97.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 10; Length 1421;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 465  
ID AAS63068 standard; cDNA; 1466 BP.  
DE Cell death protective sequence CNI-00728.  
PN WO200176532-A2.  
PD 18-OCT-2001.  
PA (COGE-) COGENT NEUROSCIENCE INC.  
Query Match 1.6%; Score 56; DB 6; Length 1466;

Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 466  
ID AAF18174 standard; DNA; 1524 BP.  
DE Lung cancer associated polynucleotide sequence SEQ ID 193.  
PN WO200055180-A2.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match 1.6%; Score 56; DB 3; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 467  
ID AAC79956 standard; cDNA; 1526 BP.  
DE Human secreted protein encoding cDNA for gene 9.  
PN WO200058357-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 3; Length 1526;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 468  
ID ABL89665 standard; cDNA; 1526 BP.  
DE Human polynucleotide SEQ ID NO 227.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 6; Length 1526;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 469  
ID AAC78187 standard; cDNA; 1574 BP.  
DE Human cancer associated gene sequence SEQ ID NO:581.  
PN WO200055350-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 3; Length 1574;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 470  
ID AAF32743 standard; cDNA; 1574 BP.  
DE Human secreted protein gene 45 SEQ ID NO:55.  
PN WO200077255-A1.  
PD 21-DEC-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 4; Length 1574;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 471  
ID AAQ80218 standard; DNA; 1651 BP.  
DE Human NDF-alpha2b clone 17 DNA.  
PN WO9428133-A1.  
PD 08-DEC-1994.  
PA (AMGE-) AMGEN INC.  
Query Match 1.6%; Score 56; DB 2; Length 1651;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 472  
ID AAC77740 standard; cDNA; 1657 BP.  
DE Human cancer associated gene sequence SEQ ID NO:134.  
PN WO200055350-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 3; Length 1657;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 473  
ID AAD05081 standard; cDNA; 1666 BP.  
DE Human secreted protein-encoding gene 5 cDNA clone HDPCJ43, SEQ ID NO:39.  
PN WO200134768-A2.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 4; Length 1666;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 474  
ID AAC98134 standard; cDNA; 1694 BP.  
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:144.  
PN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 3; Length 1694;

Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 475  
ID AA298108 standard; cDNA; 1722 BP.  
DE Human secreted protein encoding nucleotide sequence SEQ ID NO:102.  
PN WO200004140-A1.  
PD 27-JAN-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 3; Length 1722;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 476  
ID AAD11721 standard; cDNA; 1722 BP.  
DE Human secreted protein-encoding gene 71 cDNA clone HDP0256, SEQID NO:102.  
PN WO200151504-A1.  
PD 19-JUL-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 4; Length 1722;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 477  
ID ABK69818 standard; cDNA; 1722 BP.  
DE Human secreted protein gene 71 #2.  
PN WO200226931-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 6; Length 1722;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 478  
ID ADA40305 standard; cDNA; 1722 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 8; Length 1722;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 479  
ID ACC50714 standard; cDNA; 1722 BP.  
DE Human secreted protein coding sequence, SEQ ID 381.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 8; Length 1722;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 480  
ID ADA56466 standard; DNA; 1722 BP.  
DE Gene encoding human secreted protein #118.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 10; Length 1722;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 481  
ID ADM19675 standard; cDNA; 1724 BP.  
DE Novel human channel/transporter gene #237 clone 2.  
PN WO200154472-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 5; Length 1724;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 482  
ID ABL90677 standard; cDNA; 1724 BP.  
DE Human polynucleotide SEQ ID NO 1239.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 6; Length 1724;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
RESULT 483  
ID ADD19236 standard; cDNA; 1745 BP.  
DE Human cDNA from secreted protein gene 53.  
PN WO2003052377-A2.  
PD 26-JUN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 10; Length 1745;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;

RESULT 484  
ID AA265347 standard; DNA; 1779 BP.  
DE Human secreted protein gene 18.  
PN WO9958660-A1.  
PD 18-NOV-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 3; Length 1779;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
RESULT 485  
ID ADE11737 standard; cDNA; 1779 BP.  
DE Human secreted polypeptide cDNA #99.  
PN US2003100051-A1.  
PD 29-MAY-2003.  
PA (RUBE/) RUBEN S M.  
PA (FLOR/) FLORENCE K A.  
PA (NIJ/) NI J.  
PA (ROSE/) ROSEN C A.  
PA (CART/) CARTER K C.  
PA (MOOR/) MOORE P A.  
PA (OLSE/) OLSEN H S.  
PA (SHI/) SHI Y.  
PA (YOUN/) YOUNG P E.  
PA (WEI/) WEI Y.  
PA (BREW/) BREWER L A.  
PA (SOPP/) SOPPET D R.  
PA (LAF/) LAFLEUR D W.  
PA (ENDR/) ENDRESS G A.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Query Match 1.6%; Score 56; DB 10; Length 1779;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
RESULT 486  
ID ADC78218 standard; cDNA; 1803 BP.  
DE Human secreted protein encoding cDNA SEQ ID NO:25.  
PN WO2003072761-A1.  
PD 04-SEP-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 10; Length 1803;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
RESULT 487  
ID AAH84170 standard; cDNA; 1825 BP.  
DE Human cell death protective cDNA clone CNI-00714, SEQ:75.  
PN WO200145638-A2.  
PD 28-JUN-2001.  
PA (COGE-) COGENT NEUROSCIENCES INC.  
Query Match 1.6%; Score 56; DB 4; Length 1825;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
RESULT 488  
ID AAD07854 standard; cDNA; 1892 BP.  
DE Human secreted protein-encoding gene 7 cDNA clone HDPDI45, SEQ ID NO:56.  
PN WO200132675-A1.  
PD 10-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 4; Length 1892;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
RESULT 489  
ID ABL90762 standard; cDNA; 1892 BP.  
DE Human polynucleotide SEQ ID NO 1324.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.6%; Score 56; DB 6; Length 1892;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
RESULT 490  
ID ABA82901 standard; DNA; 1895 BP.  
DE Human protective DNA sequence CNI-00749.  
PN WO200176457-A2.  
PD 18-OCT-2001.  
PA (COGE-) COGENT NEUROSCIENCES INC.  
Query Match 1.6%; Score 56; DB 6; Length 1895;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
RESULT 491  
ID ABL90655 standard; cDNA; 1977 BP.

DE Human polynucleotide SEQ ID NO 1217.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 1977;  
Pred. No. 2.4e-06;  
RESULT 492  
ID AAF45091 standard; cDNA; 2018 BP.  
DE Human secreted protein coding sequence SEQ ID NO: 30.  
PN WO200077023-A1.  
PD 21-DEC-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 4; Length 2018;  
Pred. No. 2.3e-06;  
RESULT 493  
ID AAC68085 standard; cDNA; 2122 BP.  
DE Human secreted protein cDNA sequence #5.  
PN WO200058335-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 3; Length 2122;  
Pred. No. 2.3e-06;  
RESULT 494  
ID ABO54342 standard; cDNA; 2755 BP.  
DE Human ovarian antigen HNOAX46 cDNA, SEQ ID NO:222.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 2755;  
Pred. No. 2.1e-06;  
RESULT 495  
ID ABA82835 standard; DNA; 3064 BP.  
DE Human protective DNA sequence CNI-00746.  
PN WO200176457-A2.  
PD 18-OCT-2001.  
PA (COGE-) COCENT NEUROSCIENCE INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 6; Length 3064;  
Pred. No. 2.1e-06;  
RESULT 496  
ID AAF18172 standard; DNA; 3144 BP.  
DE Lung cancer associated polynucleotide sequence SEQ ID 191.  
PN WO200055180-A2.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 3; Length 3144;  
Pred. No. 2e-06;  
RESULT 497  
ID ADR41354 standard; cDNA; 3627 BP.  
DE Human CD-like molecule HHFHQ39 cDNA, SEQ ID NO:153.  
PN WO200226930-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 7; Length 3627;  
Pred. No. 2e-06;  
RESULT 498  
ID ADL61794 standard; DNA; 4773 BP.  
DE Human ovarian cancer DNA marker #20006.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.6%; Score 56; DB 5; Length 4773;  
Pred. No. 1.8e-06;  
RESULT 499  
ID ADT95739 standard; cDNA; 94 BP.  
DE Colon cancer associated human cDNA sequence #1258.  
PN US2003087818-A1.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 1.5%; Score 55; DB 11; Length 94;  
Pred. No. 1.1e-05;  
RESULT 500  
ID ABX43725 standard; cDNA; 257 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #8890.  
PN US2002137139-A1.

ID ADT95194 standard; cDNA; 96 BP.  
DE Colon cancer associated human cDNA sequence #713.  
PN US2003087818-A1.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 1.5%; Score 55; DB 11; Length 96;  
Pred. No. 1.1e-05;  
RESULT 501  
ID AAT94823 standard; cDNA; 110 BP.  
DE Colon cancer associated human cDNA sequence #342.  
PN US2003087818-A1.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 1.5%; Score 55; DB 11; Length 110;  
Pred. No. 1.1e-05;  
RESULT 502  
ID AAC13325 standard; cDNA; 129 BP.  
DE Human secreted protein 5' EST, SEQ ID NO: 17400.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST-) GENSET.  
Query Match  
Best Local Similarity 1.5%; Score 55; DB 3; Length 129;  
Pred. No. 1e-05;  
RESULT 503  
ID AAC14649 standard; cDNA; 131 BP.  
DE Human secreted protein 5' EST, SEQ ID NO: 18724.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST-) GENSET.  
Query Match  
Best Local Similarity 1.5%; Score 55; DB 3; Length 131;  
Pred. No. 1e-05;  
RESULT 504  
ID ABX50278 standard; cDNA; 138 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #207.  
PN US2002137160-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.5%; Score 55; DB 8; Length 138;  
Pred. No. 1e-05;  
RESULT 505  
ID AAK57138 standard; cDNA; 161 BP.  
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:2198.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.5%; Score 55; DB 4; Length 161;  
Pred. No. 9.5e-06;  
RESULT 506  
ID AAS58829 standard; cDNA; 172 BP.  
DE cDNA #1505 encoding portion of a human colon tumour protein.  
PN WO200173027-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 1.5%; Score 55; DB 4; Length 172;  
Pred. No. 9.3e-06;  
RESULT 507  
ID ABX38816 standard; cDNA; 210 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #3981.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 1.5%; Score 55; DB 8; Length 210;  
Pred. No. 8.8e-06;  
RESULT 508  
ID ABX43725 standard; cDNA; 257 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #8890.  
PN US2002137139-A1.



PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match  
 Best Local Similarity 1.5%; Score 55; DB 8; Length 257;  
 100.0%; Pred. No. 8.2e-06;  
 RESULT 509  
 ID ABX61239 standard; DNA; 277 BP.  
 DE Arabidopsis thaliana polynucleotide #585.  
 PN US2002142319-A1.  
 PD 03-OCT-2002.  
 PA (GORL/) GORLACH J.  
 PA (ANYI/) AN Y.  
 PA (HAMI/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (HARG/) HARGISS T R.  
 PA (YUYI/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHAW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 Query Match  
 Best Local Similarity 1.5%; Score 55; DB 10; Length 277;  
 100.0%; Pred. No. 8.1e-06;  
 RESULT 510  
 ID ABX47848 standard; cDNA; 321 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #13013.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match  
 Best Local Similarity 1.5%; Score 55; DB 8; Length 321;  
 100.0%; Pred. No. 7.7e-06;  
 RESULT 511  
 ID ABX37780 standard; cDNA; 355 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #2945.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match  
 Best Local Similarity 1.5%; Score 55; DB 8; Length 355;  
 100.0%; Pred. No. 7.5e-06;  
 RESULT 512  
 ID ABQ85688 standard; DNA; 359 BP.  
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 558.  
 PN US2002062014-A1.  
 PD 23-MAY-2002.  
 PA (GORL/) GORLACH J.  
 PA (ANYI/) AN Y.  
 PA (HAMI/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (RAIN/) RAINES T W.  
 PA (YUYI/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHAW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 PA (KRIC/) KRICKER M.  
 PA (SLAT/) SLATER T.  
 PA (DAVI/) DAVIS K R.  
 PA (ALLE/) ALLEN K.  
 PA (HOFF/) HOFFMAN N.  
 PA (HURB/) HURBAN P.

Query Match  
 Best Local Similarity 1.5%; Score 55; DB 6; Length 359;  
 100.0%; Pred. No. 7.4e-06;  
 RESULT 513  
 ID AAI83504 standard; cDNA; 381 BP.  
 DE Human polynucleotide SEQ ID NO 3564.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 55; DB 4; Length 381;  
 100.0%; Pred. No. 7.3e-06;  
 RESULT 514  
 ID ACH21043 standard; cDNA; 381 BP.  
 DE Human adult liver cDNA #655.  
 PN US2003073623-A1.  
 PD 17-APR-2003.  
 PA (DRMA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 Query Match  
 Best Local Similarity 1.5%; Score 55; DB 9; Length 381;  
 100.0%; Pred. No. 7.3e-06;  
 RESULT 515  
 ID AAI87804 standard; cDNA; 398 BP.  
 DE Human polynucleotide SEQ ID NO 7864.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 55; DB 4; Length 398;  
 100.0%; Pred. No. 7.2e-06;  
 RESULT 516  
 ID AAS35447 standard; cDNA; 439 BP.  
 DE Human cardiovascular system antigen cDNA polynucleotide SEQ ID NO 332.  
 PN WO200155321-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 55; DB 4; Length 439;  
 100.0%; Pred. No. 7e-06;  
 RESULT 517  
 ID AD845526 standard; cDNA; 439 BP.  
 DE Human cardiovascular system related polynucleotide #322.  
 PN US2003059908-A1.  
 PD 27-MAR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 55; DB 10; Length 439;  
 100.0%; Pred. No. 7e-06;  
 RESULT 518  
 ID ADJ06944 standard; DNA; 439 BP.  
 DE Human cardiovascular system associated gene SeqID332.  
 PN US2004005575-A1.  
 PD 08-JAN-2004.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 55; DB 13; Length 439;  
 100.0%; Pred. No. 7e-06;  
 RESULT 519  
 ID AAK63678 standard; cDNA; 466 BP.  
 DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:8738.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 55; DB 4; Length 466;  
 100.0%; Pred. No. 6.9e-06;  
 RESULT 520  
 ID ACN58190 standard; cDNA; 564 BP.  
 DE Cotton gynoeceum tissue EST Clone ID: LIB3829-008-Q6-K6-D6, SEQ:12971.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match  
 Best Local Similarity 1.5%; Score 55; DB 13; Length 564;  
 100.0%; Pred. No. 6.5e-06;

RESULT 521  
ID ACN53521 standard; cDNA; 568 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-008-Q1-K6-G2, SEQ:8302.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 55; DB 13; Length 568;  
Best Local Similarity 100.0%; Pred. No. 6.5e-06;  
RESULT 522  
ID ACN63058 standard; cDNA; 579 BP.  
DE Cotton carpel wall/septum EST Clone ID: LIB3831-002-Q1-N6-E12, SEQ:17839.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 55; DB 13; Length 579;  
Best Local Similarity 100.0%; Pred. No. 6.4e-06;  
RESULT 523  
ID ACN51185 standard; cDNA; 603 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-B6, SEQ:5966.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 55; DB 13; Length 603;  
Best Local Similarity 100.0%; Pred. No. 6.3e-06;  
RESULT 524  
ID AAX37373 standard; cDNA; 604 BP.  
DE Human secreted protein cDNA fragment containing gene 5.  
FN WO9909155-A1.  
PD 25-FEB-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 2; Length 604;  
Best Local Similarity 100.0%; Pred. No. 6.3e-06;  
RESULT 525  
ID AAC79824 standard; cDNA; 809 BP.  
DE Human secreted protein gene 26 SEQ ID NO:36.  
FN WO200058336-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 3; Length 809;  
Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
RESULT 526  
ID AAX30363 standard; DNA; 832 BP.  
DE DNA encoding a human secreted protein.  
FN WO9907891-A1.  
PD 18-FEB-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 2; Length 832;  
Best Local Similarity 100.0%; Pred. No. 5.7e-06;  
RESULT 527  
ID ADB47735 standard; cDNA; 832 BP.  
DE Novel human secreted protein cDNA #8.  
FN US2003054443-A1.  
PD 20-MAR-2003.  
PA (RUBE/) RUBEN S M.  
PA (SOPP/) SOPPET D R.  
PA (EBNE/) EBNEN R.  
PA (OLSE/) OLSEN H S.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (YUGG/) YU G.  
PA (NIJ/) NI J.  
PA (ROSE/) ROSEN C A.  
PA (BREW/) BREWER L A.

PA (JANA/) JANAT F.  
PA (BIRS/) BIRSE C E.  
Query Match 1.5%; Score 55; DB 10; Length 832;  
Best Local Similarity 100.0%; Pred. No. 5.7e-06;  
RESULT 528  
ID ADJ55290 standard; cDNA; 832 BP.  
DE Novel human secreted protein cDNA #8.  
FN US2004023283-A1.  
PD 05-FEB-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 12; Length 832;  
Best Local Similarity 100.0%; Pred. No. 5.7e-06;  
RESULT 529  
ID ABV25640 standard; cDNA; 974 BP.  
DE Human prostate expression marker cDNA 25631.  
FN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 55; DB 5; Length 974;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
RESULT 530  
ID AAC99900 standard; cDNA; 1001 BP.  
DE Human secreted protein gene 83 SEQ ID NO:93.  
FN WO200070042-A1.  
PD 23-NOV-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 3; Length 1001;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
RESULT 531  
ID ABL90679 standard; cDNA; 1129 BP.  
DE Human polynucleotide SEQ ID NO 1241.  
FN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 6; Length 1129;  
Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
RESULT 532  
ID ACC50489 standard; cDNA; 1142 BP.  
DE Human secreted protein coding sequence, SEQ ID 156.  
FN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 8; Length 1142;  
Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
RESULT 533  
ID ABZ71271 standard; cDNA; 1142 BP.  
DE Human secreted protein-encoding gene 82 cDNA clone HKB1E57, SEQ ID NO:92.  
FN WO200276488-A1.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 8; Length 1142;  
Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
RESULT 534  
ID ADB91177 standard; cDNA; 1142 BP.  
DE Human secreted protein cDNA #SEQ ID 123.  
FN WO2003004622-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 9; Length 1142;  
Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
RESULT 535  
ID ADC73553 standard; DNA; 1142 BP.  
DE Human secreted protein-related DNA - SEQ ID 186.  
FN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 10; Length 1142;  
Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
RESULT 536  
ID ABQ55006 standard; cDNA; 1259 BP.  
DE Human ovarian antigen HFIVR61 cDNA, SEQ ID NO:886.  
FN WO200200677-A1.  
PD 03-JAN-2002.

PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 6; Length 1259;  
Best Local Similarity 100.0%; Pred. No. 5.1e-06;  
RESULT 537  
ID AAA64408 standard; cDNA; 1473 BP.  
DE DNA encoding a human TANGO 223 polypeptide.  
PN WO200050442-A2.  
PD 31-AUG-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 55; DB 3; Length 1473;  
Best Local Similarity 100.0%; Pred. No. 4.8e-06;  
RESULT 538  
ID AAA64425 standard; cDNA; 1473 BP.  
DE DNA encoding a human TANGO 223 variant polypeptide.  
PN WO200050442-A2.  
PD 31-AUG-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 55; DB 3; Length 1473;  
Best Local Similarity 100.0%; Pred. No. 4.8e-06;  
RESULT 539  
ID AAA64424 standard; cDNA; 1473 BP.  
DE DNA encoding a human TANGO 223 variant polypeptide.  
PN WO200050442-A2.  
PD 31-AUG-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 55; DB 3; Length 1473;  
Best Local Similarity 100.0%; Pred. No. 4.8e-06;  
RESULT 540  
ID AAA64426 standard; cDNA; 1473 BP.  
DE DNA encoding a human TANGO 223 variant polypeptide.  
PN WO200050442-A2.  
PD 31-AUG-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 55; DB 3; Length 1473;  
Best Local Similarity 100.0%; Pred. No. 4.8e-06;  
RESULT 541  
ID AAF16012 standard; cDNA; 1539 BP.  
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:447.  
PN WO200055174-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match 1.5%; Score 55; DB 3; Length 1539;  
Best Local Similarity 100.0%; Pred. No. 4.8e-06;  
RESULT 542  
ID ADQ22078 standard; DNA; 2197 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4998.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.5%; Score 55; DB 12; Length 2197;  
Best Local Similarity 100.0%; Pred. No. 4.3e-06;  
RESULT 543  
ID AAQ80216 standard; DNA; 2335 BP.  
DE Human prionDF-alpha2b DNA.  
PN WO9428133-A1.  
PD 08-DEC-1994.  
PA (ANGE-) AMGEN INC.  
Query Match 1.5%; Score 55; DB 2; Length 2335;  
Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
RESULT 544  
ID ABQ54916 standard; cDNA; 2438 BP.  
DE Human ovarian antigen HNBV053 cDNA, SEQ ID NO:796.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 6; Length 2438;  
Best Local Similarity 100.0%; Pred. No. 4.1e-06;  
RESULT 545  
ID AAX22123 standard; DNA; 2888 BP.  
DE Human secreted protein gene 13 clone HUFAC36.  
PN WO9901020-A2.  
PD 14-JAN-1999.

PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 2; Length 2888;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
RESULT 546  
ID AAP29447 standard; cDNA; 2895 BP.  
DE Human INTERCEPT 217 cDNA.  
PN WO200100638-A2.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 55; DB 4; Length 2895;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
RESULT 547  
ID ACB66756 standard; cDNA; 2895 BP.  
DE Secreted polypeptide-related cDNA #40.  
PN US2003022279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.  
PA (BARN/) BARNES T M.  
PA (SHAR/) SHARP J D.  
PA (KIRS/) KIRST S J.  
PA (MYER/) MYERS P S.  
PA (LEIB/) LEIBY K R.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (WRIG/) WRIGHTON N.  
PA (MACK/) MACKAY C R.  
PA (GOOD/) GOODEARL A D J.  
Query Match 1.5%; Score 55; DB 8; Length 2895;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
RESULT 548  
ID ADB90805 standard; cDNA; 2895 BP.  
DE Human cDNA encoding INTERCEPT 217.  
PN US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 55; DB 9; Length 2895;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
RESULT 549  
ID ADF71539 standard; cDNA; 2895 BP.  
DE Human INTERCEPT 217 cDNA.  
PN US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 55; DB 10; Length 2895;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
RESULT 550  
ID ADQ10277 standard; cDNA; 2895 BP.  
DE Human polynucleotide #47.  
PN US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 55; DB 12; Length 2895;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
RESULT 551  
ID ABQ55051 standard; cDNA; 3036 BP.  
DE Human ovarian antigen HOCQ558 cDNA, SEQ ID NO:931.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 6; Length 3036;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
RESULT 552  
ID ACC50399 standard; cDNA; 3037 BP.  
DE Human secreted protein coding sequence, SEQ ID 66.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 8; Length 3037;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
RESULT 553  
ID AB271220 standard; cDNA; 3037 BP.  
DE Human secreted protein-encoding gene 31 cDNA clone HDPLC63, SEQ ID NO:41.  
PN WO200276488-A1.

ID 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 8; Length 3037;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
RESULT 554  
ID ADB91113 standard; cDNA; 3037 BP.  
DE Human secreted protein cDNA #SEQ ID 59.  
PN WO2003004622-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 9; Length 3037;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
RESULT 555  
ID ADC73450 standard; DNA; 3037 BP.  
DE Human secreted protein-related DNA - SEQ ID 83.  
PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 10; Length 3037;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
RESULT 556  
ID AAV02308 standard; cDNA; 3451 BP.  
DE Cell membrane proton-ATPase encoding cDNA.  
PN JP09252786-A.  
PD 30-SEP-1997.  
PA (ORY) ORIENTAL YEAST CO LTD.  
Query Match 1.5%; Score 55; DB 2; Length 3451;  
Best Local Similarity 100.0%; Pred. No. 3.7e-06;  
RESULT 557  
ID ADO08304 standard; cDNA; 6021 BP.  
DE Human NOVX polynucleotide #26.  
PN US2004018594-A1.  
PD 29-JAN-2004.  
PA (ALSC/) ALSOBROOK J P.  
PA (ANDE/) ANDERSON D W.  
PA (BOLD/) BOLDOG F L.  
PA (BURG/) BURGESS C E.  
PA (CASW/) CASMAN S J.  
PA (CHAP/) CHAPOVAL A.  
PA (EDIN/) EDINGER S R.  
PA (GERL/) GERLACH V.  
PA (GORM/) GORMAN L.  
PA (GUNT/) GUNTHER E.  
PA (GUOX/) GUO X S.  
PA (KEKU/) KEKUDA R.  
PA (LEPL/) LEFLEY D M.  
PA (LILL/) LI L.  
PA (LIUX/) LIU X.  
PA (MALY/) MALYANKAR U M.  
PA (MILL/) MILLER C E.  
PA (MILL/) MILLET I.  
PA (PADI/) PADIGARU M.  
PA (PATT/) PATTURAJAN M.  
PA (PENA/) PENA C E A.  
PA (RIEG/) RIEGER D K.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (SPYT/) SPYTEK K A.  
PA (TAUP/) TAUFIER R J.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZERR/) ZERRHUSEN B D.  
Query Match 1.5%; Score 55; DB 12; Length 6021;  
Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
RESULT 558  
ID ACA10136 standard; cDNA; 6033 BP.  
DE Human NOVX polynucleotide #26.  
PN WO200290504-A2.  
PD 14-NOV-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.5%; Score 55; DB 8; Length 6023;  
Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
RESULT 559

ID AAK82933 standard; DNA; 14063 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37745.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 4; Length 14063;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
RESULT 560  
ID AAK82934 standard; DNA; 14063 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37746.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 55; DB 4; Length 14063;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
RESULT 561  
ID ADT95066 standard; cDNA; 66 BP.  
DE Colon cancer associated human cDNA sequence #585.  
PN US2003087818-A1.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.5%; Score 54; DB 11; Length 66;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 562  
ID ADQ92259 standard; DNA; 93 BP.  
DE Human autoantigen DNA fragment MPWGP800P12530.  
PN WO2004058972-A1.  
PD 15-JUL-2004.  
PA (THIE/) THIESEN H.  
PA (LORE/) LORENZ P.  
Query Match 1.5%; Score 54; DB 12; Length 93;  
Best Local Similarity 100.0%; Pred. No. 2.1e-05;  
RESULT 563  
ID ACN47721 standard; cDNA; 180 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-014-Q1-K6-E9, SEQ:2502.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 54; DB 13; Length 180;  
Best Local Similarity 100.0%; Pred. No. 1.7e-05;  
RESULT 564  
ID ABX40273 standard; cDNA; 203 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #5438.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 54; DB 8; Length 203;  
Best Local Similarity 100.0%; Pred. No. 1.7e-05;  
RESULT 565  
ID ABV59126 standard; cDNA; 221 BP.  
DE Human prostate expression marker cDNA 59117.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 54; DB 5; Length 221;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
RESULT 566  
ID ACN60904 standard; cDNA; 226 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-029-Q6-K6-E8, SEQ:15685.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 54; DB 13; Length 226;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;

## RESULT 567

ID ABQ85662 standard; DNA; 360 BP.  
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 532.  
 PN US2002062014-A1.  
 PD 23-MAY-2002.

PA (GORL/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAMI/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (RAIN/) RAINES T M.  
 PA (YUY/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHAW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 PA (KRIC/) KRICKER M.  
 PA (SLAT/) SLATER T.  
 PA (DAVI/) DAVIS K R.  
 PA (ALLE/) ALLEN K.  
 PA (HOFF/) HOFFMAN N.  
 PA (HURB/) HURBAN P.

Query Match 1.5%; Score 54; DB 6; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;

## RESULT 568

ID AAT84939 standard; cDNA; 375 BP.  
 DE Human prostate protein HPA34 3' cDNA.  
 PN WO9733909-A2.  
 PD 18-SEP-1997.

PA (CORI-) CORIXA CORP.  
 Query Match 1.5%; Score 54; DB 2; Length 375;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;

## RESULT 569

ID AAX35869 standard; cDNA; 375 BP.  
 DE cDNA encoding a prostate tumour cell polypeptide.  
 PN WO9918210-A2.  
 PD 15-APR-1999.

PA (CORI-) CORIXA CORP.  
 Query Match 1.5%; Score 54; DB 2; Length 375;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;

## RESULT 570

ID ABX61502 standard; DNA; 385 BP.  
 DE Arabidopsis thaliana polynucleotide #848.  
 PN US2002142319-A1.  
 PD 03-OCT-2002.

PA (GORL/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAMI/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (HARG/) HARGISS T R.  
 PA (YUY/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHAW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.

Query Match 1.5%; Score 54; DB 10; Length 385;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;

## RESULT 571

ID AAI82053 standard; cDNA; 399 BP.  
 DE Human polynucleotide SEQ ID NO 2113.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.  
 Query Match 1.5%; Score 54; DB 4; Length 399;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

## RESULT 572

ID ACN54899 standard; cDNA; 407 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-027-Q6-K6-A1, SEQ:9680.

PN US2004123340-A1.  
 PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.

Query Match 1.5%; Score 54; DB 13; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

## RESULT 573

ID ABX43804 standard; cDNA; 410 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #8969.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.

PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.

Query Match 1.5%; Score 54; DB 8; Length 410;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

## RESULT 574

ID ACH19512 standard; cDNA; 417 BP.  
 DE Human adult lung cDNA #515.  
 PN US2003073623-A1.  
 PD 17-APR-2003.

PA (DRNA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.

Query Match 1.5%; Score 54; DB 9; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

## RESULT 575

ID AAI86360 standard; cDNA; 418 BP.  
 DE Human polynucleotide SEQ ID NO 6420.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.  
 Query Match 1.5%; Score 54; DB 4; Length 418;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

## RESULT 576

ID AAI87426 standard; cDNA; 423 BP.  
 DE Human polynucleotide SEQ ID NO 7486.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.  
 Query Match 1.5%; Score 54; DB 4; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

## RESULT 577

ID ABX61471 standard; DNA; 426 BP.  
 DE Arabidopsis thaliana polynucleotide #817.  
 PN US2002142319-A1.  
 PD 03-OCT-2002.

PA (GORL/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAMI/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (HARG/) HARGISS T R.  
 PA (YUY/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHAW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.

Query Match 1.5%; Score 54; DB 10; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

## RESULT 578

ID AAI88622 standard; cDNA; 438 BP.  
 DE Human polynucleotide SEQ ID NO 8682.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.

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Query Match
Best Local Similarity 1.5%; Score 54; DB 4; Length 438;
RESULT 579
ID ACH24608 standard; cDNA; 484 BP.
DE Human adult ovary cDNA #2988.
PD 17-APR-2003.
PA (DRMA/) DRVANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 1.5%; Score 54; DB 9; Length 484;
RESULT 580
ID ADR65444 standard; cDNA; 487 BP.
DE Cotton cDNA sequence, SEQ ID 6225.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 1.5%; Score 54; DB 13; Length 487;
RESULT 581
ID ACN53958 standard; cDNA; 487 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-019-Q1-K6-E3, SEQ:8739.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 54; DB 13; Length 487;
RESULT 582
ID ADL44915 standard; DNA; 510 BP.
DE Human ovarian cancer DNA marker #18805.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 54; DB 5; Length 510;
RESULT 583
ID ACN52870 standard; cDNA; 514 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-H11, SEQ:7651.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 54; DB 13; Length 514;
RESULT 584
ID AAX88727 standard; cDNA; 550 BP.
DE Human digestive system antigen coding sequence SEQ ID NO: 1043.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 54; DB 4; Length 550;
RESULT 585
ID AAS31761 standard; cDNA; 550 BP.
DE Human liver associated cDNA polynucleotide #81.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 54; DB 5; Length 550;
RESULT 586
ID ABN90116 standard; cDNA; 550 BP.
DE Human liver antigen HLDOM43 cDNA, SEQ ID NO:91.
PD 06-MAY-1999.
FN US2002042096-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 1.5%; Score 54; DB 6; Length 550;
RESULT 587
ID ADJ14983 standard; DNA; 550 BP.
DE Human liver-related contig DNA - SEQ ID 91.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 54; DB 11; Length 550;
RESULT 588
ID ACN53260 standard; cDNA; 588 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-004-Q1-N6-G11, SEQ:8041.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 54; DB 13; Length 588;
RESULT 589
ID AAC78236 standard; cDNA; 638 BP.
DE Human cancer associated gene sequence SEQ ID NO:630.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 54; DB 3; Length 638;
RESULT 590
ID ADR61268 standard; cDNA; 752 BP.
DE Cotton cDNA sequence, SEQ ID 2049.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 1.5%; Score 54; DB 13; Length 752;
RESULT 591
ID ABK30897 standard; cDNA; 796 BP.
DE Plant dwarfing/stunting related cDNA seq ID 311.
PD 31-JAN-2002.
PA (DOWC) DOW CHEM CO.
PA (REDD/) REDDY S A.
PA (LARR/) LARRINUA M I.
PA (RUEG/) RUEGGER M.
PA (WEGE/) WEGELARZ T.
PA (BLAK/) BLAKESLEE B.
PA (ORIE/) ORIEDO V B J.
PA (SAVI/) SAVICKAS J P.
PA (MCCR/) MCCREY A D.
PA (MILL/) MILLER A B.
PA (POGU/) POGUE P G.
PA (DELL/) DELLA-CIOPPA R G.
PA (WOLF/) WOLFE M G.
PA (ZHEN/) ZHENG W.
PA (GACH/) GACHOTTE D.
PA (GROS/) GROSLEY R.
PA (PELL/) PELL R.
Query Match
Best Local Similarity 1.5%; Score 54; DB 6; Length 796;
RESULT 592
ID AAX61366 standard; cDNA; 848 BP.
DE DNA encoding a human secreted protein.
PD WO9922243-A1.
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PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 2; Length 848;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
RESULT 593  
ID ACN87504 standard; DNA; 848 BP.  
DE Breast cancer related marker, seq id 8654.  
FN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 54; DB 11; Length 848;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
RESULT 594  
ID ABO3020 standard; DNA; 854 BP.  
DE Human breast specific coding sequence SEQ ID NO: 25.  
FN WO200240672-A2.  
PD 23-MAY-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 1.5%; Score 54; DB 6; Length 854;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
RESULT 595  
ID ABO54536 standard; cDNA; 883 BP.  
DE Human ovarian antigen HCABR46 cDNA, SEQ ID NO:416.  
FN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 6; Length 883;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
RESULT 596  
ID AAO5641 standard; cDNA; 923 BP.  
DE Human secreted protein-encoding gene 18 cDNA clone HDTFE17, SEQ ID NO:73.  
FN WO200134627-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 4; Length 923;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
RESULT 597  
ID AAO8435 standard; cDNA; 923 BP.  
DE Human secreted protein-encoding gene 4 cDNA clone HCRPV17, SEQ ID NO:42.  
FN WO200134643-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 8; Length 923;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
RESULT 598  
ID ADA40320 standard; cDNA; 923 BP.  
DE Human secreted protein encoding cDNA.  
FN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 8; Length 923;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
RESULT 599  
ID ADC73842 standard; DNA; 923 BP.  
DE Human secreted protein-related DNA - SEQ ID 475.  
FN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 10; Length 923;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
RESULT 600  
ID ADA56482 standard; DNA; 923 BP.  
DE Gene encoding human secreted protein #136.  
FN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 10; Length 923;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
RESULT 601  
ID ADR63577 standard; cDNA; 973 BP.  
DE Cotton cDNA sequence, SEQ ID 4358.  
FN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.

PA (ZHOU/) ZHOU Y.  
Query Match 1.5%; Score 54; DB 13; Length 973;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
RESULT 602  
ID AAC98033 standard; cDNA; 1060 BP.  
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:43.  
FN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 3; Length 1060;  
Best Local Similarity 100.0%; Pred. No. 9.9e-06;  
RESULT 603  
ID ADD19241 standard; cDNA; 1142 BP.  
DE Human cDNA from secreted protein gene 58.  
FN WO2003052377-A2.  
PD 26-JUN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 10; Length 1142;  
Best Local Similarity 100.0%; Pred. No. 9.7e-06;  
RESULT 604  
ID AAS02224 standard; cDNA; 1194 BP.  
DE Corn Wuschel (WUS) cDNA from clone p0083\_cidev71r #2.  
FN WO200123575-A2.  
PD 05-APR-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 1.5%; Score 54; DB 4; Length 1194;  
Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
RESULT 605  
ID ACC00758 standard; cDNA; 1269 BP.  
DE Zea mays oil trait related cDNA sequence SEQ ID NO:265.  
FN WO2003002751-A2.  
PD 09-JAN-2003.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 1.5%; Score 54; DB 8; Length 1269;  
Best Local Similarity 100.0%; Pred. No. 9.4e-06;  
RESULT 606  
ID ADC23630 standard; cDNA; 1269 BP.  
DE cDNA encodes protein used to alter plant oil phenotype (SeqID 135).  
FN WO2003001902-A2.  
PD 09-JAN-2003.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 1.5%; Score 54; DB 10; Length 1369;  
Best Local Similarity 100.0%; Pred. No. 9.4e-06;  
RESULT 607  
ID AAF33131 standard; cDNA; 1343 BP.  
DE Human secreted protein gene 37 SEQ ID NO:47.  
FN WO200077256-A1.  
PD 21-DEC-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 4; Length 1343;  
Best Local Similarity 100.0%; Pred. No. 9.2e-06;  
RESULT 608  
ID AA297106 standard; cDNA; 1723 BP.  
DE Human secreted protein gene 88 cDNA clone HNTSW57, SEQ ID NO:98.  
FN WO9966041-A1.  
PD 23-DEC-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 3; Length 1723;  
Best Local Similarity 100.0%; Pred. No. 8.6e-06;  
RESULT 609  
ID ACH66735 standard; cDNA; 1723 BP.  
DE Novel human secreted protein #88 cDNA.  
FN US2003065151-A1.  
PD 03-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 9; Length 1723;  
Best Local Similarity 100.0%; Pred. No. 8.6e-06;  
RESULT 610  
ID ABO54940 standard; cDNA; 1847 BP.  
DE Human ovarian antigen HTXKD84 cDNA, SEQ ID NO:820.



PD WO200200677-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 6; Length 1847;  
Best Local Similarity 100.0%; Pred. No. 8.4e-06;  
RESULT 611  
ID AAZ00477 standard; cDNA; 1931 BP.  
DE Human secreted protein cDNA # 2 encoding gene 2.  
PN WO9938881-A1.  
PD 05-AUG-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 2; Length 1931;  
Best Local Similarity 100.0%; Pred. No. 8.3e-06;  
RESULT 612  
ID ADA40295 standard; cDNA; 1931 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 8; Length 1931;  
Best Local Similarity 100.0%; Pred. No. 8.3e-06;  
RESULT 613  
ID ADC73812 standard; DNA; 1931 BP.  
DE Human secreted protein-related DNA - SEQ ID 445.  
PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 10; Length 1931;  
Best Local Similarity 100.0%; Pred. No. 8.3e-06;  
RESULT 614  
ID ADD37730 standard; cDNA; 1931 BP.  
DE Human secreted protein encoding sequence #212.  
PN WO200290526-A2.  
PD 14-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 10; Length 1931;  
Best Local Similarity 100.0%; Pred. No. 8.3e-06;  
RESULT 615  
ID ADA56463 standard; DNA; 1931 BP.  
DE Gene encoding human secreted protein #107.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 10; Length 1931;  
Best Local Similarity 100.0%; Pred. No. 8.3e-06;  
RESULT 616  
ID AAZ00411 standard; cDNA; 1932 BP.  
DE Human secreted protein cDNA encoding gene 2.  
PN WO9938881-A1.  
PD 05-AUG-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 2; Length 1932;  
Best Local Similarity 100.0%; Pred. No. 8.3e-06;  
RESULT 617  
ID ADA39736 standard; cDNA; 1932 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 8; Length 1932;  
Best Local Similarity 100.0%; Pred. No. 8.3e-06;  
RESULT 618  
ID ADC73452 standard; DNA; 1932 BP.  
DE Human secreted protein-related DNA - SEQ ID 85.  
PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 10; Length 1932;  
Best Local Similarity 100.0%; Pred. No. 8.3e-06;  
RESULT 619  
ID ADD37565 standard; cDNA; 1932 BP.  
DE Human secreted protein encoding sequence #47.  
PN WO200290526-A2.

PD 14-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 10; Length 1932;  
Best Local Similarity 100.0%; Pred. No. 8.3e-06;  
RESULT 620  
ID ADA55928 standard; DNA; 1932 BP.  
DE Gene encoding human secreted protein #107.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 10; Length 1932;  
Best Local Similarity 100.0%; Pred. No. 8.3e-06;  
RESULT 621  
ID AAF81813 standard; cDNA; 2150 BP.  
DE Human secreted protein gene 18 SEQ ID NO:37.  
PN WO200112775-A2.  
PD 22-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 4; Length 2150;  
Best Local Similarity 100.0%; Pred. No. 8e-06;  
RESULT 622  
ID AAI70845 standard; cDNA; 2369 BP.  
DE Human heparanase II cDNA clone 338524\_c102.  
PN WO200177341-A2.  
PD 18-OCT-2001.  
PA (JANC ) JANSSEN PHARM NV.  
Query Match 1.5%; Score 54; DB 6; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 7.8e-06;  
RESULT 623  
ID AAC77957 standard; cDNA; 2756 BP.  
DE Human cancer associated gene sequence SEQ ID NO:351.  
PN WO200055350-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 54; DB 3; Length 2756;  
Best Local Similarity 100.0%; Pred. No. 7.4e-06;  
RESULT 624  
ID AAT62360 standard; cDNA; 3214 BP.  
DE Human origin of replication complex ORC1 gene.  
PN WO9640977-A1.  
PD 19-DEC-1996.  
PA (COLD-) COLD SPRING HARBOR LAB.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 1.5%; Score 54; DB 2; Length 3214;  
Best Local Similarity 100.0%; Pred. No. 7.1e-06;  
RESULT 625  
ID AAT73287 standard; cDNA; 3214 BP.  
DE Human origin of replication complex protein 1 gene.  
PN US5614618-A.  
PD 25-MAR-1997.  
PA (REGC ) UNIV CALIFORNIA.  
PA (COLD-) COLD SPRING HARBOR LAB.  
Query Match 1.5%; Score 54; DB 2; Length 3214;  
Best Local Similarity 100.0%; Pred. No. 7.1e-06;  
RESULT 626  
ID ABV21457 standard; cDNA; 3552 BP.  
DE Human prostate expression marker cDNA 21448.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 54; DB 5; Length 3552;  
Best Local Similarity 100.0%; Pred. No. 6.9e-06;  
RESULT 627  
ID ABV27275 standard; cDNA; 3552 BP.  
DE Human prostate expression marker cDNA 27266.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 54; DB 5; Length 3552;  
Best Local Similarity 100.0%; Pred. No. 6.9e-06;  
RESULT 628  
ID ADL46001 standard; DNA; 3552 BP.  
DE Human ovarian cancer DNA marker #19891.

PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 1.5%; Score 54; DB 5; Length 3552;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;  
 RESULT 629  
 ID ACN90329 standard; DNA; 3552 BP.  
 DE Breast cancer related marker, seq id 11479.  
 PN US2003099974-A1.  
 PD 29-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.5%; Score 54; DB 11; Length 3552;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;  
 RESULT 630  
 ID ABL39412 standard; DNA; 29222 BP.  
 DE Human electron-transfer flavoprotein, beta polypeptide (ETFB) gene.  
 PN WO200202580-A2.  
 PD 10-JAN-2002.  
 PA (GENA-) GENAISSANCE PHARM INC.  
 Query Match 1.5%; Score 54; DB 6; Length 29222;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;  
 RESULT 631  
 ID ABK5233 standard; cDNA; 58 BP.  
 DE Human colon cancer-associated cDNA, SEQ ID No 703.  
 PN WO200212280-A2.  
 PD 14-FEB-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.5%; Score 53; DB 6; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
 RESULT 632  
 ID ABK54949 standard; cDNA; 60 BP.  
 DE Human colon cancer-associated cDNA, SEQ ID No 419.  
 PN WO200212280-A2.  
 PD 14-FEB-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.5%; Score 53; DB 6; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
 RESULT 633  
 ID AAV02148 standard; cDNA; 69 BP.  
 DE Human secreted protein AK296 3' portion including the polyA tail.  
 PN WO9739123-A2.  
 PD 23-OCT-1997.  
 PA (GEMY) GENETICS INST INC.  
 Query Match 1.5%; Score 53; DB 2; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
 RESULT 634  
 ID AAT88081 standard; cDNA; 69 BP.  
 DE 3' portion of cDNA clone encoding secreted protein AK296.  
 PN WO9739122-A2.  
 PD 23-OCT-1997.  
 PA (MURO-) MURO PHARM INC.  
 Query Match 1.5%; Score 53; DB 2; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
 RESULT 635  
 ID ADT95589 standard; cDNA; 74 BP.  
 DE Colon cancer associated human cDNA sequence #1108.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.5%; Score 53; DB 11; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;  
 RESULT 636  
 ID AAV05720 standard; cDNA; 85 BP.  
 DE Nucleotide sequence of the 3' portion from clone AZ302\_1.  
 PN WO9746683-A2.  
 PD 11-DEC-1997.  
 PA (GEMY) GENETICS INST INC.  
 Query Match 1.5%; Score 53; DB 2; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 RESULT 637  
 ID ABK54747 standard; cDNA; 90 BP.  
 DE Human colon cancer-associated cDNA, SEQ ID No 217.  
 PN WO200212280-A2.

PD 14-FEB-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.5%; Score 53; DB 6; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 RESULT 638  
 ID ADT94809 standard; cDNA; 90 BP.  
 DE Colon cancer associated human cDNA sequence #328.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.5%; Score 53; DB 11; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 RESULT 639  
 ID AAT91300 standard; cDNA; 99 BP.  
 DE Human M97-2 secreted protein cDNA 3' end.  
 PN WO9740151-A2.  
 PD 30-OCT-1997.  
 PA (GEMY) GENETICS INST INC.  
 Query Match 1.5%; Score 53; DB 2; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
 RESULT 640  
 ID AAV00420 standard; cDNA; 101 BP.  
 DE 3' fragment of clone M97\_2.  
 PN WO9740069-A2.  
 PD 30-OCT-1997.  
 PA (GEMY) GENETICS INST INC.  
 Query Match 1.5%; Score 53; DB 2; Length 101;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
 RESULT 641  
 ID ADT96268 standard; cDNA; 107 BP.  
 DE Colon cancer associated human cDNA sequence #1775.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.5%; Score 53; DB 11; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-05;  
 RESULT 642  
 ID ABQ94578 standard; DNA; 125 BP.  
 DE Tumour suppression-related oligonucleotide #229.  
 PN FR2819824-A1.  
 PD 26-JUL-2002.  
 PA (MOLE-) MOLECULAR ENGINES LAB SA.  
 Query Match 1.5%; Score 53; DB 6; Length 125;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;  
 RESULT 643  
 ID AAV21239 standard; cDNA; 144 BP.  
 DE Homo sapiens clone H698\_3 3' end.  
 PN WO9807859-A2.  
 PD 26-FEB-1998.  
 PA (GEMY) GENETICS INST INC.  
 Query Match 1.5%; Score 53; DB 2; Length 144;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;  
 RESULT 644  
 ID AAX77331 standard; DNA; 144 BP.  
 DE Human secreted protein encoding DNA (clone H698-3) 3' portion.  
 PN WO9926973-A1.  
 PD 03-JUN-1999.  
 PA (GEMY) GENETICS INST INC.  
 Query Match 1.5%; Score 53; DB 2; Length 144;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;  
 RESULT 645  
 ID ADC38850 standard; cDNA; 144 BP.  
 DE Human cDNA encoding a secreted protein #97 additional sequence.  
 PN US2002193567-A1.  
 PD 19-DEC-2002.  
 PA (GEMY) GENETICS INST INC.  
 Query Match 1.5%; Score 53; DB 10; Length 144;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;  
 RESULT 646  
 ID ABQ94618 standard; DNA; 160 BP.  
 DE Tumour suppression-related oligonucleotide #269.  
 PN FR2819824-A1.  
 PD 26-JUL-2002.

PA (MOLE-) MOLECULAR ENGINES LAB SA.  
 Query Match standard; cDNA; 170 BP.  
 Best Local Similarity 1.5%; Score 53; DB 6; Length 160;  
 RESULT 647  
 ID AAH70047 standard; cDNA; 170 BP.  
 DE Human cervical cancer marker nucleic acid 1321.  
 PN WO200142467-A2.  
 PD 14-JUN-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 4; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
 RESULT 648  
 ID ABX53070 standard; cDNA; 175 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #2999.  
 PN US2002137160-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 8; Length 175;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
 RESULT 649  
 ID ABQ55367 standard; cDNA; 197 BP.  
 DE Human ovarian antigen HNAE01 cDNA, SEQ ID NO:1247.  
 PN WO200200677-A1.  
 PD 03-JAN-2002.  
 PA (HUNA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 6; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
 RESULT 650  
 ID ABX43949 standard; cDNA; 202 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #9114.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 8; Length 202;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
 RESULT 651  
 ID ABV19221 standard; cDNA; 204 BP.  
 DE Human prostate expression marker cDNA 19212.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
 RESULT 652  
 ID ABV14996 standard; cDNA; 211 BP.  
 DE Human prostate expression marker cDNA 14987.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 3e-05;  
 RESULT 653  
 ID ABV60841 standard; cDNA; 219 BP.  
 DE Human prostate expression marker cDNA 60832.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 219;  
 Best Local Similarity 100.0%; Pred. No. 3e-05;  
 RESULT 654  
 ID ADL44460 standard; DNA; 222 BP.  
 DE Human ovarian cancer DNA marker #18350.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 222;  
 Best Local Similarity 100.0%; Pred. No. 3e-05;

RESULT 655  
 ID ABV05827 standard; cDNA; 226 BP.  
 DE Human prostate expression marker cDNA 5818.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 226;  
 Best Local Similarity 100.0%; Pred. No. 3e-05;  
 RESULT 656  
 ID ADI72068 standard; DNA; 234 BP.  
 DE Human ovarian cancer DNA marker #4810.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;  
 RESULT 657  
 ID ADL37217 standard; DNA; 234 BP.  
 DE Human ovarian cancer DNA marker #11107.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;  
 RESULT 658  
 ID ARV60929 standard; cDNA; 235 BP.  
 DE Human prostate expression marker cDNA 60920.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;  
 RESULT 659  
 ID ADL38890 standard; DNA; 240 BP.  
 DE Human ovarian cancer DNA marker #12780.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;  
 RESULT 660  
 ID ADI73085 standard; DNA; 241 BP.  
 DE Human ovarian cancer DNA marker #5827.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;  
 RESULT 661  
 ID ABV60876 standard; cDNA; 248 BP.  
 DE Human prostate expression marker cDNA 60867.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;  
 RESULT 662  
 ID ABL87207 standard; cDNA; 264 BP.  
 DE Human ovarian cancer related cDNA clone SEQ ID NO:10185.  
 PN WO200192581-A2.  
 PD 06-DEC-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 6; Length 264;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 RESULT 663  
 ID ABV07492 standard; cDNA; 269 BP.  
 DE Human prostate expression marker cDNA 7483.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 RESULT 664

ID ABK54605 standard; cDNA; 275 BP.  
DE Human colon cancer-associated cDNA, SEQ ID No 75.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.5%; Score 53; DB 6; Length 275;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
RESULT 665  
ID ABV35976 standard; cDNA; 281 BP.  
DE Human prostate expression marker cDNA 35967.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
RESULT 666  
ID ADL43493 standard; cDNA; 281 BP.  
DE Human ovarian cancer DNA marker #17383.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
RESULT 667  
ID ABV61303 standard; cDNA; 283 BP.  
DE Human prostate expression marker cDNA 61294.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 283;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
RESULT 668  
ID AAL16073 standard; cDNA; 289 BP.  
DE Human breast cancer expressed polynucleotide 8530.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 4; Length 289;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
RESULT 669  
ID AAL25205 standard; cDNA; 293 BP.  
DE Human breast cancer expressed polynucleotide 17662.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 4; Length 293;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
RESULT 670  
ID AAS29052 standard; cDNA; 295 BP.  
DE cDNA encoding for human DNA-binding protein #23.  
PN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 5; Length 295;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 671  
ID ABS68192 standard; cDNA; 295 BP.  
DE cDNA encoding human DNA-binding protein #23.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 1.5%; Score 53; DB 6; Length 295;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 672  
ID ADC25186 standard; cDNA; 295 BP.  
DE Human cDNA from extracellular matrix gene 23.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 10; Length 295;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;

RESULT 673  
ID ADL38330 standard; cDNA; 296 BP.  
DE Human ovarian cancer DNA marker #12220.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 296;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 674  
ID ADI73198 standard; cDNA; 296 BP.  
DE Human ovarian cancer DNA marker #5940.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 296;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 675  
ID AAH70049 standard; cDNA; 300 BP.  
DE Human cervical cancer marker nucleic acid 1323.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 4; Length 300;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 676  
ID AAS29128 standard; cDNA; 304 BP.  
DE cDNA encoding for human DNA-binding protein #99.  
PN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 5; Length 304;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 677  
ID ABS68268 standard; cDNA; 304 BP.  
DE cDNA encoding human DNA-binding protein #99.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 1.5%; Score 53; DB 6; Length 304;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 678  
ID ADC25262 standard; cDNA; 304 BP.  
DE Human cDNA from extracellular matrix gene 99.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 10; Length 304;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 679  
ID ABX37505 standard; cDNA; 313 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #2670.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 53; DB 8; Length 313;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 680  
ID ABV15175 standard; cDNA; 317 BP.  
DE Human prostate expression marker cDNA 15166.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 317;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 681  
ID ADI73647 standard; cDNA; 318 BP.  
DE Human ovarian cancer DNA marker #6389.  
PN WO200170979-A2.

PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 318;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 682  
ID ADL38776 standard; DNA; 318 BP.  
DE Human ovarian cancer DNA marker #12666.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 318;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 683  
ID AA184550 standard; cDNA; 320 BP.  
DE Human polynucleotide SEQ ID NO 4610.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 53; DB 4; Length 320;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 684  
ID ABV60936 standard; cDNA; 323 BP.  
DE Human prostate expression marker cDNA 60987.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 323;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 685  
ID ADL43688 standard; DNA; 328 BP.  
DE Human ovarian cancer DNA marker #17578.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 328;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
RESULT 686  
ID ABT22555 standard; DNA; 331 BP.  
DE Breast cancer marker gene SEQ ID No 928.  
PN WO200285298-A2.  
PD 31-OCT-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 53; DB 10; Length 331;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 687  
ID ADI72852 standard; DNA; 332 BP.  
DE Human ovarian cancer DNA marker #5594.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 332;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 688  
ID ADL37991 standard; DNA; 332 BP.  
DE Human ovarian cancer DNA marker #11881.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 332;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 689  
ID ADL37149 standard; DNA; 336 BP.  
DE Human ovarian cancer DNA marker #11039.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 336;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 690  
ID ADI72000 standard; DNA; 336 BP.  
DE Human ovarian cancer DNA marker #4742.  
PN WO200170979-A2.  
PD 27-SEP-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 336;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 691  
ID ABQ86019 standard; DNA; 337 BP.  
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 889.  
PN US2002062014-A1.  
PD 23-MAY-2002.  
PA (GORL/) GORLACH J.  
PA (ANYI/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (VUYI/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHAW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER W.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
Query Match 1.5%; Score 53; DB 6; Length 337;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 692  
ID ABV48996 standard; cDNA; 338 BP.  
DE Human prostate expression marker cDNA 48987.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 338;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 693  
ID ABV60873 standard; cDNA; 338 BP.  
DE Human prostate expression marker cDNA 60864.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 338;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 694  
ID ABZ08610 standard; cDNA; 338 BP.  
DE Human leukocyte derived cDNA SEQ ID NO 8601.  
PN WO200257414-A2.  
PD 25-JUL-2002.  
PA (BIOC-) BIOCARDIA INC.  
Query Match 1.5%; Score 53; DB 6; Length 338;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 695  
ID ABV60943 standard; cDNA; 343 BP.  
DE Human prostate expression marker cDNA 60934.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 343;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 696  
ID ACN47065 standard; cDNA; 344 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-006-Q1-N6-F1, SEQ:1846.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 344;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 697

ID AAI93468 standard; cDNA; 346 BP.  
DE Human polynucleotide SEQ ID NO 13528.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 53; DB 4; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 698  
ID ADL43786 standard; DNA; 346 BP.  
DE Human ovarian cancer DNA marker #17676.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 699  
ID AAI87539 standard; cDNA; 347 BP.  
DE Human polynucleotide SEQ ID NO 7599.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 53; DB 4; Length 347;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 700  
ID ABX38206 standard; cDNA; 347 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #3371.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 53; DB 8; Length 347;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 701  
ID ADI73011 standard; DNA; 350 BP.  
DE Human ovarian cancer DNA marker #5753.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 350;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 702  
ID ADL38146 standard; DNA; 350 BP.  
DE Human ovarian cancer DNA marker #12036.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 350;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 703  
ID ADI72157 standard; DNA; 351 BP.  
DE Human ovarian cancer DNA marker #4899.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 351;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 704  
ID ADL37304 standard; DNA; 351 BP.  
DE Human ovarian cancer DNA marker #11194.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 351;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 705  
ID ABV60857 standard; cDNA; 352 BP.  
DE Human prostate expression marker cDNA 60848.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 706  
ID ABV56898 standard; cDNA; 352 BP.  
DE Human prostate expression marker cDNA 56889.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 707  
ID ADI73560 standard; DNA; 358 BP.  
DE Human ovarian cancer DNA marker #6302.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 358;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 708  
ID ADL38690 standard; DNA; 358 BP.  
DE Human ovarian cancer DNA marker #12580.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 358;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 709  
ID ABL85588 standard; cDNA; 361 BP.  
DE Human ovarian cancer related cDNA clone SEQ ID NO:8566.  
PN WO200192581-A2.  
PD 06-DEC-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 1.5%; Score 53; DB 6; Length 361;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 710  
ID ABV54973 standard; cDNA; 367 BP.  
DE Human prostate expression marker cDNA 54964.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 367;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 711  
ID AAI83125 standard; cDNA; 369 BP.  
DE Human polynucleotide SEQ ID NO 3185.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 53; DB 4; Length 369;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 712  
ID ACN50919 standard; cDNA; 373 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-002-Q1-N6-B10, SEQ:5700.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 373;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
RESULT 713  
ID ABV44911 standard; cDNA; 375 BP.  
DE Human prostate expression marker cDNA 44902.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 375;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 714  
ID ADL44584 standard; DNA; 375 BP.  
DE Human ovarian cancer DNA marker #18474.  
PN WO200170979-A2.  
PD 27-SEP-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 375;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 715  
ID ADL43601 standard; DNA; 380 BP.  
DE Human ovarian cancer DNA marker #17491.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 380;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 716  
ID ABV42927 standard; cDNA; 382 BP.  
DE Human prostate expression marker cDNA 42918.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 382;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 717  
ID ABV34060 standard; cDNA; 383 BP.  
DE Human prostate expression marker cDNA 34051.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 383;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 718  
ID ADL44116 standard; DNA; 383 BP.  
DE Human ovarian cancer DNA marker #18006.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 383;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 719  
ID ADL44714 standard; DNA; 384 BP.  
DE Human ovarian cancer DNA marker #18604.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 384;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 720  
ID ADL45160 standard; DNA; 385 BP.  
DE Human ovarian cancer DNA marker #19050.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 385;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 721  
ID ABV57076 standard; cDNA; 386 BP.  
DE Human prostate expression marker cDNA 57067.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 386;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 722  
ID ADL44375 standard; DNA; 386 BP.  
DE Human ovarian cancer DNA marker #18265.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 386;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 723  
ID ADL43635 standard; DNA; 388 BP.  
DE Human ovarian cancer DNA marker #17525.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 1.5%; Score 53; DB 5; Length 388;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 724  
ID AAL20088 standard; cDNA; 389 BP.  
DE Human breast cancer expressed polynucleotide 12545.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 4; Length 389;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 725  
ID ABX47205 standard; cDNA; 389 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #12370.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 53; DB 8; Length 389;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 726  
ID ADL43918 standard; DNA; 390 BP.  
DE Human ovarian cancer DNA marker #17808.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 390;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 727  
ID ABX37469 standard; cDNA; 392 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #2634.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 53; DB 8; Length 392;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 728  
ID ABX39417 standard; cDNA; 393 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #4582.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 53; DB 8; Length 393;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 729  
ID ACR86032 standard; DNA; 393 BP.  
DE Breast cancer related marker, seq id 7182.  
PN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 53; DB 11; Length 393;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 730  
ID ABX36090 standard; cDNA; 395 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #1255.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 53; DB 8; Length 395;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 731  
ID AAF94819 standard; cDNA; 396 BP.  
DE Human ovarian cancer associated coding sequence SEQ ID NO: 10.



PN WO200118046-A2.  
PD 15-MAR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 1.5%; Score 53; DB 4; Length 396;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 732  
ID ABL48769 standard; cDNA; 396 BP.  
DE Ovarian carcinoma sequence isolate 21921.  
PN US2002004491-A1.  
PD 10-JAN-2002.  
PA (XUJ/) XU J.  
PA (STOL/) STOLK J A.  
PA (ALCA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 6; Length 396;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 733  
ID ABT03086 standard; cDNA; 396 BP.  
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 10.  
PN WO200239885-A2.  
PD 23-MAY-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.5%; Score 53; DB 6; Length 396;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 734  
ID ADM10679 standard; cDNA; 396 BP.  
DE Human ovarian carcinoma-associated cDNA 21921.  
PN US2003206918-A1.  
PD 06-NOV-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.5%; Score 53; DB 11; Length 396;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 735  
ID ADJ11009 standard; cDNA; 396 BP.  
DE Representative human ovarian carcinoma cDNA SeqID 10.  
PN US2003232056-A1.  
PD 18-DEC-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.5%; Score 53; DB 12; Length 396;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 736  
ID ADM43270 standard; cDNA; 396 BP.  
DE Human ovarian carcinoma cDNA #10.  
PN US2003129192-A1.  
PD 10-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.5%; Score 53; DB 12; Length 396;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 737  
ID AA182664 standard; cDNA; 397 BP.  
DE Human polynucleotide SEQ ID NO 2724.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 4; Length 397;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 738  
ID ABZ08435 standard; cDNA; 402 BP.  
DE Human leukocyte derived cDNA SEQ ID NO 8426.  
PN WO200257414-A2.  
PD 25-JUL-2002.  
PA (BIOC-) BIOCARDIA INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 6; Length 402;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 739  
ID ABV56394 standard; cDNA; 404 BP.  
DE Human prostate expression marker cDNA 56385.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 404;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 740  
ID AAI83931 standard; cDNA; 405 BP.  
DE Human polynucleotide SEQ ID NO 3991.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 53; DB 4; Length 405;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 741  
ID ABV60840 standard; cDNA; 406 BP.  
DE Human prostate expression marker cDNA 60831.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 406;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 742  
ID ABV60716 standard; cDNA; 407 BP.  
DE Human prostate expression marker cDNA 60707.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 407;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 743  
ID ABX41098 standard; cDNA; 408 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #8263.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHALAGAN N.  
PA (TRON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 53; DB 8; Length 408;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 744  
ID ADL37087 standard; DNA; 410 BP.  
DE Human ovarian cancer DNA marker #10977.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 410;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 745  
ID ADI71936 standard; DNA; 410 BP.  
DE Human ovarian cancer DNA marker #4678.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 410;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 746  
ID ACN52913 standard; cDNA; 411 BP.  
DE Cotton androscium tissue EST Clone ID: LIB3828-019-Q1-N6-D10, SEQ:7694.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 411;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 747  
ID AAI85186 standard; cDNA; 413 BP.  
DE Human polynucleotide SEQ ID NO 5246.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 53; DB 4; Length 413;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 748  
ID ADL44101 standard; DNA; 414 BP.  
DE Human ovarian cancer DNA marker #17991.  
PN WO200170979-A2.

PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 414;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 749  
ID ABX39680 standard; cDNA; 418 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #4845.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 53; DB 8; Length 418;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 750  
ID ABV56833 standard; cDNA; 420 BP.  
DE Human prostate expression marker cDNA 56824.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 420;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 751  
ID AAI89729 standard; cDNA; 422 BP.  
DE Human polynucleotide SEQ ID NO 9789.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 53; DB 4; Length 422;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 752  
ID ABV38062 standard; cDNA; 425 BP.  
DE Human prostate expression marker cDNA 38053.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 425;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 753  
ID AAI87325 standard; cDNA; 426 BP.  
DE Human polynucleotide SEQ ID NO 7385.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 53; DB 4; Length 426;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 754  
ID ABV44823 standard; cDNA; 426 BP.  
DE Human prostate expression marker cDNA 44814.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 426;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 755  
ID ABV39037 standard; cDNA; 426 BP.  
DE Human prostate expression marker cDNA 39028.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 426;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
RESULT 756  
ID ABK62058 standard; cDNA; 428 BP.  
DE Human EST from P450TEC cDNA #24.  
PN WO200181585-A2.  
PD 01-NOV-2001.  
PA (CYTO-) CYTOCHROMA INC.  
Query Match 1.5%; Score 53; DB 6; Length 428;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 757  
ID ABV83644 standard; cDNA; 430 BP.  
DE Human breast specific gene SEQ ID NO 87.  
PN WO200266605-A2.  
PD 29-AUG-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 1.5%; Score 53; DB 6; Length 430;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 758  
ID ADL37205 standard; DNA; 433 BP.  
DE Human ovarian cancer DNA marker #11095.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 433;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 759  
ID ADL44530 standard; DNA; 433 BP.  
DE Human ovarian cancer DNA marker #18420.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 433;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 760  
ID ADI72056 standard; DNA; 433 BP.  
DE Human ovarian cancer DNA marker #4798.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 433;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 761  
ID ADL44027 standard; DNA; 434 BP.  
DE Human ovarian cancer DNA marker #17917.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 434;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 762  
ID ABV35678 standard; cDNA; 436 BP.  
DE Human prostate expression marker cDNA 35669.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 436;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 763  
ID ACN50643 standard; cDNA; 436 BP.  
DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-N6-H2, SEQ:5424.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 436;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 764  
ID ABV44483 standard; cDNA; 437 BP.  
DE Human prostate expression marker cDNA 44474.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 437;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 765  
ID ADI70485 standard; DNA; 440 BP.  
DE Human ovarian cancer DNA marker #3227.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;

RESULT 766  
 ID ADI76810 standard; DNA; 440 BP.  
 DE Human ovarian cancer DNA marker #9552.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 440;  
 Pred. No. 2.4e-05;  
 RESULT 767  
 ID ACN49982 standard; cDNA; 441 BP.  
 DE Cotton primed seed EST Clone ID: LIB3825-033-Q6-N6-F1, SEQ:4763.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 13; Length 441;  
 Pred. No. 2.4e-05;  
 RESULT 768  
 ID ABV56410 standard; cDNA; 443 BP.  
 DE Human prostate expression marker cDNA 56401.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 443;  
 Pred. No. 2.4e-05;  
 RESULT 769  
 ID ABV05431 standard; cDNA; 445 BP.  
 DE Human prostate expression marker cDNA 5422.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 445;  
 Pred. No. 2.4e-05;  
 RESULT 770  
 ID AAI83049 standard; cDNA; 447 BP.  
 DE Human polynucleotide SEQ ID NO 3109.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 4; Length 447;  
 Pred. No. 2.4e-05;  
 RESULT 771  
 ID ABZ08656 standard; cDNA; 450 BP.  
 DE Human leukocyte derived cDNA SEQ ID NO 8647.  
 PN WO200257414-A2.  
 PD 25-JUL-2002.  
 PA (BIOC-) BIOCARDIA INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 6; Length 450;  
 Pred. No. 2.4e-05;  
 RESULT 772  
 ID ACN91903 standard; DNA; 450 BP.  
 DE Breast cancer related marker, seq id 13053.  
 PN US200309974-A1.  
 PD 29-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 11; Length 450;  
 Pred. No. 2.4e-05;  
 RESULT 773  
 ID AAI87364 standard; cDNA; 453 BP.  
 DE Human polynucleotide SEQ ID NO 7424.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 4; Length 453;  
 Pred. No. 2.4e-05;  
 RESULT 774  
 ID AAI19946 standard; cDNA; 457 BP.  
 DE Human breast cancer expressed polynucleotide 12403.  
 PN WO200151628-A2.  
 PD 19-JUL-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match  
 Best Local Similarity 1.5%; Score 53; DB 4; Length 457;  
 Pred. No. 2.4e-05;  
 RESULT 775  
 ID ABV48620 standard; cDNA; 457 BP.  
 DE Human prostate expression marker cDNA 48611.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 457;  
 Pred. No. 2.4e-05;  
 RESULT 776  
 ID ABV54284 standard; cDNA; 459 BP.  
 DE Human prostate expression marker cDNA 54275.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 459;  
 Pred. No. 2.4e-05;  
 RESULT 777  
 ID ADR60402 standard; cDNA; 460 BP.  
 DE Cotton cDNA sequence, SEQ ID 1183.  
 PN US2004181830-A1.  
 PD 16-SEP-2004.  
 PA (KOVA/) KOVALIC D K.  
 PA (ZHOU/) ZHOU Y.  
 PA (CAOY/) CAO Y.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 13; Length 460;  
 Pred. No. 2.4e-05;  
 RESULT 778  
 ID ACN61220 standard; cDNA; 460 BP.  
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-033-Q1-N6-H12, SEQ:16001.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 13; Length 460;  
 Pred. No. 2.4e-05;  
 RESULT 779  
 ID ABV34102 standard; cDNA; 462 BP.  
 DE Human prostate expression marker cDNA 34093.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 462;  
 Pred. No. 2.4e-05;  
 RESULT 780  
 ID ABV42965 standard; cDNA; 462 BP.  
 DE Human prostate expression marker cDNA 42956.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 462;  
 Pred. No. 2.4e-05;  
 RESULT 781  
 ID AAI10366 standard; cDNA; 463 BP.  
 DE Human breast cancer expressed polynucleotide 2823.  
 PN WO200151628-A2.  
 PD 19-JUL-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 4; Length 463;  
 Pred. No. 2.4e-05;  
 RESULT 782  
 ID ADL40902 standard; DNA; 463 BP.  
 DE Human ovarian cancer DNA marker #14792.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 1.5%; Score 53; DB 5; Length 463;  
 Pred. No. 2.4e-05;  
 RESULT 783  
 ID ACN51887 standard; cDNA; 469 BP.

DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-C10, SEQ:6668.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 469;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 784  
ID ACN50594 standard; cDNA; 469 BP.  
DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-N6-B6, SEQ:5375.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 469;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 785  
ID ACN62049 standard; cDNA; 469 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-024-Q6-N6-E4, SEQ:16830.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 469;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 786  
ID ABV14952 standard; cDNA; 472 BP.  
DE Human prostate expression marker cDNA 14943.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 13; Length 472;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 787  
ID ABV61434 standard; cDNA; 474 BP.  
DE Human prostate expression marker cDNA 61425.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 474;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 788  
ID ACN51912 standard; cDNA; 477 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-E5, SEQ:6693.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 477;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 789  
ID ABV7607 standard; cDNA; 478 BP.  
DE Human prostate expression marker cDNA 7598.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 478;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 790  
ID ACN51993 standard; cDNA; 478 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-E1, SEQ:6774.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 478;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 791  
ID ABV56511 standard; cDNA; 479 BP.  
DE Human prostate expression marker cDNA 56502.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 479;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 792  
ID ACN51787 standard; cDNA; 480 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-008-Q1-N6-A12, SEQ:6568.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 480;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 793  
ID ACN52021 standard; cDNA; 485 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-G4, SEQ:6802.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 485;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 794  
ID ABV19079 standard; cDNA; 486 BP.  
DE Human prostate expression marker cDNA 39070.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 486;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
RESULT 795  
ID ADL43471 standard; DNA; 491 BP.  
DE Human ovarian cancer DNA marker #17361.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 491;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 796  
ID ABV56664 standard; cDNA; 496 BP.  
DE Human prostate expression marker cDNA 56655.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 797  
ID ACN62281 standard; cDNA; 496 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-027-Q6-N6-E4, SEQ:17062.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 798  
ID ABV12935 standard; cDNA; 498 BP.  
DE Human prostate expression marker cDNA 12926.  
PN WO200160860-A2.

PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 498;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 799  
ID ACN46935 standard; cDNA; 499 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-005-Q1-N6-D10, SEQ:1716.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 499;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 800  
ID ACN5816 standard; cDNA; 499 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-012-Q6-N6-D11, SEQ:13597.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 499;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 801  
ID ACN61218 standard; cDNA; 500 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-033-Q1-N6-H10, SEQ:15999.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 500;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 802  
ID ABV56694 standard; cDNA; 504 BP.  
DE Human prostate expression marker cDNA 56685.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 504;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 803  
ID ACN57794 standard; cDNA; 506 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-005-Q6-N6-H9, SEQ:12575.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 506;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 804  
ID ACN61287 standard; cDNA; 512 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-035-Q1-N6-E12, SEQ:16068.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 512;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 805  
ID ABV57086 standard; cDNA; 516 BP.  
DE Human prostate expression marker cDNA 57077.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 1.5%; Score 53; DB 5; Length 516;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 806  
ID ACN61335 standard; cDNA; 517 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-036-Q1-N6-H9, SEQ:16116.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 517;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 807  
ID ACN56421 standard; cDNA; 521 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-027-Q6-N6-D4, SEQ:11202.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 521;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 808  
ID ADL45090 standard; DNA; 522 BP.  
DE Human ovarian cancer DNA marker #18980.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 522;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 809  
ID ABO59079 standard; cDNA; 522 BP.  
DE Human colon cancer related nucleotide sequence SEQ ID NO:2774.  
PN WO200229086-A2.  
PD 11-APR-2002.  
PA (FARB) BAYER CORP.  
Query Match 1.5%; Score 53; DB 6; Length 522;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 810  
ID ABV60707 standard; cDNA; 524 BP.  
DE Human prostate expression marker cDNA 60698.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 524;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 811  
ID ADL42046 standard; DNA; 524 BP.  
DE Human ovarian cancer DNA marker #15936.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 524;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 812  
ID ACN61425 standard; cDNA; 527 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-015-Q1-N6-H7, SEQ:16206.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 527;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
RESULT 813  
ID ACN47028 standard; cDNA; 528 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-006-Q1-N6-B12, SEQ:1809.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 528;  
Pred. No. 2.3e-05;  
RESULT 814  
ID ACN53350 standard; cDNA; 528 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-N6-F8, SEQ:8131.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 528;  
Pred. No. 2.3e-05;  
RESULT 815  
ID ADR64205 standard; cDNA; 529 BP.  
DE Cotton cDNA sequence, SEQ ID 4986.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 529;  
Pred. No. 2.3e-05;  
RESULT 816  
ID ACN46946 standard; cDNA; 529 BP.  
DE Cotton prined seed EST Clone ID: LIB3825-005-Q1-N6-E12, SEQ:1727.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 529;  
Pred. No. 2.3e-05;  
RESULT 817  
ID ACN50477 standard; cDNA; 530 BP.  
DE Cotton mature seed EST Clone ID: LIB3827-001-Q1-N6-C4, SEQ:5258.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 530;  
Pred. No. 2.3e-05;  
RESULT 818  
ID ABV56527 standard; cDNA; 531 BP.  
DE Human prostate expression marker cDNA 56518.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 5; Length 531;  
Pred. No. 2.3e-05;  
RESULT 819  
ID ADI75666 standard; DNA; 531 BP.  
DE Human ovarian cancer DNA marker #8408.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 5; Length 531;  
Pred. No. 2.3e-05;  
RESULT 820  
ID ADI69320 standard; DNA; 531 BP.  
DE Human ovarian cancer DNA marker #2062.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 5; Length 531;  
Pred. No. 2.3e-05;  
RESULT 821  
ID ACN62126 standard; cDNA; 533 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-025-Q6-N6-E11, SEQ:16907.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 533;  
Pred. No. 2.3e-05;  
RESULT 822  
ID ACN58719 standard; cDNA; 534 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-011-Q6-N6-B7, SEQ:13500.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 534;  
Pred. No. 2.3e-05;  
RESULT 823  
ID ABV03766 standard; cDNA; 535 BP.  
DE Human prostate expression marker cDNA 3757.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 5; Length 535;  
Pred. No. 2.3e-05;  
RESULT 824  
ID ABV37538 standard; cDNA; 536 BP.  
DE Human prostate expression marker cDNA 37529.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 5; Length 536;  
Pred. No. 2.3e-05;  
RESULT 825  
ID ACN52447 standard; cDNA; 537 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-015-Q1-N6-E10, SEQ:7228.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 537;  
Pred. No. 2.3e-05;  
RESULT 826  
ID ACN62214 standard; cDNA; 538 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-026-Q6-N6-E2, SEQ:16995.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 538;  
Pred. No. 2.3e-05;  
RESULT 827  
ID ADL43972 standard; DNA; 539 BP.  
DE Human ovarian cancer DNA marker #17862.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 5; Length 539;  
Pred. No. 2.3e-05;  
RESULT 828  
ID ACN55798 standard; cDNA; 539 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-N6-F7, SEQ:10579.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.  
PA (FENG/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 539;  
Pred. No. 2.3e-05;  
RESULT 829  
ID ACN57165 standard; cDNA; 541 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-014-Q6-N6-G1, SEQ:11946.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENG/) FINCHER K L.  
PA (FENG/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 541;  
Pred. No. 2.3e-05;  
RESULT 830  
ID ACN49713 standard; cDNA; 542 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-025-Q6-N6-G12, SEQ:4494.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENG/) FINCHER K L.  
PA (FENG/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 542;  
Pred. No. 2.3e-05;  
RESULT 831  
ID ABK11289 standard; cDNA; 545 BP.  
DE Human cDNA encoding novel secreted protein from clone HMWBT59 #1.  
PN WO200155207-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 4; Length 545;  
Pred. No. 2.3e-05;  
RESULT 832  
ID ADC06720 standard; cDNA; 545 BP.  
DE Human TM4SF clone HMWBT59 cDNA - SEQ ID 12.  
PN US2003039993-A1.  
PD 27-FEB-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 545;  
Pred. No. 2.3e-05;  
RESULT 833  
ID ABX16283 standard; cDNA; 545 BP.  
DE Human cDNA encoding partial tetraspan superfamily member #2.  
PN US2002151479-A1.  
PD 17-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 545;  
Pred. No. 2.3e-05;  
RESULT 834  
ID ACN58252 standard; cDNA; 546 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-008-Q6-N6-A9, SEQ:13033.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENG/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 546;  
Pred. No. 2.3e-05;  
RESULT 835  
ID ACN62109 standard; cDNA; 547 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-025-Q6-N6-C2, SEQ:16890.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENG/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.

Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 547;  
Pred. No. 2.3e-05;  
RESULT 836  
ID ACN45312 standard; cDNA; 552 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-K6-C5, SEQ:93.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENG/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 552;  
Pred. No. 2.3e-05;  
RESULT 837  
ID AAL10265 standard; cDNA; 554 BP.  
DE Human breast cancer expressed polynucleotide 2722.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 4; Length 554;  
Pred. No. 2.3e-05;  
RESULT 838  
ID ACN4785 standard; cDNA; 557 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-N6-A5, SEQ:25566.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENG/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 557;  
Pred. No. 2.3e-05;  
RESULT 839  
ID ACN47210 standard; cDNA; 557 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-008-Q1-N6-D6, SEQ:1991.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENG/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 557;  
Pred. No. 2.3e-05;  
RESULT 840  
ID ABT08060 standard; cDNA; 558 BP.  
DE Human breast specific coding sequence SEQ ID NO: 6.  
PN WO200266607-A2.  
PD 29-AUG-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 6; Length 558;  
Pred. No. 2.3e-05;  
RESULT 841  
ID ACN56272 standard; cDNA; 561 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-N6-E6, SEQ:11053.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENG/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 561;  
Pred. No. 2.3e-05;  
RESULT 842  
ID ACN47476 standard; cDNA; 563 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-011-Q1-N6-E7, SEQ:2257.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENG/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 563;  
Pred. No. 2.3e-05;



RESULT 843  
ID ACN56344 standard; cDNA; 565 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-034-Q6-N6-B10, SEQ:111125.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENG/) FINCHER K L.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 565;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
RESULT 844  
ID ACN45417 standard; cDNA; 565 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-G5, SEQ:198.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 565;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
RESULT 845  
ID ABV57082 standard; cDNA; 567 BP.  
DE Human prostate expression marker cDNA 57073.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 567;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
RESULT 846  
ID ACN53005 standard; cDNA; 569 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-020-Q1-N6-E7, SEQ:7786.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 569;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
RESULT 847  
ID ADI73065 standard; DNA; 570 BP.  
DE Human ovarian cancer DNA marker #5807.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 570;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
RESULT 848  
ID ADL38200 standard; DNA; 570 BP.  
DE Human ovarian cancer DNA marker #12090.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 570;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
RESULT 849  
ID ACN52610 standard; cDNA; 574 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-N6-G6, SEQ:7391.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 574;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
RESULT 850  
ID ACN56366 standard; cDNA; 574 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-034-Q6-N6-D1, SEQ:111147.  
PN US2004123340-A1.  
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 574;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
RESULT 851  
ID ACN45381 standard; cDNA; 577 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-C7, SEQ:162.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 577;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
RESULT 852  
ID ACN53147 standard; cDNA; 578 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-022-Q1-N6-E3, SEQ:7928.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 578;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
RESULT 853  
ID ACN51300 standard; cDNA; 583 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-C2, SEQ:6081.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 583;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
RESULT 854  
ID ACN52339 standard; cDNA; 593 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-F10, SEQ:7120.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 53; DB 13; Length 593;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
RESULT 855  
ID AAH71472 standard; cDNA; 597 BP.  
DE Human cervical cancer marker nucleic acid 2746.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 4; Length 597;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
RESULT 856  
ID ACN88304 standard; DNA; 597 BP.  
DE Breast cancer related marker, seq id 9454.  
PN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 53; DB 11; Length 597;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
RESULT 857  
ID AAH71474 standard; cDNA; 612 BP.  
DE Human cervical cancer marker nucleic acid 2748.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 4; Length 612;

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Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 858
ID AAH71551 standard; cDNA; 621 BP.
DE Human cervical cancer marker nucleic acid 2825.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 621;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 859
ID ABV12980 standard; cDNA; 629 BP.
DE Human prostate expression marker cDNA 12971.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 629;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 860
ID ADI72791 standard; DNA; 638 BP.
DE Human ovarian cancer DNA marker #5533.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 638;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 861
ID ADJ37930 standard; DNA; 638 BP.
DE Human ovarian cancer DNA marker #11820.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 638;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 862
ID AAL23651 standard; cDNA; 644 BP.
DE Human breast cancer expressed polynucleotide 16108.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 644;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 863
ID AAL14804 standard; cDNA; 693 BP.
DE Human breast cancer expressed polynucleotide 7261.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 864
ID ABQ65666 standard; DNA; 704 BP.
DE Arabidopsis thaliana polynucleotide SEQ ID NO 243.
PN US2002059663-A1.
PD 16-MAY-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WESS/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HOFFMAN P.
Query Match
Best Local Similarity 1.5%; Score 53; DB 6; Length 704;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 865
ID ADI72280 standard; DNA; 705 BP.
DE Human ovarian cancer DNA marker #5022.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 705;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 866
ID ADJ37424 standard; DNA; 705 BP.
DE Human ovarian cancer DNA marker #11314.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 705;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 867
ID AAL24889 standard; cDNA; 722 BP.
DE Human breast cancer expressed polynucleotide 17346.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 868
ID ADI71984 standard; DNA; 723 BP.
DE Human ovarian cancer DNA marker #4726.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 723;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 869
ID ADJ37134 standard; DNA; 723 BP.
DE Human ovarian cancer DNA marker #11024.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 723;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 870
ID AAL25251 standard; cDNA; 731 BP.
DE Human breast cancer expressed polynucleotide 17708.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 731;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 871
ID ABI90099 standard; cDNA; 735 BP.
DE Human polynucleotide SEQ ID NO 661.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 6; Length 735;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 872
ID AAC78154 standard; cDNA; 736 BP.
DE Human cancer associated gene sequence SEQ ID NO:548.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 3; Length 736;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 873
ID AAL24897 standard; cDNA; 739 BP.
DE Human breast cancer expressed polynucleotide 17354.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 739;
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Best Local Similarity 100.0%; Pred. No. 2.1e-05;  
RESULT 874  
ID ADL44766 standard; DNA; 752 BP.  
DE Human ovarian cancer DNA marker #18656.  
PN WO200170979-A2.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 752;  
Best Local Similarity 100.0%; Pred. No. 2.1e-05;  
RESULT 875  
ID ADL43864 standard; DNA; 755 BP.  
DE Human ovarian cancer DNA marker #17754.  
PN WO200170979-A2.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 755;  
Best Local Similarity 100.0%; Pred. No. 2.1e-05;  
RESULT 876  
ID AAH71500 standard; cDNA; 764 BP.  
DE Human cervical cancer marker nucleic acid 2774.  
PN WO200142467-A2.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 764;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 877  
ID AAX27402 standard; DNA; 826 BP.  
DE Human secreted protein gene 92 clone HLYAF80.  
PN WO9902546-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 2; Length 826;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 878  
ID ADAJ9947 standard; cDNA; 826 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 8; Length 826;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 879  
ID ADA07281 standard; cDNA; 826 BP.  
DE Human cDNA from secreted protein gene 92.  
PN US2003054412-A1.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAF/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLSE/) OLSEN H S.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
Query Match 1.5%; Score 53; DB 9; Length 826;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 880  
ID ADD37625 standard; cDNA; 826 BP.  
DE Human secreted protein encoding sequence #107.  
PN WO200290526-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 10; Length 826;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 881  
ID ADA56135 standard; DNA; 826 BP.  
DE Gene encoding human secreted protein #314.  
PN WO2002102994-A2.

PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 10; Length 826;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 882  
ID ADN40950 standard; cDNA; 826 BP.  
DE Novel human secreted protein cDNA seqid 72.  
PN US2004044191-A1.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAF/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLSE/) OLSEN H.  
PA (EBNE/) EBNER R.  
PA (BIER/) BIRSE C E.  
Query Match 1.5%; Score 53; DB 12; Length 826;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 883  
ID ABV14600 standard; cDNA; 830 BP.  
DE Human prostate expression marker cDNA 14591.  
PN WO200160860-A2.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 5; Length 830;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 884  
ID ABV83628 standard; cDNA; 844 BP.  
DE Human breast specific gene SEQ ID NO 71.  
PN WO200286605-A2.  
PA (DIAD-) DIADEXUS INC.  
Query Match 1.5%; Score 53; DB 6; Length 844;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 885  
ID AAL19845 standard; cDNA; 852 BP.  
DE Human breast cancer expressed polynucleotide 12302.  
PN WO200151628-A2.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 53; DB 4; Length 852;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 886  
ID ABT22217 standard; DNA; 857 BP.  
DE Breast cancer marker gene SEQ ID No 590.  
PN WO200285298-A2.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 53; DB 10; Length 857;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 887  
ID ACN84830 standard; DNA; 874 BP.  
DE Breast cancer related marker, seq id 5980.  
PN US200309974-A1.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 53; DB 11; Length 874;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 888  
ID AAA87690 standard; cDNA; 892 BP.  
DE Human secreted protein gene 25 SEQ ID NO:35.  
PN WO200043495-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 3; Length 892;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 889

ID ABV83635 standard; cDNA; 895 BP.  
DE Human breast specific gene SEQ ID NO 78.  
PN WO200266605-A2.  
PD 29-AUG-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 1.5%; Score 53; DB 6; Length 895;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 890  
ID AAH33168 standard; cDNA; 896 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:224.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 4; Length 896;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
RESULT 891  
ID ACN80464 standard; DNA; 933 BP.  
DE Breast cancer related marker, seq id 1614.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 53; DB 11; Length 933;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
RESULT 892  
ID ABV83640 standard; cDNA; 954 BP.  
DE Human breast specific gene SEQ ID NO 83.  
PN WO200266605-A2.  
PD 29-AUG-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 1.5%; Score 53; DB 6; Length 954;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
RESULT 893  
ID AA252527 standard; cDNA; 1034 BP.  
DE Human secreted protein clone ya66\_1 nucleotide sequence SEQ ID NO:105.  
PN WO958642-A2.  
PD 18-NOV-1999.  
PA (GENY) GENETICS INST INC.  
Query Match 1.5%; Score 53; DB 3; Length 1034;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
RESULT 894  
ID AAA26358 standard; cDNA; 1052 BP.  
DE Human secreted protein gene 13 SEQ ID NO:23.  
PN WO200006698-A1.  
PD 10-FEB-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 3; Length 1052;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
RESULT 895  
ID ADC73847 standard; DNA; 1052 BP.  
DE Human secreted protein-related DNA - SEQ ID 480.  
PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 10; Length 1052;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
RESULT 896  
ID ADD37736 standard; cDNA; 1052 BP.  
DE Human secreted protein encoding sequence #218.  
PN WO200290526-A2.  
PD 14-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 10; Length 1052;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
RESULT 897  
ID ADA56496 standard; DNA; 1052 BP.  
DE Gene encoding human secreted protein #172.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 10; Length 1052;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
RESULT 898  
ID ADL71419 standard; cDNA; 1052 BP.  
DE Novel human secreted protein cDNA seqid 23.  
PN US2004034196-A1.  
PD 19-FEB-2004.  
PA (KOMA/) KOMATSULIS G A.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (DUAN/) DUAN D R.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAPL/) LAFLEUR D W.  
PA (WEIY/) WEI Y.  
Query Match 1.5%; Score 53; DB 12; Length 1052;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
RESULT 899  
ID ABT08073 standard; cDNA; 1074 BP.  
DE Human breast specific coding sequence SEQ ID NO: 19.  
PN WO200266607-A2.  
PD 29-AUG-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 1.5%; Score 53; DB 6; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
RESULT 900  
ID ADR60456 standard; cDNA; 1083 BP.  
DE Cotton cDNA sequence, SEQ ID 1237.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 1.5%; Score 53; DB 13; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
RESULT 901  
ID AAS72542 standard; cDNA; 1087 BP.  
DE DNA encoding novel human diagnostic protein #8346.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 53; DB 5; Length 1087;  
Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
RESULT 902  
ID AAS26600 standard; cDNA; 1095 BP.  
DE Human cDNA encoding a novel secreted protein, Seq ID 779.  
PN WO200155322-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 4; Length 1095;  
Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
RESULT 903  
ID ABX73941 standard; DNA; 1095 BP.  
DE Human novel polynucleotide #769.  
PN US2002132753-A1.  
PD 19-SEP-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 1.5%; Score 53; DB 8; Length 1095;  
Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
RESULT 904  
ID AAS26184 standard; cDNA; 1096 BP.  
DE Human cDNA encoding a novel secreted protein, Seq ID 363.  
PN WO200155322-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 4; Length 1096;  
Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
RESULT 905  
ID ABX73525 standard; DNA; 1096 BP.  
DE Human novel polynucleotide #353.  
PN US2002132753-A1.  
PD 19-SEP-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.

Query Match  
Best Local Similarity 1.5%; Score 53; DB 8; Length 1096;  
RESULT 906  
ID AAX04325 standard; cDNA; 1376 BP.  
DE Human secreted protein gene 15 clone HSEDS04.  
PN WO9856804-A1.  
PD 17-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 6; Length 1145;  
RESULT 907  
ID ADO25557 standard; DNA; 1185 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8377.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 6; Length 1145;  
RESULT 908  
ID AAX25130 standard; cDNA; 1223 BP.  
DE Soybean isoflavone reductase cDNA clone seq3.pk0034.g5.  
PN WO9914351-A1.  
PD 25-MAR-1999.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 1185;  
RESULT 909  
ID AAX38425 standard; cDNA; 1223 BP.  
DE Soybean isoflavone reductase cDNA clone seq3.pk0034.g5.  
PN US6054636-A.  
PD 25-APR-2000.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 3; Length 1223;  
RESULT 910  
ID ADJ32833 standard; cDNA; 1223 BP.  
DE Soybean isoflavone reductase cDNA.  
PN US6617493-B1.  
PD 09-SEP-2003.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 1223;  
RESULT 911  
ID AAH49320 standard; cDNA; 1300 BP.  
DE V. vinifera aquaporin PIP2-1 cDNA.  
PN WO200166793-A2.  
PD 13-SEP-2001.  
PA (GSFU-) GSF FORSCHUNGSZENTRUM UNWELT & GESUNDHEIT.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 5; Length 1300;  
RESULT 912  
ID AAC85035 standard; DNA; 1355 BP.  
DE Soybean HES1 homologue DNA sequence (clone ID 701010572CPR9854).  
PN WO200104314-A2.  
PD 18-JAN-2001.  
PA (PHAA) PHARMACIA CORP.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 5; Length 1355;  
RESULT 913  
ID AAS00834 standard; cDNA; 1369 BP.  
DE Human cDNA clone HOFMU69 encoding cancer related protein 8.  
PN WO200118014-A1.  
PD 15-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 5; Length 1369;  
RESULT 914  
ID ADO26094 standard; DNA; 1371 BP.  
DE Cotton LDOX polynucleotide seqid 132.  
PN WO2004046336-A2.  
PD 03-JUN-2004.  
PA (MONS) MONSANTO TECHNOLOGY LLC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 1371;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;  
RESULT 915  
ID AAX04325 standard; DNA; 1376 BP.  
DE Human secreted protein gene 15 clone HSEDS04.  
PN WO9856804-A1.  
PD 17-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 2; Length 1376;  
RESULT 916  
ID ABO54525 standard; cDNA; 1442 BP.  
DE Human ovarian antigen HOFMU69 cDNA, SEQ ID NO:405.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 6; Length 1442;  
RESULT 917  
ID AAC82696 standard; cDNA; 1445 BP.  
DE Murine variant Zalpha32 cDNA.  
PN WO2000071717-A1.  
PD 30-NOV-2000.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 4; Length 1445;  
RESULT 918  
ID ADG42426 standard; cDNA; 1445 BP.  
DE Mouse cDNA encoding variant Zalpha-32.  
PN US2003207793-A1.  
PD 06-NOV-2003.  
PA (CONK/) CONKLIN D C.  
PA (GAOZ/) GAO Z.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 1445;  
RESULT 919  
ID AAS41436 standard; cDNA; 1516 BP.  
DE cDNA encoding novel human enzyme polypeptide #652.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 4; Length 1516;  
RESULT 920  
ID ADO05149 standard; DNA; 1550 BP.  
DE Citrus X paradisi epsilon cyclase homologue H5 DNA.  
PN WO2004027869-A1.  
PD 01-APR-2004.  
PA (SUNG-) SUNGENE GMBH & CO KGAA.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 1550;  
RESULT 921  
ID AAT28255 standard; cDNA; 1558 BP.  
DE Survival motor neuron gene, clone T-BCD541.  
PN EP708178-A1.  
PD 24-APR-1996.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 2; Length 1558;  
RESULT 922  
ID AAT18828 standard; cDNA; 1560 BP.  
DE Human survival motor neuron gene cDNA clone T-BCD541.  
PN EP711833-A2.  
PD 15-MAY-1996.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 2; Length 1560;  
RESULT 923  
ID AAT18831 standard; cDNA; 1582 BP.  
DE Human survival motor neuron variant gene cDNA clone C-BCD541.  
PN EP711833-A2.  
PD 15-MAY-1996.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 2; Length 1582;

Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 924  
 ID AAT28259 standard; cDNA; 1582 BP.  
 DE Survival motor neuron gene, clone C-BCD541.  
 PN EP708178-A1.  
 PD 24-APR-1996.  
 PA (INEM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 Query Match 1.5%; Score 53; DB 2; Length 1582;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 925  
 ID ADI43284 standard; DNA; 1585 BP.  
 DE Plant transcription factor polynucleotide #1178.  
 PN US2004019927-A1.  
 PD 29-JAN-2004.  
 PA (SHER ) SHERMAN B K.  
 PA (RIEC ) RIECHMANN J L.  
 PA (JIAN ) JIANG C.  
 PA (HEAR ) HEARD J E.  
 PA (HAAR ) HAAKE V.  
 PA (CREE ) CREELMAN R A.  
 PA (RATC ) RATCLIFFE O.  
 PA (ADAM ) ADAM L J.  
 PA (REUB ) REUBER T L.  
 PA (KEDD ) KEDDIE J.  
 PA (BROU ) BROUN P E.  
 PA (PILG ) PILGRIM M L.  
 PA (DUBE ) DUBELL A N.  
 PA (PINE ) PINEDA O.  
 PA (YUGG ) YU G.  
 Query Match 1.5%; Score 53; DB 12; Length 1585;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 926  
 ID ADE55267 standard; DNA; 1589 BP.  
 DE Human gene ALI37271, SEQ ID NO 1081.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GHEO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 Query Match 1.5%; Score 53; DB 10; Length 1589;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 927  
 ID ADE55264 standard; DNA; 1589 BP.  
 DE Human gene ALI37271, SEQ ID NO 1078.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GHEO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 Query Match 1.5%; Score 53; DB 10; Length 1589;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 928  
 ID ADE58406 standard; DNA; 1591 BP.  
 DE Toxicity-related gene, SEQ ID 3432.  
 PN WO2003064624-A2.  
 PD 07-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 1.5%; Score 53; DB 10; Length 1591;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 929  
 ID ADE52986 standard; DNA; 1591 BP.  
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3528.  
 PN WO2003065993-A2.  
 PD 14-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 1.5%; Score 53; DB 10; Length 1591;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 930  
 ID ABR42053 standard; DNA; 1591 BP.  
 DE Toxicity modelling related rat gene SEQ ID No 1755.  
 PN WO200295000-A2.  
 PD 28-NOV-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 1.5%; Score 53; DB 10; Length 1591;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;

RESULT 931  
 ID AAV33190 standard; cDNA; 1694 BP.  
 DE Secreted protein BD380\_1 cDNA.  
 PN WO9838209-A2.  
 PD 03-SEP-1998.  
 PA (GEMY ) GENETICS INST INC.  
 Query Match 1.5%; Score 53; DB 2; Length 1694;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 932  
 ID AA252500 standard; cDNA; 1707 BP.  
 DE Human secreted protein clone yb124\_1 nucleotide sequence SEQ ID NO:51.  
 PN WO9958642-A2.  
 PD 18-NOV-1999.  
 PA (GEMY ) GENETICS INST INC.  
 Query Match 1.5%; Score 53; DB 3; Length 1707;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 933  
 ID AAA27151 standard; cDNA; 1763 BP.  
 DE Human p52 cDNA.  
 PN WO200029578-A1.  
 PD 25-MAY-2000.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 1.5%; Score 53; DB 3; Length 1763;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 934  
 ID AA200457 standard; cDNA; 1772 BP.  
 DE Human secreted protein cDNA encoding gene 48.  
 PN WO9938881-A1.  
 PD 05-AUG-1999.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.5%; Score 53; DB 3; Length 1812;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 935  
 ID AAA16649 standard; cDNA; 1812 BP.  
 DE Human secreted protein clone pw460\_5 nucleotide sequence SEQ ID NO:63.  
 PN WO200009552-A1.  
 PD 24-FEB-2000.  
 PA (GEMY ) GENETICS INST INC.  
 Query Match 1.5%; Score 53; DB 3; Length 1812;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 936  
 ID ADQ24551 standard; DNA; 1816 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7371.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 1.5%; Score 53; DB 12; Length 1816;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 937  
 ID ABR88010 standard; cDNA; 1827 BP.  
 DE cDNA encoding human 83378 metal transporter protein.  
 PN WO200240656-A2.  
 PD 23-MAY-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 1.5%; Score 53; DB 6; Length 1827;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 938  
 ID AAF21914 standard; DNA; 1882 BP.  
 DE Human breast and ovarian cancer associated antigen gene SEQ ID 301.  
 PN WO200055173-A1.  
 PD 21-SEP-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.5%; Score 53; DB 3; Length 1882;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 RESULT 939  
 ID ADM47920 standard; DNA; 1882 BP.  
 DE Polynucleotide sequence #338 useful in producing transgenic plants.  
 PN US200323670-A1.  
 PD 18-DEC-2003.  
 PA (EDGE/) EDGERTON M D.  
 PA (CHOM/) CHOMET P S.  
 PA (LACC/) LACCETTI L B.  
 Query Match 1.5%; Score 53; DB 12; Length 1882;

Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
RESULT 940  
ID ABA06572 standard; cDNA; 1926 BP.  
DE Human cDNA SEQ ID NO: 238.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 4; Length 1926;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 941  
ID ABV83909 standard; cDNA; 1926 BP.  
DE Human polynucleotide SEQ ID NO 238.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 1.5%; Score 53; DB 6; Length 1926;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 942  
ID ABL90817 standard; cDNA; 1975 BP.  
DE Human polynucleotide SEQ ID NO 1379.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 6; Length 1975;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 943  
ID AAX27383 standard; DNA; 1977 BP.  
DE Human secreted protein gene 73 clone HCUPZ62.  
PN WO9902546-A1.  
PD 21-JAN-1999.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 2; Length 1977;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 944  
ID ADA07262 standard; cDNA; 1977 BP.  
DE Human cDNA from secreted protein gene 73.  
PN US2003064412-A1.  
PD 03-APR-2003.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAF/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHI/) SHI Y.  
PA (OLSE/) OLSEN H S.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
Query Match 1.5%; Score 53; DB 9; Length 1977;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 945  
ID ADNA1003 standard; cDNA; 1977 BP.  
DE Novel human secreted protein cDNA seqid 125.  
PN US2004044191-A1.  
PD 04-MAR-2004.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAF/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHI/) SHI Y.  
PA (OLSE/) OLSEN H.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.

Query Match 1.5%; Score 53; DB 12; Length 1977;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 946  
ID AD062413 standard; DNA; 2039 BP.  
DE Transcription factor G916 orthologous sequence, SEQ ID 880.  
PN WO2004031349-A2.  
PD 15-APR-2004.  
PA (MENDE-) MENDEL BIOTECHNOLOGY INC.  
Query Match 1.5%; Score 53; DB 12; Length 2039;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 947  
ID ABL90496 standard; cDNA; 2062 BP.  
DE Human polynucleotide SEQ ID NO 1058.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 6; Length 2062;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 948  
ID ADQ23447 standard; DNA; 2087 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6267.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.5%; Score 53; DB 12; Length 2087;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 949  
ID AAA26375 standard; cDNA; 2103 BP.  
DE Human secreted protein gene 30 SEQ ID NO:40.  
PN WO200006698-A1.  
PD 10-FEB-2000.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 3; Length 2103;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 950  
ID ADA39984 standard; cDNA; 2103 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 8; Length 2103;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 951  
ID ACC50546 standard; cDNA; 2103 BP.  
DE Human secreted protein coding sequence, SEQ ID 213.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 8; Length 2103;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 952  
ID ABZ71300 standard; cDNA; 2103 BP.  
DE Secreted protein-encoding gene 111 cDNA clone HNFPC43, SEQ ID NO:121.  
PN WO200276488-A1.  
PD 03-OCT-2002.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 8; Length 2103;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 953  
ID ADB91216 standard; cDNA; 2103 BP.  
DE Human secreted protein cDNA #SEQ ID 162.  
PN WO2003004622-A2.  
PD 16-JAN-2003.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 9; Length 2103;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 954  
ID ADC73608 standard; DNA; 2103 BP.  
DE Human secreted protein-related DNA - SEQ ID 241.  
PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 10; Length 2103;



Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 955  
ID ADA56173 standard; DNA; 2103 BP.  
DE Gene encoding human secreted protein #352.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 10; Length 2103;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 956  
ID ADL71436 standard; cDNA; 2103 BP.  
DE Novel human secreted protein cDNA seqid 40.  
PN US2004034196-A1.  
PD 19-FEB-2004.  
PA (KOMA/) KOMATSU S. G. A.  
PA (ROSE/) ROSEN C. A.  
PA (RUBEN/) RUBEN S. M.  
PA (DUAN/) DUAN D. R.  
PA (MOORE/) MOORE P. A.  
PA (SHI/) SHI Y.  
PA (LAPL/) LAPLEUR D. W.  
PA (WEI/) WEI Y.  
Query Match 1.5%; Score 53; DB 12; Length 2103;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 957  
ID ADQ24823 standard; DNA; 2178 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7643.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.5%; Score 53; DB 12; Length 2178;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 958  
ID ADP54455 standard; cDNA; 2222 BP.  
DE Human PRO cDNA sequence SEQ ID NO:431.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH/) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 13; Length 2222;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 959  
ID AAA47455 standard; cDNA; 2272 BP.  
DE Human TANGO 197 coding sequence.  
PN WO20039284-A1.  
PD 06-JUL-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 53; DB 3; Length 2272;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 960  
ID ADI00533 standard; cDNA; 2272 BP.  
DE Human TANGO 197 cDNA.  
PN US2003144193-A1.  
PD 31-JUL-2003.  
PA (ROTT/) ROTTMAN J. B.  
PA (OKEE/) O'KEEFE T. L.  
PA (OZKA/) OZKAYNAK E.  
PA (HEAL/) HEALEY J. J.  
Query Match 1.5%; Score 53; DB 10; Length 2272;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 961  
ID ADM64567 standard; cDNA; 2272 BP.  
DE Human von Willebrand factor A-like domain protein TANGO197 cDNA.  
PN US2003134786-A1.  
PD 17-JUL-2003.  
PA (ROTT/) ROTTMAN J. B.  
PA (OKEE/) O'KEEFE T. L.  
PA (OZKA/) OZKAYNAK E.  
PA (HEAL/) HEALEY J. J.  
Query Match 1.5%; Score 53; DB 11; Length 2272;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 962  
ID AAC77021 standard; cDNA; 2273 BP.  
DE Human ORFX ORF2576 polynucleotide sequence SEQ ID NO:5151.  
PN WO20032783-A1.

PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.5%; Score 53; DB 3; Length 2273;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 963  
ID ABL90769 standard; cDNA; 2317 BP.  
DE Human polynucleotide SEQ ID NO 1331.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 6; Length 2317;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 964  
ID ADO25966 standard; DNA; 2330 BP.  
DE Corn chalcone synthase (CHS) polynucleotide seqid 4.  
PN WO2004046336-A2.  
PD 03-JUN-2004.  
PA (MONS) MONSANTO TECHNOLOGY LLC.  
Query Match 1.5%; Score 53; DB 12; Length 2330;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 965  
ID ACN88807 standard; DNA; 2353 BP.  
DE Breast cancer related marker, seq id 9957.  
PN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 53; DB 11; Length 2353;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
RESULT 966  
ID ADF82123 standard; DNA; 2384 BP.  
DE Leukaemia-related DNA sequence #2679.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYIJ-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE/) HAERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KERN/) KERN W.  
Query Match 1.5%; Score 53; DB 10; Length 2384;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 967  
ID ADF82124 standard; DNA; 2384 BP.  
DE Leukaemia-related DNA sequence #2680.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYIJ-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE/) HAERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KERN/) KERN W.  
Query Match 1.5%; Score 53; DB 10; Length 2384;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 968  
ID AAC98119 standard; cDNA; 2461 BP.  
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:129.  
PN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 3; Length 2461;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 969  
ID AAH33223 standard; cDNA; 2461 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:279.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 4; Length 2461;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 970  
ID AAA27988 standard; cDNA; 2498 BP.  
DE Wheat CCR4 transcription factor nucleotide sequence #1.  
PN WO200032783-A1.

PD 08-JUN-2000.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 1.5%; Score 53; DB 3; Length 2498;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 971  
ID ABS57567 standard; cDNA; 2619 BP.  
DE Human SECP-23 cDNA from clone 7503641CD1 SEQ ID 23.  
PN WO200279441-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.5%; Score 53; DB 8; Length 2619;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 972  
ID AAH33733 standard; cDNA; 2630 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:789.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 53; DB 4; Length 2630;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 973  
ID ACF34468 standard; DNA; 2712 BP.  
DE Gene encoding anglogenesis protein BNO67.  
PN WO2003027285-A1.  
PD 03-APR-2003.  
PA (BION-) BIONOMICS LTD.  
Query Match 1.5%; Score 53; DB 8; Length 2712;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 974  
ID ABV75070 standard; DNA; 2712 BP.  
DE Human Dev20 homologue protein encoding DNA.  
PN WO200279238-A2.  
PD 10-OCT-2002.  
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.  
Query Match 1.5%; Score 53; DB 8; Length 2712;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 975  
ID ADF81962 standard; DNA; 2712 BP.  
DE Leukaemia-related DNA sequence #2518.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE/) HAPERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KERN/) KERN W.  
Query Match 1.5%; Score 53; DB 10; Length 2712;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 976  
ID ADO20179 standard; cDNA; 2712 BP.  
DE Human PRO polynucleotide #544.  
PN WO2004043361-A2.  
PD 27-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 12; Length 2712;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 977  
ID ADP55359 standard; cDNA; 2712 BP.  
DE Human PRO cDNA sequence SEQ ID NO:1335.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 13; Length 2712;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 978  
ID ADP25232 standard; cDNA; 2712 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:2410.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 13; Length 2712;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 979  
ID AAD15455 standard; cDNA; 2838 BP.  
DE Human 26583 serine/threonine phosphatase cDNA.  
PN WO200166765-A2.  
PD 13-SEP-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 53; DB 4; Length 2838;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 980  
ID ADE38448 standard; DNA; 2838 BP.  
DE Human protein 26583 gene sequence.  
PN WO2003065006-A2.  
PD 07-AUG-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 53; DB 10; Length 2838;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 981  
ID ADD45824 standard; DNA; 2857 BP.  
DE Human gene AL050155, SEQ ID NO 11493.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 1.5%; Score 53; DB 10; Length 2857;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 982  
ID ADE60246 standard; DNA; 2857 BP.  
DE Human gene AL050155, SEQ ID NO 6152.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 1.5%; Score 53; DB 10; Length 2857;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 983  
ID ADE60248 standard; DNA; 2857 BP.  
DE Human gene AL050155, SEQ ID NO 6154.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 1.5%; Score 53; DB 10; Length 2857;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 984  
ID ADE60252 standard; DNA; 2857 BP.  
DE Human gene AL050155, SEQ ID NO 6158.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 1.5%; Score 53; DB 10; Length 2857;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 985  
ID ADE60250 standard; DNA; 2857 BP.  
DE Human gene AL050155, SEQ ID NO 6156.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 1.5%; Score 53; DB 10; Length 2857;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 986  
ID AAC61886 standard; cDNA; 3030 BP.  
DE cDNA encoding a human secreted protein.  
PN WO200061755-A2.  
PD 19-OCT-2000.  
PA (CHIR) CHIRON CORP.  
Query Match 1.5%; Score 53; DB 3; Length 3030;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 987  
ID ADI42179 standard; DNA; 3118 BP.  
DE Plant transcription factor polynucleotide #364.  
PN US2004019927-A1.  
PD 29-JAN-2004.

PA (SHER/) SHERMAN B K.  
PA (RIEC/) RICHMANN J L.  
PA (JIANG/) JIANG C.  
PA (HEAR/) HEARD J E.  
PA (HAAR/) HAAKE V.  
PA (CREE/) CREELMAN R A.  
PA (RATC/) RATCLIFFE O.  
PA (ADAM/) ADAM L J.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J.  
PA (BROU/) BROUN P E.  
PA (PILG/) PILGRIM M L.  
PA (DUBE/) DUBELL A N.  
PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3118;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 988  
ID ADO02686 standard; cDNA; 3118 BP.  
DE Soybean orthologue of Thalecress transcription factor, cDNA #69.  
PN US2004045049-A1.  
PD 04-MAR-2004.  
PA (ZHAN/) ZHANG J.  
PA (FROM/) FROMM M E.  
PA (HEAR/) HEARD J E.  
PA (RIEC/) RICHMANN J L.  
PA (ADAM/) ADAM L J.  
PA (BROU/) BROUN P E.  
PA (PINE/) PINEDA O.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J S.  
PA (YUGG/) YU G.  
PA (JIAN/) JIANG C.  
PA (SAMA/) SAMAHA R S.  
PA (PILG/) PILGRIM M L.  
PA (CREE/) CREELMAN R A.  
PA (DUBE/) DUBELL A N.  
PA (RATC/) RATCLIFFE O.  
PA (KUMI/) KUMIMOTO R.  
PA (SHER/) SHERMAN B K.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3118;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 989  
ID ADO62303 standard; DNA; 3118 BP.  
DE Transcription factor G438 orthologous sequence, SEQ ID 770.  
PN WO2004031349-A2.  
PD 15-APR-2004.  
PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3118;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 990  
ID AAS21262 standard; cDNA; 3501 BP.  
DE Human cDNA sequence encoding for PRO4985 polypeptide.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 4; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 991  
ID ACAD3621 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 8; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 992  
ID ABX89159 standard; cDNA; 3501 BP.  
DE DNA encoding novel secreted and transmembrane protein PRO4985.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 8; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 993  
ID ACD41813 standard; cDNA; 3501 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #19.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 8; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 994  
ID ACA04042 standard; cDNA; 3501 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 37.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 8; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 995  
ID ADA45556 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 996  
ID ADA75987 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 997  
ID ADA18637 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 998  
ID ADA61260 standard; cDNA; 3501 BP.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 999  
ID ADB19045 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1000  
ID ADB27586 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1001  
ID ADA86065 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;

ID ADA91462 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
FN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1012  
ID ADB14525 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
FN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1013  
ID ADB18486 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
FN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1014  
ID ADA93701 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
FN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1015  
ID ADB19597 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
FN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1016  
ID ADB12909 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
FN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1017  
ID ACD98442 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
FN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1018  
ID ADA74163 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
FN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1019  
ID ADB24396 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide SEQ ID NO 37.  
FN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1020  
ID ADA81920 standard; cDNA; 3501 BP.

DE Human PRO polynucleotide #19.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1021  
ID ADA74893 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1022  
ID ADA84961 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1023  
ID ADA84409 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1024  
ID ADB29665 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1025  
ID ADA80193 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1026  
ID ADA75435 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1027  
ID ADA46660 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1028  
ID ADB24956 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide SEQ ID NO 37.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1029  
ID ADA93132 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.

PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1030  
ID ADB26482 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1031  
ID ADB30769 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1032  
ID ADA60697 standard; cDNA; 3501 BP.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1033  
ID ADB23844 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide SEQ ID NO 37.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1034  
ID ADA96173 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1035  
ID ADA80745 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1036  
ID ADA95621 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1037  
ID ADB25930 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 9; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1038  
ID ADB21415 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003082765-A1.

PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1039  
 ID ADA77194 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003068797-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1040  
 ID ADB17934 standard; cDNA; 3501 BP.  
 DE cDNA encoding human PRO polypeptide #19.  
 PN US2003077710-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1041  
 ID ADA86617 standard; cDNA; 3501 BP.  
 DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
 PN US2003082709-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1042  
 ID ADA87720 standard; cDNA; 3501 BP.  
 DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
 PN US2003082700-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1043  
 ID ADA46108 standard; cDNA; 3501 BP.  
 DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
 PN US2003054516-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1044  
 ID ADB28138 standard; cDNA; 3501 BP.  
 DE cDNA encoding human PRO polypeptide #19.  
 PN US2003082699-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1045  
 ID ADB28690 standard; cDNA; 3501 BP.  
 DE cDNA encoding human PRO polypeptide #19.  
 PN US2003082706-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1046  
 ID ADA76642 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003059909-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1047  
 ID ADA88272 standard; cDNA; 3501 BP.  
 DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
 PN US2003073213-A1.  
 PD 17-APR-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1048  
 ID ADA97277 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003082686-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1049  
 ID ADB27034 standard; cDNA; 3501 BP.  
 DE cDNA encoding human PRO polypeptide #19.  
 PN US2003022239-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1050  
 ID ADB21967 standard; cDNA; 3501 BP.  
 DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
 PN US2003087344-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1051  
 ID ADA66658 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003068793-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1052  
 ID ADB22519 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003077711-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1053  
 ID ADB23292 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide SEQ ID NO 37.  
 PN US2003077712-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1054  
 ID ADA92014 standard; cDNA; 3501 BP.  
 DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
 PN US2003082712-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1055  
 ID ADB15077 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003087352-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1056  
 ID ADB38329 standard; cDNA; 3501 BP.  
 DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
 PN US2003082766-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 9; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

ID ADB35258 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide SEQ ID NO 37.  
FN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1067  
ID ADB33602 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide SEQ ID NO 37.  
FN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1068  
ID ADB34706 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide SEQ ID NO 37.  
FN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1069  
ID ADB35810 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide SEQ ID NO 37.  
FN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1070  
ID ADB46205 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
FN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1071  
ID ADB50078 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
FN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1072  
ID ADC71625 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
FN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1073  
ID ADC59604 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
FN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1074  
ID ADC52611 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID37  
FN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1075  
ID APC5965 standard; cDNA; 3501 BP.



DE Novel human secreted and transmembrane protein cDNA Seq ID37.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1076  
ID ADC60156 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1077  
ID ADC50631 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1078  
ID ADC65158 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1079  
ID ADC54256 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID37.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1080  
ID ADC53217 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID37.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1081  
ID ADC58740 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID37.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1082  
ID ADC55618 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID37.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1083  
ID ADC58188 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID37.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1084  
ID ADD02862 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003087358-A1.

PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1085  
ID ADC89854 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1086  
ID ADC69273 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1087  
ID ADC48162 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1088  
ID ADD09691 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1089  
ID ADD04266 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1090  
ID ADC80222 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1091  
ID ADD10729 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1092  
ID ADC47610 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
Pred. No. 1.3e-05;  
RESULT 1093  
ID ADC79670 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003087358-A1.

PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1094  
 ID ADD09139 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003194775-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1095  
 ID ADD40852 standard; cDNA; 3501 BP.  
 DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
 PN US2003203438-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1096  
 ID ADD51991 standard; cDNA; 3501 BP.  
 DE cDNA encoding human PRO polypeptide #19.  
 PN US2003194769-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1097  
 ID ADD52731 standard; cDNA; 3501 BP.  
 DE cDNA encoding human PRO polypeptide #19.  
 PN US2003194792-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1098  
 ID ADD53283 standard; cDNA; 3501 BP.  
 DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
 PN US2003203437-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1099  
 ID ADD51439 standard; cDNA; 3501 BP.  
 DE cDNA encoding human PRO polypeptide #19.  
 PN US2003194779-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1100  
 ID ADD02238 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003203431-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1101  
 ID ADD01672 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003203430-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1102  
 ID ADD53854 standard; cDNA; 3501 BP.  
 DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
 PN US2003203432-A1.  
 PD 30-OCT-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1103  
 ID ADD92171 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003199030-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1104  
 ID ADD91067 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003199055-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1105  
 ID ADE03681 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003199057-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1106  
 ID ADE31978 standard; cDNA; 3501 BP.  
 DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
 PN US2003194765-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1107  
 ID ADE21910 standard; cDNA; 3501 BP.  
 DE cDNA encoding human PRO polypeptide #19.  
 PN US2003199056-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1108  
 ID ADD79134 standard; cDNA; 3501 BP.  
 DE cDNA encoding human PRO polypeptide #19.  
 PN US2003203428-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1109  
 ID ADE41670 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003194772-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1110  
 ID ADE17487 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003199023-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 1.5%; Score 53; DB 10; Length 3501;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 RESULT 1111  
 ID ADD91619 standard; cDNA; 3501 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003199053-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1112  
ID ADE33082 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1113  
ID ADE33634 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1114  
ID ADD79686 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1115  
ID ADD92723 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1116  
ID ADE19143 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1117  
ID ADE18591 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1118  
ID ADE42787 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1119  
ID ADD95576 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1120  
ID ADE22462 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1121  
ID ADD78580 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1122  
ID ADE32530 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1123  
ID ADE42222 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1124  
ID ADE80238 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1125  
ID ADE89266 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1126  
ID ADE40550 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1127  
ID ADE04349 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1128  
ID ADE32478 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1129  
ID ADG21187 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;  
RESULT 1130  
ID ADE22462 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.

RESULT 1130  
ID ADG22828 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1131  
ID ADG97163 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1132  
ID ADG80227 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1133  
ID ADG79675 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1134  
ID ADH54967 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1135  
ID ADH55519 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1136  
ID ADI63738 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1137  
ID ADI64687 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1138  
ID ADI63186 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1139  
ID ADC80774 standard; cDNA; 3501 BP.

ID ADH81600 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1140  
ID ADH81048 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1141  
ID ACD23871 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1142  
ID ACA67012 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 10; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1143  
ID ADM82217 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 11; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1144  
ID ADN15616 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 11; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1145  
ID ADN16245 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 11; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1146  
ID ADN15064 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 11; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1147  
ID ADN14512 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 53; DB 11; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1148  
ID ADC80774 standard; cDNA; 3501 BP.

DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1149  
ID ADD76222 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1150  
ID ADD87586 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1151  
ID ADD85990 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1152  
ID ADE75438 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1153  
ID ADE23014 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1154  
ID ADE23566 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1155  
ID ADE24209 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1156  
ID ADD87034 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1157  
ID ADE88900 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.

PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1158  
ID ADE18039 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1159  
ID ADE88348 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1160  
ID ADE94368 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1161  
ID ADE90779 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1162  
ID ADE94920 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1163  
ID ADE93030 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1164  
ID ADF34611 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1165  
ID ADE91926 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
RESULT 1166  
ID ADE90227 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003199063-A1.

PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1176  
ID ADG16423 standard; cDNA; 3501 BP.  
DE CDNA encoding human PRO polypeptide #19.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1177  
ID ADG04882 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1178  
ID ADG19149 standard; cDNA; 3501 BP.  
DE CDNA encoding human PRO polypeptide #19.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1179  
ID ADG12986 standard; cDNA; 3501 BP.  
DE CDNA encoding human PRO polypeptide #19.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1180  
ID ADG08043 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 CDNA.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1181  
ID ADG15213 standard; cDNA; 3501 BP.  
DE CDNA encoding human PRO polypeptide #19.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1182  
ID ADP96611 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1183  
ID ADG05796 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1184  
ID ADG23380 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 CDNA.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.

PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1167  
ID ADE31374 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 CDNA.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1168  
ID ADG01953 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1169  
ID ADG21739 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 CDNA.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1170  
ID ADG19809 standard; cDNA; 3501 BP.  
DE CDNA encoding human PRO polypeptide #19.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1171  
ID ADF97715 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1172  
ID ADG23932 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 CDNA.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1173  
ID ADF98286 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1174  
ID ADG03117 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1175  
ID ADP98838 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003207353-A1.  
PD 06-NOV-2003.

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Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1185
ID ADG03669 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1186
ID ADG24570 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1187
ID ADG06867 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1188
ID ADG07419 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1189
ID ADG54914 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1190
ID ADG60578 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1191
ID ADG61682 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1192
ID ADG81883 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1193
ID ADG57122 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1194
ID ADG56570 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1195
ID ADG5466 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1196
ID ADG58226 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1197
ID ADG70592 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1198
ID ADG57674 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1199
ID ADG53258 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1200
ID ADG71144 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1201
ID ADG81331 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1202
ID ADH30293 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US200307723-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1203
ID ADG57122 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
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ID ADH11660 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1204  
ID ADG52082 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1205  
ID ADG53810 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1206  
ID ADG80779 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1207  
ID ADG56018 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1208  
ID ADH12284 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1209  
ID ADG61130 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1210  
ID ADH28217 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1211  
ID ADG54362 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1212  
ID ADG59402 standard; cDNA; 3501 BP.

DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1213  
ID ADI80826 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1214  
ID ADG09569 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1215  
ID ADI15040 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1216  
ID ADG08917 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1217  
ID ADI14372 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1218  
ID ADI17967 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1219  
ID ADJ63248 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1220  
ID ADJ77143 standard; cDNA; 3501 BP.  
DE Human PRO polynucleotide #19.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1221  
ID ADJ65265 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.

PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1222  
ID ADM27401 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1223  
ID ADM42125 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1224  
ID ADM27987 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;  
RESULT 1225  
ID ADI95469 standard; cDNA; 3501 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 3501;  
RESULT 1226  
ID ADI96021 standard; cDNA; 3501 BP.  
DE Novel human secreted and transmembrane protein PRO4985 cDNA.  
PN US20030207354-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 3501;  
RESULT 1227  
ID AAQ44391 standard; cDNA to mRNA; 3581 BP.  
DE Sequence of murine OSF-4 cDNA.  
PN EP585801-A2.  
PD 09-MAR-1994.  
PA (FAB) HOECHST JAPAN LTD.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 2; Length 3581;  
RESULT 1228  
ID ADQ23054 standard; DNA; 3650 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5874.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 12; Length 3650;  
RESULT 1229  
ID ADP54957 standard; cDNA; 4090 BP.  
DE Human PRO cDNA sequence SEQ ID NO:933.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 4090;  
RESULT 1230  
ID ADS88644 standard; cDNA; 4090 BP.  
DE Human housekeeping gene cDNA sequence SEQ ID NO:187.  
PN WO2004035785-A1.

PD 29-APR-2004.  
PA (NIGA) NGK INSULATORS LTD.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 13; Length 4090;  
RESULT 1231  
ID ADL06652 standard; cDNA; 4557 BP.  
DE Human 3T3 cell conversion promoter PP13850 cDNA.  
PN CN1403477-A.  
PD 19-MAR-2003.  
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 4557;  
RESULT 1232  
ID ADL06654 standard; DNA; 4557 BP.  
DE Human 3T3 cell conversion promoter PP13850 DNA.  
PN CN1403477-A.  
PD 19-MAR-2003.  
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 4557;  
RESULT 1233  
ID ADL15662 standard; DNA; 4816 BP.  
DE Human structural and cytoskeleton-associated protein (SCAP) gene #10.  
PN WO2003062391-A2.  
PD 31-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 10; Length 4816;  
RESULT 1234  
ID ABZ26080 standard; DNA; 40116 BP.  
DE Mouse DNaseX encoding genomic DNA SEQ ID NO 7.  
PN EP1249495-A1.  
PD 16-OCT-2002.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 8; Length 40116;  
RESULT 1235  
ID AAZ23902 standard; DNA; 49999 BP.  
DE Human LOBO homologue genomic DNA fragment 4.  
PN WO950284-A2.  
PD 07-OCT-1999.  
PA (ROSE/) ROSENTHAL A.  
Query Match  
Best Local Similarity 1.5%; Score 53; DB 2; Length 49999;  
RESULT 1236  
ID ABK55207 standard; cDNA; 56 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 677.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 6; Length 56;  
RESULT 1237  
ID ADT94789 standard; cDNA; 68 BP.  
DE Colon cancer associated human cDNA sequence #308.  
PN US2003087818-A1.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 11; Length 68;  
RESULT 1238  
ID ABK54873 standard; cDNA; 72 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 343.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 6; Length 72;  
RESULT 1239  
ID ACN50126 standard; cDNA; 142 BP.  
DE Cotton non-primed seed EST Clone ID: LIB3826-001-Q1-K6-E5, SEQ:4907.  
PN US2004123340-A1.  
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 52; DB 13; Length 142;  
Best Local Similarity 100.0%; Pred. No. 6.4e-05;  
RESULT 1240  
ID ADT94954 standard; cDNA; 146 BP.  
DE Colon cancer associated human cDNA sequence #473.  
PN US2003087818-A1.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.5%; Score 52; DB 11; Length 146;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
RESULT 1241  
ID ADF57474 standard; cDNA; 153 BP.  
DE Urogenital sinus-derived expressed sequence tag, SEQ ID No 793.  
PN WO958665-A2.  
PD 18-NOV-1999.  
PA (UYVI-) UNIV VIRGINIA PATENT FOUND.  
Query Match 1.5%; Score 52; DB 3; Length 153;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
RESULT 1242  
ID ABX46255 standard; cDNA; 165 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #11420.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 52; DB 8; Length 165;  
Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
RESULT 1243  
ID ADL45094 standard; DNA; 193 BP.  
DE Human ovarian cancer DNA marker #18984.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 5; Length 193;  
Best Local Similarity 100.0%; Pred. No. 5.8e-05;  
RESULT 1244  
ID ABX45180 standard; cDNA; 210 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #10345.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 52; DB 8; Length 210;  
Best Local Similarity 100.0%; Pred. No. 5.7e-05;  
RESULT 1245  
ID ABX60856 standard; DNA; 215 BP.  
DE Arabidopsis thaliana polynucleotide #202.  
PN US2002142319-A1.  
PD 03-OCT-2002.  
PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (HARG/) HARGISS T R.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
Query Match 1.5%; Score 52; DB 10; Length 215;  
Best Local Similarity 100.0%; Pred. No. 5.6e-05;  
RESULT 1246

ID AAh69412 standard; cDNA; 226 BP.  
DE Human cervical cancer marker nucleic acid 686.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 4; Length 226;  
Best Local Similarity 100.0%; Pred. No. 5.6e-05;  
RESULT 1247  
ID ABX54617 standard; cDNA; 229 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #4546.  
PN US2002137160-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 52; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 5.5e-05;  
RESULT 1248  
ID AAD05356 standard; cDNA; 233 BP.  
DE Human secreted protein-encoding gene 14 cDNA clone HCRNO87, SEQ ID NO:67.  
PN WO200134626-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 4; Length 233;  
Best Local Similarity 100.0%; Pred. No. 5.5e-05;  
RESULT 1249  
ID ABX46273 standard; cDNA; 239 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #11438.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 52; DB 8; Length 239;  
Best Local Similarity 100.0%; Pred. No. 5.5e-05;  
RESULT 1250  
ID ACN45492 standard; cDNA; 256 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-002-Q1-K6-G3, SEQ:273.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 52; DB 13; Length 256;  
Best Local Similarity 100.0%; Pred. No. 5.3e-05;  
RESULT 1251  
ID ADK61479 standard; DNA; 260 BP.  
DE Ovarian cancer-related DNA #634 with altered ovarian cancer expression.  
PN WO2003068054-A2.  
PD 21-AUG-2003.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
Query Match 1.5%; Score 52; DB 10; Length 260;  
Best Local Similarity 100.0%; Pred. No. 5.3e-05;  
RESULT 1252  
ID ABV56597 standard; cDNA; 267 BP.  
DE Human prostate expression marker cDNA 56588.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 5; Length 267;  
Best Local Similarity 100.0%; Pred. No. 5.3e-05;  
RESULT 1253  
ID AAL16362 standard; cDNA; 271 BP.  
DE Human breast cancer expressed polynucleotide 8819.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 4; Length 271;  
Best Local Similarity 100.0%; Pred. No. 5.3e-05;

Query Match 1.5%; Score 52; DB 6; Length 306;  
Best Local Similarity 100.0%; Pred. No. 5.1e-05;  
RESULT 1263  
ID ADK61477 standard; DNA; 306 BP.  
DE Ovarian cancer-related DNA #632 with altered ovarian cancer expression.  
ID WO2003068054-A2.  
PD 21-AUG-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
Query Match 1.5%; Score 52; DB 10; Length 306;  
Best Local Similarity 100.0%; Pred. No. 5.1e-05;  
RESULT 1264  
ID ABX42505 standard; cDNA; 308 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #7670.  
ID US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARRE/) WARREN W C.  
Query Match 1.5%; Score 52; DB 8; Length 308;  
Best Local Similarity 100.0%; Pred. No. 5e-05;  
RESULT 1265  
ID ABEV04305 standard; cDNA; 314 BP.  
DE Human prostate expression marker cDNA 4296.  
ID WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 5; Length 314;  
Best Local Similarity 100.0%; Pred. No. 5e-05;  
RESULT 1266  
ID ADQ21262 standard; DNA; 320 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4082.  
ID WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PRO-) PROTEIN DESIGN LABS INC.  
Query Match 1.5%; Score 52; DB 12; Length 320;  
Best Local Similarity 100.0%; Pred. No. 5e-05;  
RESULT 1267  
ID ABX41000 standard; cDNA; 321 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #6165.  
ID US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARRE/) WARREN W C.  
Query Match 1.5%; Score 52; DB 8; Length 321;  
Best Local Similarity 100.0%; Pred. No. 5e-05;  
RESULT 1268  
ID ABV55706 standard; cDNA; 337 BP.  
DE Human prostate expression marker cDNA 55697.  
ID WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 5; Length 337;  
Best Local Similarity 100.0%; Pred. No. 4.9e-05;  
RESULT 1269  
ID ACN45670 standard; cDNA; 341 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-007-Q1-K6-C8, SEQ:451.  
ID US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 52; DB 13; Length 341;  
Best Local Similarity 100.0%; Pred. No. 4.9e-05;  
RESULT 1270  
ID ACN55002 standard; cDNA; 342 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-K6-A9, SEQ:9783.  
ID US2004123340-A1.  
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 1.5%; Score 52; DB 13; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-05;  
 RESULT 1271  
 ID ACN49021 standard; cDNA; 350 BP.  
 DE Cotton primed seed EST Clone ID: LIB3825-029-Q6-K6-A8, SEQ:3802.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 1.5%; Score 52; DB 13; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-05;  
 RESULT 1272  
 ID ABX49592 standard; cDNA; 355 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #14757.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 1.5%; Score 52; DB 8; Length 355;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
 RESULT 1273  
 ID ABX40295 standard; cDNA; 355 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #5460.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 1.5%; Score 52; DB 8; Length 355;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
 RESULT 1274  
 ID ABV48348 standard; cDNA; 358 BP.  
 DE Human prostate expression marker cDNA 48339.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 1.5%; Score 52; DB 5; Length 358;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
 RESULT 1275  
 ID ABV57991 standard; cDNA; 373 BP.  
 DE Human prostate expression marker cDNA 57982.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 1.5%; Score 52; DB 5; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
 RESULT 1276  
 ID AAS01025 standard; cDNA; 378 BP.  
 DE Sugarcane plant gene promoter cDNA isolated from clone c32A.  
 PN WO200118211-A1.  
 PD 15-MAR-2001.  
 PA (UYQU) UNIV QUEENSLAND.  
 Query Match 1.5%; Score 52; DB 4; Length 378;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
 RESULT 1277  
 ID ABV49790 standard; cDNA; 380 BP.  
 DE Human prostate expression marker cDNA 49781.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 1.5%; Score 52; DB 5; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
 RESULT 1278  
 ID ABX44845 standard; cDNA; 380 BP.

DE Bovine EST associated with lactation/muscle/fat deposition #10010.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 1.5%; Score 52; DB 8; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
 RESULT 1279  
 ID AAH70111 standard; cDNA; 384 BP.  
 DE Human cervical cancer marker nucleic acid 1385.  
 PN WO200142467-A2.  
 PD 14-JUN-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 1.5%; Score 52; DB 4; Length 384;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
 RESULT 1280  
 ID ABZ08601 standard; cDNA; 386 BP.  
 DE Human leukocyte derived cDNA SEQ ID NO 8592.  
 PN WO200257414-A2.  
 PD 25-JUL-2002.  
 PA (BIOC-) BIOCARDIA INC.  
 Query Match 1.5%; Score 52; DB 6; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
 RESULT 1281  
 ID ACH28736 standard; cDNA; 390 BP.  
 DE Human adult ovary cDNA #7116.  
 PN US2003073623-A1.  
 PD 17-APR-2003.  
 PA (DRMA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 Query Match 1.5%; Score 52; DB 9; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
 RESULT 1282  
 ID ABV47791 standard; cDNA; 391 BP.  
 DE Human prostate expression marker cDNA 47782.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 1.5%; Score 52; DB 5; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
 RESULT 1283  
 ID ABV49244 standard; cDNA; 394 BP.  
 DE Human prostate expression marker cDNA 49235.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 1.5%; Score 52; DB 5; Length 394;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
 RESULT 1284  
 ID ABX34934 standard; cDNA; 395 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #99.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 1.5%; Score 52; DB 8; Length 395;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
 RESULT 1285  
 ID AAF94851 standard; cDNA; 396 BP.  
 DE Human ovarian cancer associated coding sequence SEQ ID NO: 42.  
 PN WO200118046-A2.  
 PD 15-MAR-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match 1.5%; Score 52; DB 4; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
 RESULT 1286

ID ABL48801 standard; cDNA; 396 BP.  
DE Ovarian carcinoma sequence isolate 24356.  
PN US200204491-A1.  
PD 10-JAN-2002.  
PA (XUJJ/) XU J.  
PA (STOL/) STOLK J A.  
PA (ALCA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
Query Match 1.5%; Score 52; DB 6; Length 396;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
RESULT 1287  
ID ABL03118 standard; cDNA; 396 BP.  
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 42.  
PN WO200239885-A2.  
PD 23-MAY-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 1.5%; Score 52; DB 6; Length 396;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
RESULT 1288  
ID ADM10711 standard; cDNA; 396 BP.  
DE Human ovarian carcinoma-associated cDNA 24356.  
PN US2003206918-A1.  
PD 06-NOV-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.5%; Score 52; DB 11; Length 396;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
RESULT 1289  
ID ADJ11041 standard; cDNA; 396 BP.  
DE Representative human ovarian carcinoma cDNA SeqID 42.  
PN US2003232056-A1.  
PD 18-DEC-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.5%; Score 52; DB 12; Length 396;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
RESULT 1290  
ID ADM43302 standard; cDNA; 396 BP.  
DE Human ovarian carcinoma cDNA #42.  
PN US2003129192-A1.  
PD 10-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.5%; Score 52; DB 12; Length 396;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
RESULT 1291  
ID ACN53082 standard; cDNA; 398 BP.  
DE Cotton androecium tissue EST Clone ID: LTB3828-021-Q1-N6-P7, SEQ:7863.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 52; DB 13; Length 398;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
RESULT 1292  
ID AAT13044 standard; cDNA; 399 BP.  
DE Cotton fibre-specific cDNA clone A9.  
PN US5495070-A.  
PD 27-FEB-1996.  
PA (CETU) AGRACETUS INC.  
Query Match 1.5%; Score 52; DB 2; Length 399;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
RESULT 1293  
ID AAT30261 standard; DNA; 399 BP.  
DE Cotton fibre cell-specific cDNA clone CKFB10-A9.  
PN US5521078-A.  
PD 28-MAY-1996.  
PA (CETU) AGRACETUS INC.  
Query Match 1.5%; Score 52; DB 2; Length 399;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
RESULT 1294  
ID AAT62620 standard; cDNA to mRNA; 399 BP.  
DE Cotton fibre specific cDNA clone CKFB10-A9.  
PN US5597718-A.

PD 28-JAN-1997.  
PA (CETU) AGRACETUS.  
Query Match 1.5%; Score 52; DB 2; Length 399;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
RESULT 1295  
ID AAT70051 standard; cDNA; 399 BP.  
DE Cotton fibre specific cDNA clone A9.  
PN US5620882-A.  
PD 15-APR-1997.  
PA (CETU) AGRACETUS INC.  
Query Match 1.5%; Score 52; DB 2; Length 399;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
RESULT 1296  
ID AAZ35555 standard; DNA; 399 BP.  
DE cDNA sequence a cotton fibre gene from clone CKFB10A9.  
PN US5981834-A.  
PD 09-NOV-1999.  
PA (MONS) MONSANTO CO.  
Query Match 1.5%; Score 52; DB 3; Length 399;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
RESULT 1297  
ID AAI93256 standard; cDNA; 399 BP.  
DE Human polynucleotide SEQ ID NO 13316.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 52; DB 4; Length 399;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
RESULT 1298  
ID AAL19713 standard; cDNA; 402 BP.  
DE Human breast cancer expressed polynucleotide 12170.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 4; Length 402;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
RESULT 1299  
ID ABZ08612 standard; cDNA; 402 BP.  
DE Human leukocyte derived cDNA SEQ ID NO 8603.  
PN WO200257414-A2.  
PD 25-JUL-2002.  
PA (BIOC-) BIOCARDIA INC.  
Query Match 1.5%; Score 52; DB 6; Length 402;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
RESULT 1300  
ID ABV49258 standard; cDNA; 404 BP.  
DE Human prostate expression marker cDNA 49249.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 5; Length 404;  
Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
RESULT 1301  
ID ABX45586 standard; cDNA; 404 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #10751.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 52; DB 8; Length 404;  
Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
RESULT 1302  
ID ACH16113 standard; cDNA; 406 BP.  
DE Human adult heart cDNA #427.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.

Query Match 1.5%; Score 52; DB 9; Length 406;  
Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
RESULT 1303  
ID AAF81795 standard; cDNA; 410 BP.  
DE Human secreted protein gene 9 SEQ ID NO:19.  
PN WO200112775-A2.  
PD 22-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 4; Length 410;  
Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
RESULT 1304  
ID ADO63303 standard; DNA; 410 BP.  
DE Transcription factor G319 orthologous sequence, SEQ ID 1770.  
PN WO2004031349-A2.  
PD 15-APR-2004.  
PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
Query Match 1.5%; Score 52; DB 12; Length 410;  
Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
RESULT 1305  
ID AAI88540 standard; cDNA; 418 BP.  
DE Human polynucleotide SEQ ID NO 8600.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 52; DB 4; Length 418;  
Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
RESULT 1306  
ID ACH48626 standard; cDNA; 420 BP.  
DE Human leukocyte cDNA #220.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 1.5%; Score 52; DB 9; Length 420;  
Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
RESULT 1307  
ID ACH28837 standard; cDNA; 424 BP.  
DE Human adult ovary cDNA #7217.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 1.5%; Score 52; DB 9; Length 424;  
Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
RESULT 1308  
ID AAH33149 standard; cDNA; 425 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:205.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 4; Length 425;  
Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
RESULT 1309  
ID AAI88844 standard; cDNA; 426 BP.  
DE Human polynucleotide SEQ ID NO 8904.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 52; DB 4; Length 426;  
Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
RESULT 1310  
ID ACH30520 standard; cDNA; 426 BP.  
DE Human testis cDNA #906.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 1.5%; Score 52; DB 9; Length 426;  
Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
RESULT 1311  
ID ABV49095 standard; cDNA; 429 BP.  
DE Human prostate expression marker cDNA 49086.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 5; Length 429;  
Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
RESULT 1312  
ID AAI86320 standard; cDNA; 435 BP.  
DE Human polynucleotide SEQ ID NO 6380.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 52; DB 4; Length 435;  
Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
RESULT 1313  
ID ACH18655 standard; cDNA; 435 BP.  
DE Human adult heart cDNA #2969.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 1.5%; Score 52; DB 9; Length 435;  
Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
RESULT 1314  
ID AAH71214 standard; cDNA; 436 BP.  
DE Human cervical cancer marker nucleic acid 2488.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 4; Length 436;  
Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
RESULT 1315  
ID AAI87438 standard; cDNA; 441 BP.  
DE Human polynucleotide SEQ ID NO 7498.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 52; DB 4; Length 441;  
Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
RESULT 1316  
ID ABV56473 standard; cDNA; 442 BP.  
DE Human prostate expression marker cDNA 56464.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 5; Length 442;  
Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
RESULT 1317  
ID ABX43368 standard; cDNA; 447 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #8533.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.5%; Score 52; DB 8; Length 447;  
Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
RESULT 1318  
ID ABL87269 standard; cDNA; 451 BP.  
DE Human ovarian cancer related cDNA clone SEQ ID NO:10247.  
PN WO200192581-A2.  
PD 06-DEC-2001.



PA (CORI-) CORIXA CORP.  
Query Match 1.5%; Score 52; DB 6; Length 451;  
Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
RESULT 1319  
ID ACH24688 standard; cDNA; 457 BP.  
DE Human adult ovary cDNA #3068.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRNA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 1.5%; Score 52; DB 9; Length 457;  
Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
RESULT 1320  
ID ACH24394 standard; cDNA; 461 BP.  
DE Human adult ovary cDNA #2774.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRNA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 1.5%; Score 52; DB 9; Length 461;  
Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
RESULT 1321  
ID ADH28959 standard; DNA; 466 BP.  
DE Human chronic myelogenous leukaemia (CML) gene marker #227.  
PN US200310426-A1.  
PD 05-JUN-2003.  
PA (LINS/) LINSLEY P S.  
PA (MAOM/) MAO M.  
PA (DAIH/) DAI H.  
PA (HEYI/) HE Y.  
PA (RADI/) RADICH J P.  
Query Match 1.5%; Score 52; DB 10; Length 466;  
Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
RESULT 1322  
ID AAI92071 standard; cDNA; 467 BP.  
DE Human polynucleotide SEQ ID NO 12131.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.5%; Score 52; DB 4; Length 467;  
Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
RESULT 1323  
ID ABV56672 standard; cDNA; 467 BP.  
DE Human prostate expression marker cDNA 56663.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 5; Length 467;  
Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
RESULT 1324  
ID ACN51755 standard; cDNA; 486 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-007-Q1-N6-P4, SEQ:6536.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 52; DB 13; Length 486;  
Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
RESULT 1325  
ID ACN62774 standard; cDNA; 489 BP.  
DE Cotton carpel wall/septum EST Clone ID: LIB3831-001-Q1-K6-C8, SEQ:17555.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 52; DB 13; Length 489;  
Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
RESULT 1326  
ID ADL42859 standard; DNA; 495 BP.  
DE Human ovarian cancer DNA marker #16749.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 5; Length 495;  
Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
RESULT 1327  
ID ABV56951 standard; cDNA; 496 BP.  
DE Human prostate expression marker cDNA 56942.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 5; Length 496;  
Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
RESULT 1328  
ID ACN49058 standard; cDNA; 514 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-029-Q6-K6-E7, SEQ:3839.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 52; DB 13; Length 514;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
RESULT 1329  
ID ADI73400 standard; DNA; 515 BP.  
DE Human ovarian cancer DNA marker #6142.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 5; Length 515;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
RESULT 1330  
ID ADJ38531 standard; DNA; 515 BP.  
DE Human ovarian cancer DNA marker #12421.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.5%; Score 52; DB 5; Length 515;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
RESULT 1331  
ID ADF56917 standard; cDNA; 521 BP.  
DE Urogenital sinus-derived expressed sequence tag, SEQ ID No 236.  
PN WO9598665-A2.  
PD 18-NOV-1999.  
PA (UYVI-) UNIV VIRGINIA PATENT FOUND.  
Query Match 1.5%; Score 52; DB 3; Length 521;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
RESULT 1332  
ID ACN46717 standard; cDNA; 522 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-003-Q1-N6-C8, SEQ:1498.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.5%; Score 52; DB 13; Length 522;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
RESULT 1333  
ID ACN61692 standard; cDNA; 522 BP.  
DE Cotton gynoceum tissue EST Clone ID: LIB3829-018-Q6-N6-H8, SEQ:16473.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 13; Length 522;  
RESULT 1334  
ID ACN59983 standard; cDNA; 526 BP.  
DE Cotton gynecium tissue EST Clone ID: LIB3829-036-Q1-N6-A4, SEQ:14764.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 13; Length 526;  
RESULT 1335  
ID ACN53350 standard; cDNA; 528 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-N6-P8, SEQ:8131.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 13; Length 528;  
RESULT 1336  
ID AAS60058 standard; cDNA; 534 BP.  
DE Human cancer agent-sensitive marker #59.  
PN WO200179555-A2.  
PD 25-OCT-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 4; Length 534;  
RESULT 1337  
ID ACN55415 standard; cDNA; 536 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-023-Q6-N6-C9, SEQ:10196.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 13; Length 536;  
RESULT 1338  
ID ADR62275 standard; cDNA; 546 BP.  
DE Cotton cDNA sequence, SEQ ID 3056.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 13; Length 546;  
RESULT 1339  
ID ACN51414 standard; cDNA; 547 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-K6-G6, SEQ:6195.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 13; Length 547;  
RESULT 1340  
ID ADG33016 standard; DNA; 552 BP.  
DE Human DNA differentially expressed in patients with SLE SeqID340.  
PN WO2003090694-A2.  
PD 06-NOV-2003.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 10; Length 552;

Best Local Similarity 100.0%; Pred. No. 4.2e-05;  
RESULT 1341  
ID ACN62570 standard; cDNA; 552 BP.  
DE Cotton developing fibre EST Clone ID: LIB3830-001-Q1-N6-A1, SEQ:17351.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 13; Length 552;  
RESULT 1342  
ID ABV40163 standard; cDNA; 556 BP.  
DE Human prostate expression marker cDNA 40154.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 5; Length 556;  
RESULT 1343  
ID ABV40063 standard; cDNA; 556 BP.  
DE Human prostate expression marker cDNA 40054.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 5; Length 556;  
RESULT 1344  
ID ABV42105 standard; cDNA; 556 BP.  
DE Human prostate expression marker cDNA 42096.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 5; Length 556;  
RESULT 1345  
ID ABV43601 standard; cDNA; 556 BP.  
DE Human prostate expression marker cDNA 43592.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 5; Length 556;  
RESULT 1346  
ID ACN56091 standard; cDNA; 573 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-032-Q6-K6-C10, SEQ:10872.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 13; Length 573;  
RESULT 1347  
ID ABV57502 standard; cDNA; 574 BP.  
DE Human prostate expression marker cDNA 57493.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 5; Length 574;  
RESULT 1348  
ID ACN46463 standard; cDNA; 591 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-020-Q1-K6-D3, SEQ:1244.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 13; Length 591;

Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
RESULT 1349  
ID AAF18206 standard; DNA; 601 BP.  
DE Lung cancer associated polynucleotide sequence SEQ ID 225.  
PN WO200055180-A2.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A. 1.5%; Score 52; DB 3; Length 601;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
RESULT 1350  
ID ADC29847 standard; DNA; 619 BP.  
DE Fertilization-independent endosperm protein gene #6.  
PN WO2003026390-A2.  
PD 03-APR-2003.  
PA (PION-) PIONEER HI-BRED INT INC.  
PA (DUPO) DU PONT DE NEMOURS & CO E I. 1.5%; Score 52; DB 10; Length 619;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
RESULT 1351  
ID AAS01161 standard; cDNA; 620 BP.  
DE Fertilisation-independent endosperm cDNA clone hplc.pk003.e8.  
PN WO200116325-A2.  
PD 08-MAR-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
PA (PION-) PIONEER HI-BRED INT INC. 1.5%; Score 52; DB 4; Length 620;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
RESULT 1352  
ID ADR63368 standard; cDNA; 670 BP.  
DE Cotton cDNA sequence, SEQ ID 4149.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y. 1.5%; Score 52; DB 13; Length 723;  
PA (CAOY/) CAO Y. 1.5%; Score 52; DB 13; Length 723;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 4e-05;  
RESULT 1353  
ID ABV19321 standard; cDNA; 681 BP.  
DE Human prostate expression marker cDNA 19312.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 4e-05;  
RESULT 1354  
ID AAX30351 standard; DNA; 687 BP.  
DE DNA encoding a human secreted protein.  
PN WO9907891-A1.  
PD 18-FEB-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
RESULT 1355  
ID ADB47795 standard; cDNA; 687 BP.  
DE Novel human secreted protein cDNA #68.  
PN US2003054443-A1.  
PD 20-MAR-2003.  
PA (RUBE/) RUBEN S M.  
PA (SOPP/) SOPPET D R.  
PA (EBNE/) EBNER R.  
PA (OLSE/) OLSEN H S.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (ROSE/) ROSEN C A.  
PA (BREW/) BREWER L A.  
PA (JANA/) JANAT F.  
PA (BIRS/) BIRSE C E. 1.5%; Score 52; DB 10; Length 687;  
Query Match

Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
RESULT 1356  
ID ADJ5350 standard; cDNA; 687 BP.  
DE Novel human secreted protein cDNA #58.  
PN US2004023283-A1.  
PD 05-FEB-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
RESULT 1357  
ID ABL87011 standard; cDNA; 695 BP.  
DE Human ovarian cancer related cDNA clone SEQ ID NO:9989.  
PN WO200192581-A2.  
PD 06-DEC-2001.  
PA (CORI-) CORIAX CORP. 1.5%; Score 52; DB 6; Length 695;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
RESULT 1358  
ID ADR60499 standard; cDNA; 723 BP.  
DE Cotton cDNA sequence, SEQ ID 1280.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y. 1.5%; Score 52; DB 13; Length 723;  
PA (CAOY/) CAO Y. 1.5%; Score 52; DB 13; Length 723;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
RESULT 1359  
ID ACN54305 standard; cDNA; 723 BP.  
DE Cotton androecium tissue EST Clone ID: LIB9828-003-Q1-K6-F12, SEQ:9086.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E. 1.5%; Score 52; DB 13; Length 723;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
RESULT 1360  
ID AAL08093 standard; cDNA; 768 BP.  
DE Human breast cancer expressed polynucleotide 550.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
RESULT 1361  
ID AAL37842 standard; DNA; 783 BP.  
DE Soybean KCP-like protein encoding DNA, SEQ ID NO 34.  
PN WO20022821-A2.  
PD 21-MAR-2002.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
RESULT 1362  
ID AAC77913 standard; cDNA; 785 BP.  
DE Human cancer associated gene sequence SEQ ID NO:307.  
PN WO200055350-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC. 1.5%; Score 52; DB 3; Length 785;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
RESULT 1363  
ID ABV13906 standard; cDNA; 814 BP.  
DE Human prostate expression marker cDNA 13897.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 1.5%; Score 52; DB 5; Length 814;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 3.7e-05;  
RESULT 1364  
ID AAF91869 standard; cDNA; 840 BP.  
DE Human secreted protein-encoding gene 12 cDNA clone HFKKS66, SEQ ID NO:22.  
Query Match

PN WO200118022-A1.  
 PD 15-MAR-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 100.0%; DB 4; Length 840;  
 RESULT 1365  
 ID AC660574 standard; cDNA; 878 BP.  
 DE Polynucleotide relating to the invention SEQ ID NO: 151.  
 PN WO200257460-A2.  
 PD 25-JUL-2002.  
 PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
 Query Match  
 Best Local Similarity 100.0%; DB 6; Length 878;  
 RESULT 1366  
 ID AAL25029 standard; cDNA; 899 BP.  
 DE Human breast cancer expressed polynucleotide 17486.  
 PN WO200151628-A2.  
 PD 19-JUL-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 100.0%; DB 4; Length 899;  
 RESULT 1367  
 ID AAT65651 standard; cDNA to mRNA; 916 BP.  
 DE CDNA encoding anti-coagulant protein A.  
 PN JP09067396-A.  
 PD 11-MAR-1997.  
 PA (NORQ-) NORINSUISANSHO SANGSHI KONCHU.  
 Query Match  
 Best Local Similarity 100.0%; DB 2; Length 916;  
 RESULT 1368  
 ID AAV62000 standard; cDNA; 916 BP.  
 DE R. prolixus NO-r protein S CDNA.  
 PN JP10265497-A.  
 PD 06-OCT-1998.  
 PA (NORQ-) NORINSUISANSHO SANGSHI KONCHU.  
 Query Match  
 Best Local Similarity 100.0%; DB 2; Length 916;  
 RESULT 1369  
 ID AAI97661 standard; cDNA; 951 BP.  
 DE Human neuroblastoma expressed polynucleotide SEQ ID NO 3736.  
 PN WO200166719-A1.  
 PD 13-SEP-2001.  
 PA (CHIB-) CHIBA PREFECTURE.  
 PA (HISM-) HISAMITSU PHARM CO LTD.  
 Query Match  
 Best Local Similarity 100.0%; DB 4; Length 951;  
 RESULT 1370  
 ID AAC98222 standard; cDNA; 970 BP.  
 DE Human colon cancer antigen nucleotide sequence SEQ ID NO:232.  
 PN WO200055351-A1.  
 PD 21-SEP-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 100.0%; DB 3; Length 970;  
 RESULT 1371  
 ID ADF81829 standard; DNA; 976 BP.  
 DE Leukaemia-related DNA sequence #2385.  
 PN WO2003039443-A2.  
 PD 15-MAY-2003.  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
 PA (HAFE-) HAFERLACH T.  
 PA (SCHO-) SCHOCH C.  
 PA (KERN-) KERN W.  
 Query Match  
 Best Local Similarity 100.0%; DB 10; Length 976;  
 RESULT 1372  
 ID AAA53405 standard; cDNA; 991 BP.  
 DE Clone asm.pk0067.g5 nucleotide sequence encoding GST type III.  
 PN US6063570-A.  
 PD 16-MAY-2000.  
 PA (DUFO-) DU PONT DE NEMOURS & CO E I.  
 Query Match  
 Best Local Similarity 100.0%; DB 3; Length 991;

Best Local Similarity 100.0%; Pred. No. 3.5e-05;  
 RESULT 1373  
 ID AA294961 standard; cDNA; 991 BP.  
 DE Soybean glutathione-S-transferase cDNA clone asm.pk0067.g5.  
 PN WO200018936-A1.  
 PD 06-APR-2000.  
 PA (DUFO-) DU PONT DE NEMOURS & CO E I.  
 Query Match  
 Best Local Similarity 100.0%; DB 3; Length 991;  
 RESULT 1374  
 ID AAA59469 standard; DNA; 991 BP.  
 DE Nucleotide sequence of a soybean type III glutathione-S-transferase.  
 PN WO200047728-A2.  
 PD 17-AUG-2000.  
 PA (DUFO-) DU PONT DE NEMOURS & CO E I.  
 Query Match  
 Best Local Similarity 100.0%; DB 3; Length 991;  
 RESULT 1375  
 ID AAF31564 standard; DNA; 991 BP.  
 DE Soybean type III GST cDNA #6.  
 PN US6171839-B1.  
 PD 09-JAN-2001.  
 PA (DUFO-) DU PONT DE NEMOURS & CO E I.  
 Query Match  
 Best Local Similarity 100.0%; DB 4; Length 991;  
 RESULT 1376  
 ID AAF57531 standard; cDNA; 991 BP.  
 DE Glycine max clone SSM.PK0067.G5 sequence.  
 PN WO200121770-A2.  
 PD 29-MAR-2001.  
 PA (ZENE-) ZENECA LTD.  
 Query Match  
 Best Local Similarity 100.0%; DB 4; Length 991;  
 RESULT 1377  
 ID AAQ12431 standard; DNA; 1013 BP.  
 DE Fragment D of urate oxidase-encoding clone 9C.  
 PN EP435776-A.  
 PD 03-JUL-1991.  
 PA (SNFI-) SANOFI SA.  
 PA (SNFI-) ELP SANOFI.  
 Query Match  
 Best Local Similarity 100.0%; DB 2; Length 1013;  
 RESULT 1378  
 ID ADJ45542 standard; cDNA; 1022 BP.  
 DE cDNA encoding LXR-ligand induced transcript seq id 73.  
 PN US2004023276-A1.  
 PD 05-FEB-2004.  
 PA (WARD-) WARD T R.  
 PA (MAOM-) MAO M.  
 PA (LINS-) LINSLEY P S.  
 PA (LUND-) LUND E.  
 Query Match  
 Best Local Similarity 100.0%; DB 12; Length 1022;  
 RESULT 1379  
 ID AAX30155 standard; DNA; 1032 BP.  
 DE Human secreted protein gene 11.  
 PN WO9910363-A1.  
 PD 04-MAR-1999.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 100.0%; DB 2; Length 1032;  
 RESULT 1380  
 ID ADP04740 standard; cDNA; 1052 BP.  
 DE Sea squirt cDNA with tissue specific expression in development Seq 335.  
 PN JP2004057129-A.  
 PD 26-FEB-2004.  
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 Query Match  
 Best Local Similarity 100.0%; DB 12; Length 1052;  
 RESULT 1381  
 ID ADR65755 standard; cDNA; 1063 BP.  
 DE Cotton cDNA sequence, SEQ ID 6536.  
 PN US2004181830-A1.

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PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 13; Length 1063;
  100.0%; Pred. No. 3.5e-05;
RESULT 1382
ID ABN98364 standard; DNA; 1072 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 132.
PD US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANYI/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYI/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 6; Length 1072;
  100.0%; Pred. No. 3.4e-05;
RESULT 1383
ID ADJ80201 standard; cDNA; 1103 BP.
DE Novel human nucleic acid-associated protein coding sequence #19.
PD WO2003038052-A2.
PD 08-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 10; Length 1103;
  100.0%; Pred. No. 3.4e-05;
RESULT 1384
ID AAV34315 standard; DNA; 1114 BP.
DE Human secreted protein gene 5 clone HELDY41.
PD WO9840483-A2.
PD 17-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 2; Length 1114;
  100.0%; Pred. No. 3.4e-05;
RESULT 1385
ID AAD44666 standard; cDNA; 1114 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HELDY41, SEQ ID NO:41.
PD US200207287-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYI/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 6; Length 1114;
  100.0%; Pred. No. 3.4e-05;
RESULT 1386
ID AAD44884 standard; cDNA; 1114 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HELDY41, SEQ ID NO:41.
PD US2002076756-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYI/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 6; Length 1114;
  100.0%; Pred. No. 3.4e-05;
RESULT 1387
ID ACC00855 standard; cDNA; 1130 BP.
DE Zea mays oil trait related cDNA sequence SEQ ID NO:500.
PD WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 8; Length 1130;
  100.0%; Pred. No. 3.4e-05;
RESULT 1390
ID AAT39050 standard; cDNA; 1174 BP.
DE cDNA encoding cellulytic enzyme #4 of the invention.
PD WO9629397-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYI/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 12; Length 1114;
  100.0%; Pred. No. 3.4e-05;
RESULT 1389
ID ACC00855 standard; cDNA; 1130 BP.
DE Zea mays oil trait related cDNA sequence SEQ ID NO:500.
PD WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 8; Length 1130;
  100.0%; Pred. No. 3.4e-05;
RESULT 1390
ID AAT39050 standard; cDNA; 1174 BP.
DE cDNA encoding cellulytic enzyme #4 of the invention.
PD WO9629397-A1.

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PD 26-SEP-1996.  
PA (NOVO ) NOVO-NORDISK AS.  
Query Match 1.5%; Score 52; DB 2; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
RESULT 1391  
ID AAV3096 standard; cDNA; 1174 BP.  
DE Monocomponent endoglucanase encoding cDNA.  
PN EP843041-A1.  
PD 20-MAY-1998.  
PA (NOVO ) NOVO-NORDISK AS.  
Query Match 1.5%; Score 52; DB 2; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
RESULT 1392  
ID ADP73934 standard; DNA; 1174 BP.  
DE DNA encoding the Thielavia terrestris cellulase protein SeqID 3.  
PN WO2004053039-A2.  
PD 24-JUN-2004.  
PA (NOVO ) NOVOZYMES AS.  
Query Match 1.5%; Score 52; DB 12; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
RESULT 1393  
ID AAX07565 standard; cDNA; 1230 BP.  
DE Homo sapiens fetal kidney clone AK296 secreted protein gene.  
PN WO9900405-A1.  
PD 07-JAN-1999.  
PA (GENY ) GENETICS INST INC.  
Query Match 1.5%; Score 52; DB 2; Length 1230;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
RESULT 1394  
ID AAH25190 standard; cDNA; 1231 BP.  
DE Nucleotide sequence of a human transferrin.  
PN WO200146254-A1.  
PD 28-JUN-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 4; Length 1231;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
RESULT 1395  
ID AAA40490 standard; cDNA; 1248 BP.  
DE Human fetal kidney cDNA fragment AK296\_li.  
PN WO200037630-A1.  
PD 29-JUN-2000.  
PA (GENY ) GENETICS INST INC.  
Query Match 1.5%; Score 52; DB 3; Length 1248;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
RESULT 1396  
ID AAA53975 standard; cDNA; 1291 BP.  
DE TRIB-AP53 tumour suppressor gene.  
PN WO200055178-A1.  
PD 21-SEP-2000.  
PA (EXEL-) EXELIXIS INC.  
Query Match 1.5%; Score 52; DB 3; Length 1291;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
RESULT 1397  
ID ACC00641 standard; cDNA; 1301 BP.  
DE Zea mays oil trait related cDNA sequence SEQ ID NO:31.  
PN WO2003002751-A2.  
PD 09-JAN-2003.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 1.5%; Score 52; DB 8; Length 1301;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
RESULT 1398  
ID ABQ54352 standard; cDNA; 1319 BP.  
DE Human ovarian antigen HNOF50 cDNA, SEQ ID NO:232.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 6; Length 1319;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
RESULT 1399  
ID AAC78172 standard; cDNA; 1334 BP.  
DE Human cancer associated gene sequence SEQ ID NO:566.  
PN WO200055350-A1.

PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 3; Length 1334;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
RESULT 1400  
ID AAF21860 standard; DNA; 1336 BP.  
DE Human breast and ovarian cancer associated antigen gene SEQ ID 247.  
PN WO200055173-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 3; Length 1336;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
RESULT 1401  
ID ADI42533 standard; DNA; 1338 BP.  
DE Plant transcription factor polynucleotide #631.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER/) SHERMAN B K.  
PA (RIEC/) RIECHMANN J L.  
PA (JIAN/) JIANG C.  
PA (HEAR/) HEARD J E.  
PA (HAAK/) HAAKE V.  
PA (CREE/) CREELMAN R A.  
PA (RATC/) RATCLIFFE O.  
PA (ADAM/) ADAM L J.  
PA (KEDD/) KEDDIE J.  
PA (BROU/) BROUN P E.  
PA (PILG/) PILGRIM M L.  
PA (DUBE/) DUBELL A N.  
PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
Query Match 1.5%; Score 52; DB 12; Length 1338;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
RESULT 1402  
ID ADO02862 standard; cDNA; 1338 BP.  
DE Soybean orthologue of Thalecress transcription factor, cDNA #139.  
PN US2004045049-A1.  
PD 04-MAR-2004.  
PA (ZHAN/) ZHANG J.  
PA (FROM/) FROMM M E.  
PA (HEAR/) HEARD J E.  
PA (RIEC/) RIECHMANN J L.  
PA (ADAM/) ADAM L J.  
PA (BROU/) BROUN P E.  
PA (PINE/) PINEDA O.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J S.  
PA (YUGG/) YU G.  
PA (JIAN/) JIANG C.  
PA (SAMA/) SAMAHA R S.  
PA (PILG/) PILGRIM M L.  
PA (CREE/) CREELMAN R A.  
PA (DUBE/) DUBELL A N.  
PA (RATC/) RATCLIFFE O.  
PA (KUMI/) KUMIMOTO R.  
PA (SHER/) SHERMAN B K.  
Query Match 1.5%; Score 52; DB 12; Length 1338;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
RESULT 1403  
ID AAB05201 standard; cDNA; 1439 BP.  
DE Human secreted protein-encoding gene 23 cDNA clone H15BL03, SEQ ID NO:91.  
PN WO200134769-A2.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 4; Length 1439;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1404  
ID ADR63648 standard; cDNA; 1449 BP.  
DE Cotton cDNA sequence, SEQ ID 4429.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.

PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 1.5%; Score 52; DB 13; Length 1449;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1405  
ID ACN92580 standard; DNA; 1453 BP.  
DE Breast cancer related marker, seq id 13730.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.5%; Score 52; DB 11; Length 1453;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1406  
ID ABX92051 standard; cDNA; 1457 BP.  
DE Lung specific nucleic acid (LSNA) #93.  
PN WO200268633-A2.  
PD 06-SEP-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 1.5%; Score 52; DB 6; Length 1457;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1407  
ID AAS27566 standard; cDNA; 1462 BP.  
DE cDNA encoding novel signal transduction pathway protein, Seq ID 601.  
PN WO200154733-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 4; Length 1462;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1408  
ID ADB93744 standard; cDNA; 1462 BP.  
DE Human cDNA encoding a novel protein #591.  
PN US2002168711-A1.  
PD 14-NOV-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 1.5%; Score 52; DB 10; Length 1462;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1409  
ID ACC62522 standard; cDNA; 1479 BP.  
DE Human secreted protein #48 coding sequence SEQ ID 58.  
PN WO200299066-A2.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 8; Length 1479;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1410  
ID AAX84967 standard; DNA; 1494 BP.  
DE Human secreted protein gene No. 35.  
PN WO9924836-A1.  
PD 20-MAY-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 2; Length 1494;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1411  
ID ADA39887 standard; cDNA; 1494 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 8; Length 1494;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1412  
ID ACD18893 standard; cDNA; 1494 BP.  
DE Novel human secreted protein cDNA #35.  
PN US2003028003-A1.  
PD 06-FEB-2003.  
PA (FENG/) FENG P.  
PA (RUBE/) RUBEN S M.  
PA (EBNE/) EBNER R. S.  
PA (OLSE/) OLSEN H S.  
PA (NIJU/) NI J.  
Query Match 1.5%; Score 52; DB 6; Length 1612;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1413  
ID ADA56077 standard; DNA; 1494 BP.  
DE Gene encoding human secreted protein #256.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 10; Length 1494;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1414  
ID ADG78284 standard; cDNA; 1494 BP.  
DE Human secreted protein cDNA #35.  
PN US2003211472-A1.  
PD 13-NOV-2003.  
PA (FENG/) FENG P.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (EBNE/) EBNER R. S.  
PA (OLSE/) OLSEN H S.  
PA (NIJU/) NI J.  
PA (WEIY/) WEI Y.  
PA (SOPP/) SOPPET D R.  
PA (MOOR/) MOORE P A.  
PA (KYAW/) KYAW H.  
PA (LAPL/) LAPLEUR D W.  
PA (SHIY/) SHI Y.  
PA (JANA/) JANAT F.  
PA (ENDR/) ENDRESS G A.  
PA (CART/) CARTER K C.  
PA (BIRS/) BIRSE C E.  
Query Match 1.5%; Score 52; DB 8; Length 1494;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1415  
ID ADN60575 standard; cDNA; 1494 BP.  
DE Human secreted polynucleotide #35.  
PN US2004038277-A1.  
PD 26-FEB-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 12; Length 1494;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1416  
ID AAA27985 standard; cDNA; 1495 BP.  
DE Corn CCR4 transcription factor nucleotide sequence #2.  
PN WO200032783-A1.  
PD 08-JUN-2000.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 1.5%; Score 52; DB 3; Length 1495;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1417  
ID AAC59407 standard; cDNA; 1576 BP.  
DE Human secreted protein cDNA #16.  
PN WO200056765-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 3; Length 1576;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
RESULT 1418  
ID ABL90003 standard; cDNA; 1612 BP.  
DE Human polynucleotide SEQ ID NO 565.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 6; Length 1612;



Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1419  
ID AAC76111 standard; cDNA; 1644 BP.  
DE Human ORFX ORF1666 polynucleotide sequence SEQ ID NO:3331.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.5%; Score 52; DB 3; Length 1644;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1420  
ID ADO22714 standard; DNA; 1661 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5534.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.5%; Score 52; DB 12; Length 1661;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1421  
ID AAL60889 standard; cDNA; 1673 BP.  
DE Human placental protein 11 splice variant (plap11) cDNA.  
PN WO2003046180-A2.  
PD 05-JUN-2003.  
PA (GSET) GENSET SA.  
Query Match 1.5%; Score 52; DB 9; Length 1673;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1422  
ID AAC98165 standard; cDNA; 1689 BP.  
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:175.  
PN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.5%; Score 52; DB 3; Length 1689;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1423  
ID AAZ34311 standard; cDNA; 1738 BP.  
DE Human PRO213-1 nucleotide sequence.  
PN WO9946281-A2.  
PD 16-SEP-1999.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 2; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1424  
ID AAC78585 standard; cDNA; 1738 BP.  
DE Human PRO213-1 nucleotide sequence SEQ ID NO:505.  
PN WO200053756-A2.  
PD 14-SEP-2000.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 3; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1425  
ID AAA75702 standard; cDNA; 1738 BP.  
DE cDNA clone DNA30943-1163 encoding a PRO213 polypeptide.  
PN WO200053752-A2.  
PD 14-SEP-2000.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 3; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1426  
ID AAC58226 standard; cDNA; 1738 BP.  
DE Human PRO213 nucleotide sequence SEQ ID NO:3.  
PN WO200053754-A1.  
PD 14-SEP-2000.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 3; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1427  
ID ACA63879 standard; cDNA; 1738 BP.  
DE Novel human secreted and transmembrane protein PRO213-1 cDNA.  
PN US2002192706-A1.  
PD 19-DEC-2002.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 8; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1428  
ID ACA72043 standard; cDNA; 1738 BP.  
DE Human secreted and transmembrane PRO polypeptide #33 cDNA.  
PN US2002177553-A1.  
PD 28-NOV-2002.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 8; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1429  
ID ABX92683 standard; cDNA; 1738 BP.  
DE cDNA encoding human PRO213-1 polypeptide.  
PN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 8; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1430  
ID ACA66424 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO213-1.  
PN US2003004102-A1.  
PD 02-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 8; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1431  
ID ADA25044 standard; cDNA; 1738 BP.  
DE Novel human secreted and transmembrane protein PRO213-1 cDNA.  
PN US2003050241-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 9; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1432  
ID ACD30025 standard; cDNA; 1738 BP.  
DE Novel human secreted and transmembrane protein PRO213-1 cDNA.  
PN US2003050240-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 9; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1433  
ID ADA12705 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO213-1.  
PN US2003055216-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 9; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1434  
ID ACD29440 standard; cDNA; 1738 BP.  
DE Novel human secreted and transmembrane polypeptide cDNA #128.  
PN US2003049633-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 9; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1435  
ID ADB74011 standard; cDNA; 1738 BP.  
DE Human PRO polynucleotide sequence #128.  
PN US2003045462-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1436  
ID ADB76727 standard; cDNA; 1738 BP.  
DE Human PRO polynucleotide sequence #128.  
PN US2003083248-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1437  
ID ADC44153 standard; cDNA; 1738 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003054986-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1438  
ID ADC61913 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003049684-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1439  
ID ADC63877 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003054405-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1440  
ID ADC66977 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003060406-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1441  
ID ADC69101 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003064407-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1442  
ID ADC63161 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003068648-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1443  
ID ADC68226 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003069178-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1444  
ID ADC41546 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1445  
ID ADC67601 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1446  
ID ADC62537 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003216561-A1.

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PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1447  
ID ADC42170 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1448  
ID ADE49539 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1449  
ID ADE35593 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1450  
ID ADE16707 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1451  
ID ADD73322 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003203436-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1452  
ID ADD72680 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003194781-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1453  
ID ADE17331 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003203433-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1454  
ID ADF47345 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003195333-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 10; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1455  
ID ADG53102 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003216561-A1.

PD 20-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 10; Length 1738;  
RESULT 1456  
ID ADG60422 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003206915-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 10; Length 1738;  
RESULT 1457  
ID ADI61182 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003077700-A1.  
PD 24-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 10; Length 1738;  
RESULT 1458  
ID ACD42844 standard; cDNA; 1738 BP.  
DE Novel human secreted and transmembrane protein PRO213-1 cDNA.  
PN US2003050239-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 10; Length 1738;  
RESULT 1459  
ID ADE48839 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003104536-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;  
RESULT 1460  
ID ADE89940 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003130181-A1.  
PD 10-JUL-2003.  
PA (ASHK/) ASHKENAZI A J.  
PA (BAKE/) BAKER K P.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GIRM/) GIRMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (KUOS/) KUO S S.  
PA (NAPI/) NAPIER M A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (SHEL/) SHELTON D L.  
PA (STEW/) STEWART T A.  
PA (TUNA/) TUNAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;  
RESULT 1461  
ID ADF61580 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.

PN US2003195345-A1.  
PD 16-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;  
RESULT 1462  
ID ADF40272 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003198994-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;  
RESULT 1463  
ID ADF46068 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003195148-A1.  
PD 16-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;  
RESULT 1464  
ID ADF24464 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003204055-A1.  
PD 30-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;  
RESULT 1465  
ID ADF40896 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003199021-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;  
RESULT 1466  
ID ADF23840 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003203402-A1.  
PD 30-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;  
RESULT 1467  
ID ADF33823 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003194780-A1.  
PD 16-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;  
RESULT 1468  
ID ADF27290 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003199436-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;  
RESULT 1469  
ID ADF27926 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003199437-A1.  
PD 23-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;  
RESULT 1470  
ID ADF41520 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003199435-A1.

PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1471  
ID ADF33199 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003211091-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1472  
ID ADF25565 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003211092-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1473  
ID ADF26666 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003199674-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1474  
ID ADF34455 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003194410-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1475  
ID ADF46692 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003195344-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1476  
ID ADG50678 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003207803-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1477  
ID ADG50054 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1478  
ID ADG51926 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1479  
ID ADG49430 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003216305-A1.  
PD 20-NOV-2003.

PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1480  
ID ADG48806 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2003216560-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1481  
ID ADG51302 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2004005312-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1482  
ID ADG59246 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2004005657-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1483  
ID ADG62702 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2004006219-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1484  
ID ADH25727 standard; cDNA; 1738 BP.  
DE Human neurotrophin homologue related nucleotide sequence SEQ ID NO:505.  
PN EP1386931-A1.  
PD 04-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1485  
ID ADM17504 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2004048332-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1486  
ID ADL07338 standard; cDNA; 1738 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.  
PN US2004063921-A1.  
PD 01-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1487  
ID ADT92579 standard; cDNA; 1738 BP.  
DE Human PRO213-1 cDNA sequence.  
PN AU2002330288-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 1.5%; Score 52; DB 12; Length 1738;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
RESULT 1488  
ID AAZ33891 standard; cDNA; 1743 BP.  
DE Human PRO213 nucleotide sequence.  
PN WO9946281-A2.  
PD 16-SEP-1999.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 1.5%; Score 52; DB 2; Length 1743;  
RESULT 1489  
ID AAC78458 standard; cDNA; 1743 BP.  
DE Human PRO213 (UNQ187) nucleotide sequence SEQ ID NO:1.  
PN WO200053756-A2.  
PD 14-SEP-2000.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 3; Length 1743;  
RESULT 1490  
ID ABL98258 standard; cDNA; 1743 BP.  
DE Human PRO1449 cDNA sequence SEQ ID NO:373.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 6; Length 1743;  
RESULT 1491  
ID AAL44159 standard; DNA; 1743 BP.  
DE Beta vulgaris dihydroorotase gene sequence.  
PN WO200252012-A2.  
PD 04-JUL-2002.  
PA (CROP-) CROPDISEIGN NV.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 6; Length 1743;  
RESULT 1492  
ID ABL95747 standard; cDNA; 1743 BP.  
DE Human angiogenesis related cDNA PRO1449 SEQ ID NO: 373.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 6; Length 1743;  
RESULT 1493  
ID ACA63459 standard; cDNA; 1743 BP.  
DE Novel human secreted and transmembrane protein PRO213 cDNA.  
PN US2002192706-A1.  
PD 19-DEC-2002.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 8; Length 1743;  
RESULT 1494  
ID ACA71623 standard; cDNA; 1743 BP.  
DE Human secreted and transmembrane polypeptide PRO213 cDNA.  
PN US200217553-A1.  
PD 28-NOV-2002.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 8; Length 1743;  
RESULT 1495  
ID ABX92263 standard; cDNA; 1743 BP.  
DE cDNA encoding human PRO213 polypeptide.  
PN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 8; Length 1743;  
RESULT 1496  
ID ACA66004 standard; cDNA; 1743 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO213.  
PN US2003004102-A1.  
PD 02-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 8; Length 1743;  
RESULT 1497  
ID ADA24540 standard; cDNA; 1743 BP.  
DE Novel human secreted and transmembrane protein PRO213 cDNA.  
PN US2003050241-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 9; Length 1743;  
RESULT 1498  
ID ACD29605 standard; cDNA; 1743 BP.  
DE Novel human secreted and transmembrane protein PRO213 cDNA.  
PN US2003050240-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 9; Length 1743;  
RESULT 1499  
ID ADA12201 standard; cDNA; 1743 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO213.  
PN US2003055216-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 9; Length 1743;  
RESULT 1500  
ID ACD29020 standard; cDNA; 1743 BP.  
DE Novel human secreted and transmembrane polypeptide cDNA #1.  
PN US2003049633-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 1.5%; Score 52; DB 9; Length 1743;

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OM nucleic - nucleic search, using sw model

Run on: March 28, 2005, 20:57:22 ; Search time 591 Seconds  
(without alignments)  
9911.795 Million cell updates/sec

Title: US-10-015-388A-53

Perfect score: 3580

Sequence: 1 gacgggtccctccggtcgtg.....cagcaacagccggtgcgctt 3580

Scoring table: OXFGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database :

Issued Patents\_NA.\*  
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2: /cgm2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgm2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgm2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgm2\_6/ptodata/1/ina/PTCUS\_COMB.seq.\*  
6: /cgm2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	995	27.8	2240	4	US-09-799-451-571
2	201	5.6	2223	4	US-09-799-451-817
3	64	1.8	601	4	US-09-949-016-144142
4	64	1.8	601	4	US-09-949-016-144200
5	64	1.8	601	4	US-09-949-016-144258
6	64	1.8	601	4	US-09-949-016-144316
7	64	1.8	53394	4	US-09-949-016-15817
8	64	1.8	53394	4	US-09-949-016-15818
9	64	1.8	53394	4	US-09-949-016-15819
10	64	1.8	53394	4	US-09-949-016-15820
11	62	1.7	134890	3	US-09-949-016-15602
12	59	1.6	1193	3	US-09-372-422A-23
13	59	1.6	194537	4	US-09-949-016-15828
14	59	1.6	201529	3	US-09-949-016-12740
15	58	1.6	7023	3	US-09-313-300-6
16	58	1.6	1023	4	US-09-229-947-38
17	58	1.6	1048	4	US-09-489-847-38
18	58	1.6	1057	4	US-09-716-129-16
19	58	1.6	1361	4	US-09-489-847-64
20	58	1.6	1375	4	US-09-489-847-120
21	58	1.6	1376	4	US-09-489-847-66
22	58	1.6	1411	3	US-08-964-127-5
23	58	1.6	1411	3	US-09-496-692-5
24	58	1.6	1411	4	US-10-000-273-5
25	58	1.6	1618	4	US-09-800-729-29
26	58	1.6	1733	3	US-09-073-569-1
27	58	1.6	1810	4	US-09-369-247-11

1.6	2038	4	US-09-885-723-6	Sequence 6, Appl
1.6	2202	4	US-09-396-149-3	Sequence 3, Appl
1.6	2205	3	US-08-888-077A-41	Sequence 41, Appl
1.6	2369	4	US-09-057-996-13	Sequence 13, Appl
1.6	2719	3	US-08-706-216-1	Sequence 1, Appl
1.6	2719	4	US-09-650-284B-1	Sequence 1, Appl
1.6	2964	4	US-09-578-063-25	Sequence 25, Appl
1.6	1069	3	US-09-372-422A-7	Sequence 7, Appl
1.6	1315	3	US-09-164-193-1	Sequence 1, Appl
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1.6	1375	3	US-09-372-422A-37	Sequence 37, Appl
1.6	1454	3	US-09-372-422A-19	Sequence 19, Appl
1.6	1485	3	US-09-372-422A-39	Sequence 39, Appl
1.6	2235	4	US-09-569-804-20	Sequence 20, Appl
1.6	2581	4	US-09-369-247-51	Sequence 51, Appl
1.6	2584	4	US-09-716-129-47	Sequence 47, Appl
1.6	487	3	US-09-257-179-22	Sequence 22, Appl
1.6	601	4	US-09-949-016-154650	Sequence 154650, Appl
1.6	931	4	US-09-482-273-31	Sequence 31, Appl
1.6	1138	4	US-09-800-729-44	Sequence 44, Appl
1.6	1722	4	US-09-482-273-102	Sequence 102, Appl
1.6	1825	3	US-09-461-697-75	Sequence 75, Appl
1.6	275110	4	US-09-949-016-12706	Sequence 12706, A
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1.5	131	4	US-09-513-999C-18724	Sequence 18724, A
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1.5	601	4	US-09-949-016-48621	Sequence 48621, A
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1.5	1723	4	US-10-012-542-98	Sequence 98, Appl
1.5	1723	4	US-10-115-123-98	Sequence 98, Appl
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1.5	3214	1	US-08-484-106-17	Sequence 17, Appl
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1.5	247299	4	US-09-949-016-17590	Sequence 17590, A
1.5	144	1	US-08-702-344-26	Sequence 26, Appl
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1.5	396	4	US-09-825-294-10	Sequence 10, Appl
1.5	396	4	US-09-970-966-10	Sequence 10, Appl
1.5	826	3	US-09-227-357-102	Sequence 102, Appl
1.5	1034	4	US-09-311-021-105	Sequence 105, Appl
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1.5	1223	3	US-09-154-874-4	Sequence 4, Appl
1.5	1223	4	US-08-931-668-4	Sequence 4, Appl
1.5	1223	4	US-09-468-175-4	Sequence 4, Appl
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1.5	1977	3	US-09-227-357-83	Sequence 83, Appl
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1.5	396	4	US-09-825-294-42	Sequence 42, Appl
1.5	396	4	US-09-970-966-42	Sequence 42, Appl
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1.5	399	1	US-08-298-687A-13	Sequence 13, Appl
1.5	399	1	US-08-530-787-12	Sequence 12, Appl
1.5	399	1	US-08-298-829-13	Sequence 13, Appl
1.5	399	2	US-08-787-335-12	Sequence 12, Appl
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1.5	687	4	US-09-774-639-45	Sequence 45, Appl
1.5	991	3	US-08-924-747-25	Sequence 25, Appl
1.5	991	3	US-09-247-373B-25	Sequence 25, Appl



C 101	52	1.5	991	3	US-09-296-715-25	Sequence 25, Appl	174	51	1.4	13193	4	US-09-949-016-17515	Sequence 17515, A
C 102	52	1.5	1013	1	US-07-920-519-30	Sequence 30, Appl	175	51	1.4	14079	4	US-09-949-016-11993	Sequence 11993, A
C 103	52	1.5	1013	1	US-08-086-410-23	Sequence 30, Appl	176	50	1.4	80	3	US-09-284-627-15	Sequence 15, Appl
C 104	52	1.5	1013	1	US-08-314-586-30	Sequence 30, Appl	C 177	50	1.4	85	4	US-09-621-976-14741	Sequence 14741, A
C 105	52	1.5	1032	3	US-09-257-179-21	Sequence 21, Appl	C 178	50	1.4	100	4	US-09-621-976-12774	Sequence 12774, A
C 106	52	1.5	1114	3	US-09-152-060-41	Sequence 41, Appl	C 179	50	1.4	105	3	US-09-284-627-23	Sequence 23, Appl
C 107	52	1.5	1114	3	US-08-872-437-1	Sequence 1, Appl	C 180	50	1.4	138	4	US-09-621-976-9595	Sequence 9595, Ap
C 108	52	1.5	1174	2	US-08-651-136C-11	Sequence 11, Appl	C 181	50	1.4	141	4	US-09-621-976-8705	Sequence 8705, Ap
C 109	52	1.5	1174	3	US-09-229-911A-11	Sequence 11, Appl	C 182	50	1.4	185	4	US-09-513-999C-24016	Sequence 24016, A
C 110	52	1.5	1291	4	US-09-524-101D-5	Sequence 5, Appl	C 183	50	1.4	188	4	US-09-621-976-10364	Sequence 10364, A
C 111	52	1.5	1842	4	US-09-482-273-90	Sequence 90, Appl	C 184	50	1.4	194	4	US-09-621-976-15317	Sequence 15317, A
C 112	52	1.5	1976	4	US-09-920-759-10	Sequence 10, Appl	C 185	50	1.4	222	3	US-08-481-190-15	Sequence 15, Appl
C 113	52	1.5	2202	3	US-09-388-743-1	Sequence 1, Appl	C 186	50	1.4	222	5	PCT-US93-00869-15	Sequence 15, Appl
C 114	52	1.5	2202	4	US-10-044-543-1	Sequence 1, Appl	C 187	50	1.4	223	3	US-09-792-594-11	Sequence 11, Appl
C 115	52	1.5	6200	3	US-09-439-923-1	Sequence 1, Appl	C 188	50	1.4	231	4	US-09-621-976-16456	Sequence 16456, A
C 116	52	1.5	6200	4	US-09-711-202A-1	Sequence 1, Appl	C 189	50	1.4	323	4	US-09-621-976-10374	Sequence 10374, A
C 117	52	1.5	6200	4	US-09-711-205A-1	Sequence 1, Appl	C 190	50	1.4	323	4	US-09-621-976-16131	Sequence 16131, A
C 118	51	1.4	94	3	US-09-404-879A-261	Sequence 261, App	C 191	50	1.4	391	4	US-09-621-976-18858	Sequence 18858, A
C 119	51	1.4	94	4	US-09-338-933-261	Sequence 261, App	C 192	50	1.4	396	4	US-09-640-173-33	Sequence 33, Appl
C 120	51	1.4	94	4	US-09-215-681-261	Sequence 261, App	C 193	50	1.4	396	4	US-09-640-173-57	Sequence 57, Appl
C 121	51	1.4	94	4	US-09-215-003A-261	Sequence 261, App	C 194	50	1.4	396	4	US-09-713-550-33	Sequence 33, Appl
C 122	51	1.4	94	4	US-09-667-857-261	Sequence 261, App	C 195	50	1.4	396	4	US-09-713-550-57	Sequence 57, Appl
C 123	51	1.4	195	4	US-09-621-976-15314	Sequence 15314, A	C 196	50	1.4	396	4	US-09-825-294-33	Sequence 33, Appl
C 124	51	1.4	215	4	US-09-621-976-15321	Sequence 15321, A	C 197	50	1.4	396	4	US-09-825-294-57	Sequence 57, Appl
C 125	51	1.4	279	4	US-09-621-976-10220	Sequence 10220, A	C 198	50	1.4	396	4	US-09-970-966-33	Sequence 33, Appl
C 126	51	1.4	299	4	US-09-621-976-10211	Sequence 10211, A	C 199	50	1.4	396	4	US-09-970-966-57	Sequence 57, Appl
C 127	51	1.4	327	4	US-09-621-976-16141	Sequence 16141, A	C 200	50	1.4	458	1	US-08-524-757-1	Sequence 1, Appl
C 128	51	1.4	341	4	US-09-621-976-16135	Sequence 16135, A	C 201	50	1.4	540	1	US-09-313-434C-15	Sequence 15, Appl
C 129	51	1.4	347	4	US-09-621-976-16136	Sequence 16136, A	C 202	50	1.4	568	1	US-08-582-257-20	Sequence 20, Appl
C 130	51	1.4	351	4	US-09-621-976-16140	Sequence 16140, A	C 203	50	1.4	572	2	US-08-582-238-20	Sequence 20, Appl
C 131	51	1.4	554	4	US-09-696-169A-14	Sequence 14, Appl	C 204	50	1.4	601	4	US-09-949-016-109436	Sequence 109436, A
C 132	51	1.4	569	4	US-09-461-325-44	Sequence 44, Appl	C 205	50	1.4	601	4	US-09-949-016-39835	Sequence 39835, A
C 133	51	1.4	569	4	US-10-012-542-44	Sequence 44, Appl	C 206	50	1.4	601	4	US-09-949-016-39836	Sequence 39836, A
C 134	51	1.4	569	4	US-10-115-123-44	Sequence 44, Appl	C 207	50	1.4	601	4	US-09-949-016-39837	Sequence 39837, A
C 135	51	1.4	685	3	US-09-227-357-66	Sequence 66, Appl	C 208	50	1.4	601	4	US-09-949-016-75976	Sequence 75976, A
C 136	51	1.4	711	4	US-09-621-976-17854	Sequence 17854, A	C 209	50	1.4	601	4	US-09-949-016-109435	Sequence 109435, A
C 137	51	1.4	763	4	US-09-743-207-3	Sequence 3, Appl	C 210	50	1.4	601	4	US-09-949-016-109436	Sequence 109436, A
C 138	51	1.4	966	1	US-08-514-014-7	Sequence 7, Appl	C 211	50	1.4	601	4	US-09-949-016-109437	Sequence 109437, A
C 139	51	1.4	966	2	US-08-833-823-7	Sequence 7, Appl	C 212	50	1.4	601	4	US-09-949-016-112463	Sequence 112463, A
C 140	51	1.4	976	2	US-08-504-459-9	Sequence 9, Appl	C 213	50	1.4	601	4	US-09-949-016-116454	Sequence 116454, A
C 141	51	1.4	1117	3	US-09-247-373B-33	Sequence 33, Appl	C 214	50	1.4	601	4	US-09-949-016-123892	Sequence 123892, A
C 142	51	1.4	1632	4	US-09-912-628-3	Sequence 3, Appl	C 215	50	1.4	601	4	US-09-949-016-123892	Sequence 123892, A
C 143	51	1.4	1738	2	US-08-379-482A-2	Sequence 2, Appl	C 216	50	1.4	601	4	US-09-949-016-160858	Sequence 160858, A
C 144	51	1.4	1886	4	US-09-594-506-31	Sequence 31, Appl	C 217	50	1.4	601	4	US-09-949-016-160859	Sequence 160859, A
C 145	51	1.4	1910	2	US-09-009-438-1	Sequence 1, Appl	C 218	50	1.4	601	4	US-09-949-016-160860	Sequence 160860, A
C 146	51	1.4	1910	3	US-09-207-493-1	Sequence 1, Appl	C 219	50	1.4	601	4	US-09-949-016-164245	Sequence 164245, A
C 147	51	1.4	1949	4	US-09-461-325-26	Sequence 26, Appl	C 220	50	1.4	675	4	US-09-621-976-2461	Sequence 2461, Ap
C 148	51	1.4	1949	4	US-10-012-542-26	Sequence 26, Appl	C 221	50	1.4	831	4	US-09-904-615-25	Sequence 25, Appl
C 149	51	1.4	1949	4	US-10-115-123-26	Sequence 26, Appl	C 222	50	1.4	844	4	US-09-904-615-25	Sequence 25, Appl
C 150	51	1.4	1951	3	US-09-465-558-35	Sequence 35, Appl	C 223	50	1.4	911	2	US-08-924-759-9	Sequence 9, Appl
C 151	51	1.4	1963	4	US-09-482-273-91	Sequence 91, Appl	C 224	50	1.4	911	3	US-09-248-335-9	Sequence 9, Appl
C 152	51	1.4	1965	4	US-09-482-273-27	Sequence 27, Appl	C 225	50	1.4	981	4	US-09-780-717-4	Sequence 4, Appl
C 153	51	1.4	2060	4	US-09-345-473E-5	Sequence 5, Appl	C 226	50	1.4	997	4	US-09-907-794A-376	Sequence 376, App
C 154	51	1.4	2065	3	US-09-370-473-5	Sequence 5, Appl	C 227	50	1.4	997	4	US-09-905-125A-376	Sequence 376, App
C 155	51	1.4	2409	3	US-09-293-322C-8	Sequence 8, Appl	C 228	50	1.4	997	4	US-09-905-125A-376	Sequence 376, App
C 156	51	1.4	2409	4	US-09-839-497A-8	Sequence 8, Appl	C 229	50	1.4	997	4	US-09-906-700-376	Sequence 376, App
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C 158	51	1.4	2589	4	US-09-689-366-1	Sequence 1, Appl	C 231	50	1.4	997	4	US-09-904-903A-376	Sequence 376, App
C 159	51	1.4	2589	5	PCT-US96-12860-1	Sequence 1, Appl	C 232	50	1.4	997	4	US-09-905-064-376	Sequence 376, App
C 160	51	1.4	2790	3	US-08-800-291B-1	Sequence 1, Appl	C 233	50	1.4	997	4	US-09-905-381A-376	Sequence 376, App
C 161	51	1.4	2821	4	US-09-702-705-1669	Sequence 1669, Ap	C 234	50	1.4	997	4	US-09-906-618-376	Sequence 376, App
C 162	51	1.4	2821	4	US-09-736-457-1669	Sequence 1669, Ap	C 235	50	1.4	1001	2	US-08-728-259A-10	Sequence 10, Appl
C 163	51	1.4	2821	4	US-09-671-325-1669	Sequence 1669, Ap	C 236	50	1.4	1001	2	US-08-473-486-10	Sequence 10, Appl
C 164	51	1.4	2821	4	US-09-658-824-1669	Sequence 1669, Ap	C 237	50	1.4	1024	4	US-09-328-475C-50	Sequence 50, Appl
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C 166	51	1.4	3394	3	US-09-344-441-2	Sequence 2, Appl	C 239	50	1.4	1051	3	US-09-248-335-67	Sequence 67, Appl
C 167	51	1.4	4055	4	US-09-620-312D-706	Sequence 706, App	C 240	50	1.4	1051	4	US-09-358-055B-10	Sequence 10, Appl
C 168	51	1.4	4064	4	US-09-873-737A-3	Sequence 3, Appl	C 241	50	1.4	1051	4	US-09-893-238-10	Sequence 10, Appl
C 169	51	1.4	4235	4	US-09-174-937-4	Sequence 4, Appl	C 242	50	1.4	1100	3	US-09-248-335-67	Sequence 67, Appl
C 170	51	1.4	8643	4	US-10-029-907-4	Sequence 4, Appl	C 243	50	1.4	1100	3	US-09-248-335-53	Sequence 53, Appl
C 171	51	1.4	9589	1	US-07-925-695-1	Sequence 1, Appl	C 244	50	1.4	1118	3	US-07-861-458C-4	Sequence 4, Appl
C 172	51	1.4	9589	1	US-07-925-695-1	Sequence 1, Appl	C 245	50	1.4	1118	3	US-09-614-912-181	Sequence 181, App
C 173	51	1.4	9589	1	US-07-925-695-2	Sequence 2, Appl	C 246	50	1.4	1123	3	US-09-152-060-15	Sequence 15, Appl

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C 248	50	1.4	1133	4	US-10-282-048-1	Sequence 1, Appli	C 321	50	1.4	2230	3	US-08-378-313-24	Sequence 24, Appli
C 249	50	1.4	1159	3	US-09-410-464-14	Sequence 14, Appli	C 322	50	1.4	2239	3	US-09-196-390-1	Sequence 1, Appli
C 250	50	1.4	1172	1	US-07-945-288-9	Sequence 9, Appli	C 323	50	1.4	2239	4	US-09-952-677-1	Sequence 1, Appli
C 251	50	1.4	1172	1	US-08-462-831-9	Sequence 9, Appli	C 324	50	1.4	2287	4	US-09-949-016-134	Sequence 134, App
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C 255	50	1.4	1242	3	US-08-413-974-1	Sequence 1, Appli	C 328	50	1.4	2301	3	US-09-232-201-8	Sequence 8, Appli
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C 260	50	1.4	1249	4	US-09-461-325-128	Sequence 128, App	C 333	50	1.4	2378	3	US-08-802-805D-20	Sequence 20, Appli
C 261	50	1.4	1249	4	US-10-012-542-128	Sequence 128, App	C 334	50	1.4	2378	4	US-08-860-370-1	Sequence 1, Appli
C 262	50	1.4	1249	4	US-10-115-123-128	Sequence 128, App	C 335	50	1.4	2550	6	5258287-23	Patent No. 5258287
C 263	50	1.4	1260	4	US-09-461-325-93	Sequence 93, Appli	C 336	50	1.4	2550	6	5258287-23	Patent No. 5258287
C 264	50	1.4	1260	4	US-10-012-542-93	Sequence 93, Appli	C 337	50	1.4	2625	4	US-09-270-767-10080	Sequence 10080, A
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C 276	50	1.4	1546	4	US-09-901-151-1	Sequence 1, Appli	C 349	50	1.4	4239	4	US-09-815-048-1	Sequence 1, Appli
C 277	50	1.4	1604	1	US-09-403-463A-5	Sequence 5, Appli	C 350	50	1.4	5503	2	US-08-726-012B-1	Sequence 1, Appli
C 278	50	1.4	1604	1	US-08-665-966-9	Sequence 9, Appli	C 351	50	1.4	5503	4	US-09-023-655-989	Sequence 989, App
C 279	50	1.4	1604	3	US-09-041-780-9	Sequence 9, Appli	C 352	50	1.4	6065	4	US-09-800-729-35	Sequence 35, Appli
C 280	50	1.4	1696	4	US-09-835-811-1	Sequence 1, Appli	C 353	50	1.4	7724	4	US-08-486-049-1	Sequence 1, Appli
C 281	50	1.4	1700	2	US-08-897-340-4	Sequence 4, Appli	C 354	50	1.4	7855	4	US-09-949-016-12431	Sequence 12431, A
C 282	50	1.4	1700	3	US-09-252-329-4	Sequence 4, Appli	C 355	50	1.4	10106	4	US-09-949-016-14269	Sequence 14269, A
C 283	50	1.4	1728	3	US-08-985-925-7	Sequence 7, Appli	C 356	50	1.4	10106	4	US-09-949-016-14270	Sequence 14270, A
C 284	50	1.4	1748	4	US-09-546-049-7	Sequence 7, Appli	C 357	50	1.4	10106	4	US-09-949-016-14271	Sequence 14271, A
C 285	50	1.4	1748	4	US-08-635-967-1	Sequence 1, Appli	C 358	50	1.4	10442	4	US-09-596-141C-1	Sequence 1, Appli
C 286	50	1.4	1771	4	US-09-907-794A-158	Sequence 158, App	C 359	50	1.4	10442	4	US-09-595-526C-1	Sequence 1, Appli
C 287	50	1.4	1771	4	US-09-866-028-35	Sequence 36, Appli	C 360	50	1.4	10474	4	US-09-596-141C-7	Sequence 7, Appli
C 288	50	1.4	1771	4	US-09-905-125A-158	Sequence 158, App	C 361	50	1.4	10474	4	US-09-596-141C-9	Sequence 9, Appli
C 289	50	1.4	1771	4	US-09-902-775A-158	Sequence 158, App	C 362	50	1.4	10474	4	US-09-595-526C-7	Sequence 7, Appli
C 290	50	1.4	1771	4	US-09-906-700-158	Sequence 158, App	C 363	50	1.4	10474	4	US-09-595-526C-9	Sequence 9, Appli
C 291	50	1.4	1771	4	US-09-944-457-36	Sequence 36, Appli	C 364	50	1.4	13584	4	US-09-991-258-17	Sequence 17, Appli
C 292	50	1.4	1771	4	US-09-903-603A-158	Sequence 158, App	C 365	50	1.4	15450	4	US-09-470-661A-1	Sequence 1, Appli
C 293	50	1.4	1771	4	US-09-904-920A-158	Sequence 158, App	C 366	50	1.4	21360	4	US-09-949-016-12857	Sequence 12857, A
C 294	50	1.4	1771	4	US-09-905-064-158	Sequence 158, App	C 367	50	1.4	21361	4	US-09-949-016-16245	Sequence 16245, A
C 295	50	1.4	1771	4	US-09-905-381A-158	Sequence 158, App	C 368	50	1.4	24395	4	US-09-949-016-14758	Sequence 14758, A
C 296	50	1.4	1771	4	US-09-906-618-158	Sequence 158, App	C 369	50	1.4	24405	4	US-09-949-016-12040	Sequence 12040, A
C 297	50	1.4	1781	3	US-09-499-302A-1	Sequence 1, Appli	C 370	50	1.4	24405	4	US-09-949-016-17346	Sequence 17346, A
C 298	50	1.4	1813	5	PCT-US94-12883-3	Sequence 3, Appli	C 371	50	1.4	25969	4	US-09-949-016-13397	Sequence 13397, A
C 299	50	1.4	1883	4	US-09-419-679-13	Sequence 13, Appli	C 372	50	1.4	26760	4	US-09-949-016-15894	Sequence 15894, A
C 300	50	1.4	1898	1	US-08-342-411A-1	Sequence 1, Appli	C 373	50	1.4	27670	4	US-09-949-016-16226	Sequence 16226, A
C 301	50	1.4	1937	4	US-09-647-143-1	Sequence 1, Appli	C 374	50	1.4	31739	4	US-09-949-016-16226	Sequence 16226, A
C 302	50	1.4	1998	3	US-09-232-200-68	Sequence 68, Appli	C 375	50	1.4	36858	4	US-09-949-016-17406	Sequence 17406, A
C 303	50	1.4	1998	3	US-09-232-197-68	Sequence 68, Appli	C 376	50	1.4	36858	4	US-09-949-016-17095	Sequence 17095, A
C 304	50	1.4	1998	3	US-09-232-201-68	Sequence 68, Appli	C 377	50	1.4	39823	4	US-09-949-016-15700	Sequence 15700, A
C 305	50	1.4	1998	4	US-09-232-195-68	Sequence 68, Appli	C 378	50	1.4	42428	4	US-09-949-016-13879	Sequence 13879, A
C 306	50	1.4	2083	4	US-09-716-129-41	Sequence 41, Appli	C 379	50	1.4	44249	4	US-09-949-016-14485	Sequence 14485, A
C 307	50	1.4	2087	3	US-09-232-191-6	Sequence 6, Appli	C 380	50	1.4	44249	4	US-09-949-016-14491	Sequence 14491, A
C 308	50	1.4	2087	3	US-09-232-200-6	Sequence 6, Appli	C 381	50	1.4	45314	4	US-09-949-016-14927	Sequence 14927, A
C 309	50	1.4	2087	3	US-09-232-197-6	Sequence 6, Appli	C 382	50	1.4	50797	4	US-09-949-016-16346	Sequence 16346, A
C 310	50	1.4	2087	3	US-09-232-201-6	Sequence 6, Appli	C 383	50	1.4	50797	4	US-09-949-016-16347	Sequence 16347, A
C 311	50	1.4	2087	4	US-09-232-195-6	Sequence 6, Appli	C 384	50	1.4	51822	4	US-09-949-016-15233	Sequence 15233, A
C 312	50	1.4	2206	4	US-09-907-794A-3	Sequence 3, Appli	C 385	50	1.4	52636	4	US-09-949-016-14839	Sequence 14839, A
C 313	50	1.4	2206	4	US-09-905-125A-3	Sequence 3, Appli	C 386	50	1.4	52598	4	US-09-491-356C-1	Sequence 1, Appli
C 314	50	1.4	2206	4	US-09-902-775A-3	Sequence 3, Appli	C 387	50	1.4	57811	4	US-09-949-016-13192	Sequence 13192, A
C 315	50	1.4	2206	4	US-09-906-700-3	Sequence 3, Appli	C 388	50	1.4	60304	4	US-09-949-016-12218	Sequence 12218, A
C 316	50	1.4	2206	4	US-09-903-603A-3	Sequence 3, Appli	C 389	50	1.4	60304	4	US-09-949-016-15791	Sequence 15791, A
C 317	50	1.4	2206	4	US-09-904-920A-3	Sequence 3, Appli	C 390	50	1.4	62804	3	US-08-800-960-3	Sequence 3, Appli
C 318	50	1.4	2206	4	US-09-909-064-3	Sequence 3, Appli	C 391	50	1.4	62804	3	US-10-096-960-3	Sequence 3, Appli
C 319	50	1.4	2206	4	US-09-905-381A-3	Sequence 3, Appli	C 392	50	1.4	63183	4	US-09-949-016-13047	Sequence 13047, A

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394	50	1.4	71863	4	US-09-949-016-15112	Sequence 15112, A	c 467	49	1.4	229	4	US-09-702-1705-195	Sequence 195, App
395	50	1.4	84462	4	US-09-949-016-15116	Sequence 15116, A	c 468	49	1.4	229	4	US-09-736-457-195	Sequence 195, App
396	50	1.4	84425	4	US-09-949-016-17402	Sequence 17402, A	c 469	49	1.4	229	4	US-09-614-1248-195	Sequence 195, App
397	50	1.4	117391	4	US-09-949-016-13945	Sequence 13945, A	c 470	49	1.4	229	4	US-09-671-325-195	Sequence 195, App
398	50	1.4	118382	4	US-09-949-016-15996	Sequence 15996, A	c 471	49	1.4	229	4	US-09-589-184-195	Sequence 195, App
399	50	1.4	118382	4	US-09-949-016-15997	Sequence 15997, A	c 472	49	1.4	229	4	US-09-658-824-195	Sequence 195, App
400	50	1.4	118382	4	US-09-949-016-13763	Sequence 13763, A	c 473	49	1.4	240	1	US-08-628-417-6	Sequence 6, Appli
401	50	1.4	137226	4	US-09-949-016-17030	Sequence 17030, A	c 474	49	1.4	255	4	US-09-621-976-9406	Sequence 9406, Ap
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403	50	1.4	139552	4	US-09-949-016-15300	Sequence 15300, A	c 476	49	1.4	271	2	US-08-731-272A-29	Sequence 29, Appl
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405	50	1.4	151261	4	US-09-949-016-13242	Sequence 13242, A	c 478	49	1.4	289	1	US-08-341-568-3	Sequence 3, Appli
406	50	1.4	157822	4	US-09-949-016-16723	Sequence 16723, A	c 479	49	1.4	289	2	US-08-911-020-3	Sequence 3, Appli
407	50	1.4	192506	4	US-09-949-016-15830	Sequence 15830, A	c 480	49	1.4	289	4	US-09-621-976-10009	Sequence 10009, A
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409	50	1.4	276237	4	US-09-949-016-17504	Sequence 17504, A	c 482	49	1.4	351	4	US-09-621-976-15134	Sequence 15134, A
410	50	1.4	636591	4	US-09-949-016-11808	Sequence 11808, A	c 483	49	1.4	358	4	US-09-621-976-927	Sequence 927, App
411	49	1.4	636591	4	US-09-949-016-13388	Sequence 13388, A	c 484	49	1.4	382	4	US-09-621-976-18855	Sequence 18855, A
412	49	1.4	57	4	US-09-621-976-12150	Sequence 12150, A	c 485	49	1.4	396	4	US-09-640-173-18	Sequence 18, Appl
413	49	1.4	61	3	US-09-457-959-7	Sequence 7, Appli	c 486	49	1.4	396	4	US-09-640-173-53	Sequence 53, Appl
414	49	1.4	61	4	US-10-079-178-7	Sequence 7, Appli	c 487	49	1.4	396	4	US-09-713-550-18	Sequence 18, Appl
415	49	1.4	63	4	US-09-621-976-12231	Sequence 12231, A	c 488	49	1.4	396	4	US-09-713-550-53	Sequence 53, Appl
416	49	1.4	63	4	US-09-621-976-13480	Sequence 13480, A	c 489	49	1.4	396	4	US-09-825-294-18	Sequence 18, Appl
417	49	1.4	68	4	US-09-621-976-11613	Sequence 11613, A	c 490	49	1.4	396	4	US-09-825-294-53	Sequence 53, Appl
418	49	1.4	68	4	US-09-621-976-11912	Sequence 11912, A	c 491	49	1.4	396	4	US-09-970-966-18	Sequence 18, Appl
419	49	1.4	69	4	US-09-621-976-12005	Sequence 12005, A	c 492	49	1.4	396	4	US-09-970-966-53	Sequence 53, Appl
420	49	1.4	70	4	US-09-621-976-12006	Sequence 12006, A	c 493	49	1.4	444	3	US-08-688-988-44	Sequence 44, Appl
421	49	1.4	75	4	US-09-621-976-13579	Sequence 13579, A	c 494	49	1.4	472	4	US-08-270-767-12212	Sequence 97, Appl
422	49	1.4	76	4	US-09-621-976-12456	Sequence 12456, A	c 495	49	1.4	474	3	US-08-516-859A-97	Sequence 97, Appl
423	49	1.4	81	4	US-09-513-999C-17324	Sequence 17324, A	c 496	49	1.4	474	3	US-09-586-472-97	Sequence 97, Appl
424	49	1.4	90	3	US-09-065-058-16	Sequence 16, Appl	c 497	49	1.4	474	3	US-09-528-706-97	Sequence 97, Appl
425	49	1.4	91	3	US-09-404-879A-201	Sequence 201, App	c 498	49	1.4	495	4	US-09-220-132-186	Sequence 186, App
426	49	1.4	91	4	US-09-338-933-201	Sequence 201, App	c 499	49	1.4	530	4	US-09-461-325-28	Sequence 28, Appl
427	49	1.4	91	4	US-09-215-681-201	Sequence 201, App	c 500	49	1.4	530	4	US-10-012-542-28	Sequence 28, Appl
428	49	1.4	91	4	US-09-621-976-14925	Sequence 14925, A	c 501	49	1.4	530	4	US-10-115-123-28	Sequence 28, Appl
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430	49	1.4	91	4	US-09-667-857-201	Sequence 201, App	c 503	49	1.4	570	1	US-08-298-687A-10	Sequence 10, Appl
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432	49	1.4	100	3	US-09-062-451-30	Sequence 30, Appl	c 505	49	1.4	601	4	US-09-949-016-164575	Sequence 164575,
433	49	1.4	100	3	US-09-598-326-30	Sequence 30, Appl	c 506	49	1.4	601	4	US-08-530-797-9	Sequence 9, Appli
434	49	1.4	100	4	US-09-289-198-30	Sequence 30, Appl	c 507	49	1.4	609	2	US-08-787-335-9	Sequence 9, Appli
435	49	1.4	100	4	US-09-429-755-30	Sequence 30, Appl	c 508	49	1.4	612	4	US-09-902-540-1357	Sequence 1357, Ap
436	49	1.4	100	4	US-09-699-295-30	Sequence 30, Appl	c 509	49	1.4	615	3	US-09-105-542A-2	Sequence 2, Appli
437	49	1.4	101	3	US-09-404-879A-293	Sequence 293, App	c 510	49	1.4	647	4	US-09-495-050A-54	Sequence 54, Appl
438	49	1.4	101	4	US-09-338-933-293	Sequence 293, App	c 511	49	1.4	728	3	US-09-091-037-5	Sequence 5, Appli
439	49	1.4	101	4	US-09-215-681-293	Sequence 293, App	c 512	49	1.4	740	2	US-08-713-000-8	Sequence 8, Appli
440	49	1.4	101	4	US-09-667-857-293	Sequence 293, App	c 513	49	1.4	740	2	US-08-975-316-8	Sequence 8, Appli
441	49	1.4	101	4	US-09-216-003A-293	Sequence 293, App	c 514	49	1.4	740	2	US-09-211-710-8	Sequence 8, Appli
442	49	1.4	102	4	US-09-621-976-11436	Sequence 11436, A	c 515	49	1.4	740	3	US-09-615-192A-8	Sequence 8, Appli
443	49	1.4	110	4	US-09-621-976-12025	Sequence 12025, A	c 516	49	1.4	740	3	US-09-169-789-8	Sequence 8, Appli
444	49	1.4	120	1	US-08-153-058B-28	Sequence 28, Appl	c 517	49	1.4	740	3	US-09-615-192A-8	Sequence 8, Appli
445	49	1.4	120	1	US-08-060-952C-44	Sequence 44, Appl	c 518	49	1.4	741	2	US-08-975-316-8	Sequence 58, Appl
446	49	1.4	120	2	US-08-151-477A-28	Sequence 28, Appl	c 519	49	1.4	741	3	US-09-615-192A-58	Sequence 58, Appl
447	49	1.4	120	3	US-08-819-867-58	Sequence 58, Appl	c 520	49	1.4	741	3	US-09-621-976-1894	Sequence 1894, Ap
448	49	1.4	120	3	US-08-464-011B-44	Sequence 44, Appl	c 521	49	1.4	741	4	US-09-169-789-58	Sequence 58, Appl
449	49	1.4	120	4	US-09-378-535-58	Sequence 58, Appl	c 522	49	1.4	746	3	US-09-013-810-1	Sequence 1, Appli
450	49	1.4	130	4	US-09-621-976-12892	Sequence 12892, A	c 523	49	1.4	748	1	US-08-361-457B-3	Sequence 3, Appli
451	49	1.4	140	1	US-08-628-417-5	Sequence 5, Appli	c 524	49	1.4	748	1	US-08-484-332C-3	Sequence 3, Appli
452	49	1.4	140	4	US-09-621-976-17449	Sequence 17449, A	c 525	49	1.4	785	4	US-09-518-036-9	Sequence 9, Appli
453	49	1.4	141	3	US-08-737-078A-1	Sequence 1, Appli	c 526	49	1.4	785	4	US-10-279-130-9	Sequence 9, Appli
454	49	1.4	141	5	PCT-US94-04706-1	Sequence 1, Appli	c 527	49	1.4	788	3	US-09-615-192A-96	Sequence 96, Appl
455	49	1.4	145	4	US-09-621-976-16688	Sequence 16688, A	c 528	49	1.4	788	4	US-09-169-789-96	Sequence 96, Appl
456	49	1.4	145	4	US-09-621-976-16691	Sequence 16691, A	c 529	49	1.4	795	1	US-09-270-767-14068	Sequence 14068, A
457	49	1.4	146	4	US-09-621-976-16686	Sequence 16686, A	c 530	49	1.4	796	1	US-08-104-073-2	Sequence 2, Appli
458	49	1.4	146	4	US-09-621-976-16695	Sequence 16695, A	c 531	49	1.4	812	3	US-09-091-097-7	Sequence 7, Appli
459	49	1.4	148	4	US-09-621-976-17447	Sequence 17447, A	c 532	49	1.4	812	3	US-09-621-976-2725	Sequence 2725, Ap
460	49	1.4	148	4	US-09-621-976-17450	Sequence 17450, A	c 533	49	1.4	890	4	Sequence 21, Appl	
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462	49	1.4	184	4	US-09-621-976-12893	Sequence 12893, A	c 535	49	1.4	958	2	US-08-757-046A-5	Sequence 5, Appli
463	49	1.4	194	4	US-09-621-976-9596	Sequence 9596, App	c 536	49	1.4	958	3	US-09-447-208-5	Sequence 5, Appli
464	49	1.4	214	4	US-09-621-976-9843	Sequence 9843, Ap	c 537	49	1.4	958	3	US-09-135-988-5	Sequence 5, Appli
465	49	1.4	216	1	US-08-686-878A-34	Sequence 34, Appl	c 538	49	1.4	958	3	US-09-277-716-5	Sequence 5, Appli

C 539	49	1.4	958	3	US-08-597-274A-5	Sequence 5, Appli	C 612	49	1.4	1776	3	US-09-258-016-10	Sequence 10, Appl
C 540	49	1.4	958	3	US-08-908-909-5	Sequence 5, Appli	C 613	49	1.4	1776	3	US-09-257-825B-10	Sequence 10, Appl
C 541	49	1.4	958	3	US-09-609-161B-5	Sequence 5, Appli	C 614	49	1.4	1781	4	US-09-818-512-1	Sequence 1, Appl
C 542	49	1.4	958	3	US-08-990-103-5	Sequence 5, Appli	C 615	49	1.4	1801	4	US-09-709-103-3	Sequence 3, Appli
C 543	49	1.4	958	4	US-09-746-485A-5	Sequence 5, Appli	C 616	49	1.4	1801	4	US-09-439-410A-3	Sequence 3, Appli
C 544	49	1.4	958	4	US-10-126-135-5	Sequence 5, Appli	C 617	49	1.4	1817	1	US-08-473-981A-5	Sequence 5, Appli
C 545	49	1.4	958	4	US-10-126-798-5	Sequence 5, Appli	C 618	49	1.4	1817	2	US-08-474-087-5	Sequence 5, Appli
C 546	49	1.4	958	4	US-10-126-777-5	Sequence 5, Appli	C 619	49	1.4	1835	3	US-09-485-549-1	Sequence 1, Appli
C 547	49	1.4	959	4	US-09-578-030-5	Sequence 5, Appli	C 620	49	1.4	1858	2	US-08-909-965C-11	Sequence 11, Appl
C 548	49	1.4	971	4	US-09-800-729-49	Sequence 49, Appl	C 621	49	1.4	1872	3	US-09-801-052-1	Sequence 1, Appli
C 549	49	1.4	1045	1	US-09-270-767-12552	Sequence 12552, A	C 622	49	1.4	1872	4	US-10-020-121-1	Sequence 1, Appli
C 550	49	1.4	1066	1	US-08-157-101A-4	Sequence 4, Appli	C 623	49	1.4	1878	3	US-09-465-558-39	Sequence 39, Appl
C 551	49	1.4	1075	3	US-08-400-006B-6	Sequence 6, Appli	C 624	49	1.4	1921	4	US-09-057-936-7	Sequence 7, Appli
C 552	49	1.4	1091	4	US-09-328-985-1	Sequence 1, Appli	C 625	49	1.4	1931	3	US-09-019-942-2	Sequence 2, Appli
C 553	49	1.4	1134	3	US-09-248-335-29	Sequence 29, Appl	C 626	49	1.4	1931	3	US-09-099-041A-1	Sequence 1, Appli
C 554	49	1.4	1141	4	US-09-800-729-78	Sequence 78, Appl	C 627	49	1.4	1931	3	US-09-245-281-1	Sequence 1, Appli
C 555	49	1.4	1154	3	US-08-651-136C-7	Sequence 7, Appli	C 628	49	1.4	1931	3	US-09-470-271-2	Sequence 2, Appli
C 556	49	1.4	1154	3	US-09-229-911A-7	Sequence 7, Appli	C 629	49	1.4	1931	3	US-09-207-359B-1	Sequence 1, Appli
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C 560	49	1.4	1198	3	US-09-248-335-27	Sequence 27, Appl	C 633	49	1.4	1934	3	US-08-776-844-1	Sequence 1, Appli
C 561	49	1.4	1201	4	US-09-461-325-36	Sequence 36, Appl	C 634	49	1.4	1934	4	US-09-909-325-1	Sequence 1, Appli
C 562	49	1.4	1201	4	US-10-012-542-36	Sequence 36, Appl	C 635	49	1.4	1934	4	US-09-909-326-1	Sequence 1, Appli
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C 568	49	1.4	1378	3	US-09-149-476-208	Sequence 208, App	C 641	49	1.4	2203	4	US-10-224-562-1	Sequence 1, Appli
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C 576	49	1.4	1487	4	US-09-723-971-3	Sequence 3, Appli	C 649	49	1.4	2331	4	US-09-866-028-54	Sequence 54, Appl
C 577	49	1.4	1490	2	US-08-553-367A-5	Sequence 5, Appli	C 650	49	1.4	2331	4	US-09-944-457-54	Sequence 54, Appl
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C 583	49	1.4	1522	3	US-09-413-574-1	Sequence 1, Appli	C 656	49	1.4	2625	4	US-09-358-055B-18	Sequence 18, Appl
C 584	49	1.4	1540	3	US-08-977-001-2	Sequence 2, Appli	C 657	49	1.4	2625	4	US-09-893-238-18	Sequence 18, Appl
C 585	49	1.4	1540	4	US-09-560-761B-3	Sequence 3, Appli	C 658	49	1.4	2671	6	5168051-9	Patent No. 5168051
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C 590	49	1.4	1578	3	US-09-664-800-1	Sequence 1, Appli	C 663	49	1.4	2760	1	US-08-101-593-1	Sequence 1, Appli
C 591	49	1.4	1578	3	US-09-665-309-1	Sequence 1, Appli	C 664	49	1.4	2760	1	US-08-101-593-3	Sequence 3, Appli
C 592	49	1.4	1578	3	US-09-664-800-1	Sequence 1, Appli	C 665	49	1.4	2836	3	US-08-747-221B-24	Sequence 24, Appl
C 593	49	1.4	1641	1	US-08-300-903A-8	Sequence 8, Appli	C 666	49	1.4	2836	3	US-08-747-221B-26	Sequence 26, Appl
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C 595	49	1.4	1641	4	US-10-385-072-8	Sequence 8, Appli	C 668	49	1.4	2836	3	US-09-005-051-26	Sequence 26, Appl
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C 597	49	1.4	1662	4	US-09-668-097A-13	Sequence 13, Appl	C 670	49	1.4	2836	2	US-09-403-942P-26	Sequence 26, Appl
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C 599	49	1.4	1670	3	US-08-829-839-1	Sequence 1, Appli	C 672	49	1.4	2908	3	US-09-930-181-1	Sequence 1, Appli
C 600	49	1.4	1670	4	US-09-624-594-1	Sequence 1, Appli	C 673	49	1.4	3001	4	US-09-539-333D-153	Sequence 153, App
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C 603	49	1.4	1736	3	US-09-672-785-3	Sequence 3, Appli	C 676	49	1.4	3350	2	US-08-288-065A-1	Sequence 1, Appli
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C 605	49	1.4	1736	3	US-09-182-816-24	Sequence 24, Appl	C 678	49	1.4	3350	5	PCT-US95-10245-1	Sequence 1, Appli
C 606	49	1.4	1736	3	US-09-471-528-22	Sequence 22, Appl	C 679	49	1.4	3375	3	US-09-511-625B-67	Sequence 67, Appl
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C 609	49	1.4	1736	3	US-09-634-530-24	Sequence 24, Appl	C 682	49	1.4	3437	2	US-10-208-349-17	Sequence 17, Appl
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C 611	49	1.4	1776	3	US-08-655-352-10	Sequence 10, Appl	C 684	49	1.4	3715	4	US-09-234-245-1	Sequence 1, Appli

C 685	49	1.4	3975	4	US-09-270-767-3	Sequence 3, Appli	c 758	48	1.3	72	4	US-09-621-976-14815	Sequence 14815, A
C 686	49	1.4	5173	1	US-08-242-677-1	Sequence 1, Appli	c 759	48	1.3	72	4	US-09-621-976-14842	Sequence 14842, A
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C 689	49	1.4	6409	4	US-10-159-151-1	Sequence 1, Appli	c 762	48	1.3	73	4	US-09-621-976-14729	Sequence 14729, A
C 690	49	1.4	7286	3	US-09-331-581-3	Sequence 3, Appli	c 763	48	1.3	74	4	US-09-621-976-14963	Sequence 14963, A
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C 693	49	1.4	12379	4	US-09-991-258-14	Sequence 14, Appli	c 766	48	1.3	76	4	US-09-621-976-14831	Sequence 14831, A
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C 696	49	1.4	64190	4	US-09-949-016-14712	Sequence 14712, A	c 769	48	1.3	77	4	US-09-621-976-14176	Sequence 14176, A
C 697	49	1.4	64190	4	US-09-949-016-14713	Sequence 14713, A	c 770	48	1.3	77	4	US-08-781-986A-2883	Sequence 2883, Ap
C 698	49	1.4	76401	4	US-09-949-016-17153	Sequence 17153, A	c 771	48	1.3	78	4	US-09-621-976-14824	Sequence 14824, A
C 699	49	1.4	84171	4	US-09-949-016-16356	Sequence 16356, A	c 772	48	1.3	78	4	US-09-621-976-15092	Sequence 15092, A
C 700	49	1.4	86877	4	US-09-949-016-15491	Sequence 15491, A	c 773	48	1.3	79	4	US-09-621-976-15090	Sequence 15090, A
C 701	49	1.4	86877	4	US-09-949-016-15492	Sequence 15492, A	c 774	48	1.3	80	1	US-07-920-281C-25	Sequence 25, Appli
C 702	49	1.4	192506	4	US-09-949-016-15830	Sequence 15830, A	c 775	48	1.3	80	3	US-08-466-277-25	Sequence 25, Appli
C 703	49	1.4	193303	4	US-09-497-855A-37	Sequence 37, Appli	c 776	48	1.3	80	4	US-09-688-842-25	Sequence 25, Appli
C 704	49	1.4	193303	4	US-09-497-855A-44	Sequence 44, Appli	c 777	48	1.3	81	4	US-09-621-976-12198	Sequence 12198, A
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C 706	48	1.3	50	4	US-09-621-976-14715	Sequence 14715, A	c 779	48	1.3	81	4	US-09-621-976-13601	Sequence 13601, A
C 707	48	1.3	52	4	US-09-621-976-13828	Sequence 13828, A	c 780	48	1.3	82	4	US-09-621-976-11689	Sequence 11689, A
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C 710	48	1.3	54	4	US-09-621-976-14994	Sequence 14994, A	c 783	48	1.3	82	4	US-09-621-976-11888	Sequence 11888, A
C 711	48	1.3	55	4	US-09-621-976-14535	Sequence 14535, A	c 784	48	1.3	82	4	US-09-621-976-11944	Sequence 11944, A
C 712	48	1.3	55	4	US-09-621-976-14800	Sequence 14800, A	c 785	48	1.3	82	4	US-09-621-976-11949	Sequence 11949, A
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C 717	48	1.3	57	4	US-09-621-976-13937	Sequence 13937, A	c 790	48	1.3	82	4	US-09-621-976-12131	Sequence 12131, A
C 718	48	1.3	58	4	US-09-621-976-8006	Sequence 8006, Ap	c 791	48	1.3	82	4	US-09-621-976-12137	Sequence 12137, A
C 719	48	1.3	58	4	US-09-621-976-14827	Sequence 14827, A	c 792	48	1.3	82	4	US-09-621-976-12322	Sequence 12322, A
C 720	48	1.3	59	4	US-09-621-976-13084	Sequence 13084, A	c 793	48	1.3	82	4	US-09-621-976-12434	Sequence 12434, A
C 721	48	1.3	59	4	US-09-621-976-13752	Sequence 13752, A	c 794	48	1.3	82	4	US-09-621-976-13499	Sequence 13499, A
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C 724	48	1.3	60	4	US-09-621-976-13761	Sequence 13761, A	c 797	48	1.3	83	4	US-09-621-976-12175	Sequence 12175, A
C 725	48	1.3	60	4	US-09-621-976-14742	Sequence 14742, A	c 798	48	1.3	83	4	US-09-621-976-12195	Sequence 12195, A
C 726	48	1.3	60	4	US-09-621-976-14884	Sequence 14884, A	c 799	48	1.3	83	4	US-09-621-976-12429	Sequence 12429, A
C 727	48	1.3	60	4	US-10-079-178-8	Sequence 8, Appli	c 800	48	1.3	83	4	US-09-621-976-12450	Sequence 12450, A
C 728	48	1.3	61	4	US-09-621-976-11967	Sequence 11967, A	c 801	48	1.3	83	4	US-09-621-976-14751	Sequence 14751, A
C 729	48	1.3	61	4	US-09-621-976-1680	Sequence 1480, A	c 802	48	1.3	83	4	US-09-621-976-14959	Sequence 14959, A
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C 731	48	1.3	61	4	US-09-621-976-14754	Sequence 14754, A	c 804	48	1.3	84	1	US-08-738-367-3	Sequence 3, Appli
C 732	48	1.3	61	4	US-09-621-976-14799	Sequence 14799, A	c 805	48	1.3	84	4	US-09-621-976-14571	Sequence 14571, A
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C 734	48	1.3	61	4	US-09-621-976-14948	Sequence 14948, A	c 807	48	1.3	85	4	US-09-621-976-13395	Sequence 13395, A
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C 741	48	1.3	64	4	US-09-621-976-14858	Sequence 14858, A	c 814	48	1.3	90	1	US-08-677-944-2	Sequence 2, Appli
C 742	48	1.3	65	4	US-09-621-976-14743	Sequence 14743, A	c 815	48	1.3	90	3	US-09-254-048A-1	Sequence 1, Appli
C 743	48	1.3	65	4	US-09-621-976-14853	Sequence 14853, A	c 816	48	1.3	90	3	US-09-921-203-1	Sequence 1, Appli
C 744	48	1.3	66	4	US-09-621-976-12404	Sequence 12404, A	c 817	48	1.3	90	4	US-09-816-089A-2	Sequence 2, Appli
C 745	48	1.3	66	4	US-09-621-976-14819	Sequence 14819, A	c 818	48	1.3	90	4	US-10-106-832-1	Sequence 1, Appli
C 746	48	1.3	67	4	US-09-621-976-11909	Sequence 11909, A	c 819	48	1.3	91	4	US-09-621-976-12161	Sequence 12161, A
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C 753	48	1.3	70	4	US-09-621-976-14750	Sequence 14750, A	c 826	48	1.3	98	2	US-08-471-907A-42	Sequence 42, Appli
C 754	48	1.3	71	4	US-09-816-089A-5	Sequence 5, Appli	c 827	48	1.3	98	4	US-09-621-976-11744	Sequence 11744, A
C 755	48	1.3	71	4	US-09-621-976-14905	Sequence 14905, A	c 828	48	1.3	98	4	US-09-621-976-12160	Sequence 12160, A
C 756	48	1.3	72	4	US-09-621-976-9837	Sequence 9837, Ap	c 829	48	1.3	98	4	US-09-621-976-15091	Sequence 15091, A
C 757	48	1.3	72	4	US-09-621-976-10145	Sequence 10145, A	c 830	48	1.3	102	4	US-09-621-976-14804	Sequence 14804, A

C 831	48	1.3	104	4	US-09-621-976-9392	Sequence 9392, Ap	C 904	48	1.3	246	4	US-09-621-976-16288	Sequence 16288, A
C 832	48	1.3	105	2	US-08-735-381-2	Sequence 2, Appl	C 905	48	1.3	249	4	US-09-621-976-1322	Sequence 1322, Ap
C 833	48	1.3	105	3	US-09-183-619-1	Sequence 1, Appl	C 906	48	1.3	249	4	US-09-621-976-16291	Sequence 16291, A
C 834	48	1.3	105	3	US-09-201-674-2	Sequence 2, Appl	C 907	48	1.3	249	4	US-09-621-976-16292	Sequence 16292, A
C 835	48	1.3	105	4	US-09-621-976-13820	Sequence 13820, A	C 908	48	1.3	249	4	US-09-621-976-16292	Sequence 16292, A
C 836	48	1.3	106	4	US-09-621-976-13079	Sequence 12079, A	C 909	48	1.3	250	4	US-09-621-976-18144	Sequence 18144, A
C 837	48	1.3	109	4	US-09-621-976-14592	Sequence 14592, A	C 909	48	1.3	250	4	US-09-621-976-18893	Sequence 18893, A
C 838	48	1.3	111	3	US-09-297-533-23	Sequence 23, Appl	C 910	48	1.3	253	2	US-08-520-678A-25	Sequence 25, Appl
C 839	48	1.3	111	3	US-09-621-976-14677	Sequence 14677, A	C 911	48	1.3	253	2	US-08-897-126-25	Sequence 25, Appl
C 840	48	1.3	117	1	US-08-702-344-3	Sequence 3, Appl	C 912	48	1.3	253	2	US-09-621-976-17799	Sequence 17799, A
C 841	48	1.3	121	3	US-09-297-533-20	Sequence 20, Appl	C 913	48	1.3	257	2	US-08-520-678A-24	Sequence 24, Appl
C 842	48	1.3	123	4	US-09-621-976-12330	Sequence 12330, A	C 914	48	1.3	257	3	US-08-897-126-24	Sequence 24, Appl
C 843	48	1.3	127	4	US-09-621-976-13933	Sequence 13933, A	C 915	48	1.3	259	3	US-09-621-976-16294	Sequence 16294, A
C 844	48	1.3	132	4	US-09-621-976-13992	Sequence 13992, A	C 916	48	1.3	260	2	US-08-520-678A-29	Sequence 29, Appl
C 845	48	1.3	134	4	US-09-621-976-18433	Sequence 18433, A	C 917	48	1.3	260	3	US-08-897-126-29	Sequence 29, Appl
C 846	48	1.3	135	4	US-09-621-976-11087	Sequence 11087, A	C 918	48	1.3	263	3	US-09-091-097-26	Sequence 26, Appl
C 847	48	1.3	137	4	US-09-621-976-18434	Sequence 18434, A	C 919	48	1.3	266	4	US-09-621-976-16813	Sequence 16813, A
C 848	48	1.3	139	4	US-09-621-976-8632	Sequence 8632, Ap	C 920	48	1.3	266	4	US-09-621-976-16936	Sequence 16936, A
C 849	48	1.3	142	4	US-09-621-976-18001	Sequence 18001, A	C 921	48	1.3	270	2	US-08-520-678A-30	Sequence 30, Appl
C 850	48	1.3	146	4	US-09-621-976-8550	Sequence 8550, Ap	C 922	48	1.3	270	3	US-08-897-126-30	Sequence 30, Appl
C 851	48	1.3	146	4	US-09-621-976-16115	Sequence 16115, A	C 923	48	1.3	271	4	US-09-621-976-10380	Sequence 10380, A
C 852	48	1.3	147	4	US-09-621-976-8551	Sequence 8551, Ap	C 924	48	1.3	272	4	US-09-621-976-16932	Sequence 16932, A
C 853	48	1.3	147	4	US-09-621-976-10254	Sequence 10254, A	C 925	48	1.3	272	4	US-09-270-767-11902	Sequence 11902, A
C 854	48	1.3	147	4	US-09-621-976-10283	Sequence 10283, A	C 926	48	1.3	273	4	US-09-809-545A-31	Sequence 31, Appl
C 855	48	1.3	150	4	US-09-621-976-8656	Sequence 8656, Ap	C 927	48	1.3	282	4	US-09-621-976-18648	Sequence 18648, A
C 856	48	1.3	153	4	US-09-621-976-18058	Sequence 18058, A	C 928	48	1.3	283	4	US-09-621-976-16989	Sequence 16989, A
C 857	48	1.3	156	4	US-09-621-976-9095	Sequence 9095, Ap	C 929	48	1.3	289	4	US-09-621-976-15142	Sequence 15142, A
C 858	48	1.3	157	4	US-09-621-976-10271	Sequence 10271, A	C 930	48	1.3	293	4	US-09-621-976-16965	Sequence 16965, A
C 859	48	1.3	157	4	US-09-621-976-16781	Sequence 16781, A	C 931	48	1.3	298	4	US-09-621-976-3871	Sequence 3871, Ap
C 860	48	1.3	159	4	US-09-621-976-11782	Sequence 11782, A	C 932	48	1.3	298	4	US-09-621-976-16226	Sequence 16226, A
C 861	48	1.3	159	4	US-09-621-976-17448	Sequence 17448, A	C 933	48	1.3	304	4	US-09-621-976-16099	Sequence 16099, A
C 862	48	1.3	160	4	US-09-621-976-10335	Sequence 10335, A	C 934	48	1.3	316	4	US-09-513-999C-838	Sequence 838, App
C 863	48	1.3	160	4	US-09-621-976-18071	Sequence 18071, A	C 935	48	1.3	318	4	US-09-621-976-10247	Sequence 10247, A
C 864	48	1.3	162	4	US-09-621-976-18068	Sequence 18068, A	C 936	48	1.3	326	4	US-09-621-976-16024	Sequence 16024, A
C 865	48	1.3	163	4	US-09-621-976-9608	Sequence 9608, Ap	C 937	48	1.3	329	4	US-09-621-976-16012	Sequence 16012, A
C 866	48	1.3	164	4	US-09-621-976-8070	Sequence 8070, Ap	C 938	48	1.3	331	4	US-09-621-976-16100	Sequence 16100, A
C 867	48	1.3	165	4	US-09-621-976-8127	Sequence 8127, Ap	C 939	48	1.3	332	4	US-09-621-976-16031	Sequence 16031, A
C 868	48	1.3	165	4	US-09-621-976-19195	Sequence 19195, A	C 940	48	1.3	332	4	US-09-621-976-16050	Sequence 16050, A
C 869	48	1.3	166	4	US-09-621-976-8651	Sequence 8651, Ap	C 941	48	1.3	332	4	US-09-621-976-16053	Sequence 16053, A
C 870	48	1.3	166	4	US-09-621-976-18390	Sequence 18390, A	C 942	48	1.3	333	4	US-09-621-976-16032	Sequence 16032, A
C 871	48	1.3	166	4	US-09-621-976-11249	Sequence 11249, A	C 943	48	1.3	333	4	US-09-621-976-16045	Sequence 16045, A
C 872	48	1.3	176	4	US-09-621-976-13903	Sequence 13903, A	C 944	48	1.3	334	4	US-09-621-976-16044	Sequence 16044, A
C 873	48	1.3	177	4	US-09-621-976-1047	Sequence 1047, Ap	C 945	48	1.3	334	4	US-09-621-976-16434	Sequence 16434, A
C 874	48	1.3	179	4	US-09-621-976-9575	Sequence 9575, Ap	C 946	48	1.3	335	4	US-09-621-976-16038	Sequence 16038, A
C 875	48	1.3	179	4	US-09-621-976-18054	Sequence 18054, A	C 947	48	1.3	335	4	US-09-621-976-16061	Sequence 16061, A
C 876	48	1.3	182	4	US-09-621-976-16234	Sequence 16234, A	C 948	48	1.3	336	4	US-09-621-976-16013	Sequence 16013, A
C 877	48	1.3	184	4	US-09-513-998C-36135	Sequence 36135, A	C 949	48	1.3	338	4	US-09-621-976-16041	Sequence 16041, A
C 878	48	1.3	185	4	US-09-621-976-18779	Sequence 18779, A	C 950	48	1.3	339	4	US-09-621-976-16015	Sequence 16015, A
C 879	48	1.3	189	4	US-09-621-976-18761	Sequence 18761, A	C 951	48	1.3	341	4	US-09-621-976-11000	Sequence 11000, A
C 880	48	1.3	190	4	US-09-621-976-16784	Sequence 16784, A	C 952	48	1.3	342	4	US-09-270-767-13044	Sequence 13044, A
C 881	48	1.3	193	4	US-09-621-976-10584	Sequence 10584, A	C 953	48	1.3	347	4	US-09-621-976-16026	Sequence 16026, A
C 882	48	1.3	194	4	US-09-621-976-801	Sequence 801, App	C 954	48	1.3	350	4	US-09-621-976-15342	Sequence 15342, A
C 883	48	1.3	196	4	US-09-644-460-40	Sequence 40, Appl	C 955	48	1.3	356	2	US-08-520-678A-22	Sequence 22, Appl
C 884	48	1.3	196	4	US-09-442-054A-42	Sequence 42, Appl	C 956	48	1.3	356	3	US-08-897-126-22	Sequence 22, Appl
C 885	48	1.3	196	4	US-09-442-054A-42	Sequence 42, Appl	C 957	48	1.3	357	4	US-09-621-976-16058	Sequence 16058, A
C 886	48	1.3	204	4	US-09-621-976-1323	Sequence 1323, Ap	C 958	48	1.3	359	4	US-09-621-976-16008	Sequence 16008, A
C 887	48	1.3	204	4	US-09-621-976-16458	Sequence 16458, A	C 959	48	1.3	359	4	US-09-621-976-16019	Sequence 16019, A
C 888	48	1.3	213	4	US-09-621-976-16536	Sequence 16536, A	C 960	48	1.3	362	4	US-09-621-976-16010	Sequence 16010, A
C 889	48	1.3	227	2	US-08-520-678A-28	Sequence 28, Appl	C 961	48	1.3	365	4	US-09-621-976-14699	Sequence 14699, A
C 890	48	1.3	227	3	US-08-897-126-28	Sequence 28, Appl	C 962	48	1.3	365	4	US-09-621-976-16042	Sequence 16042, A
C 891	48	1.3	231	4	US-09-621-976-16317	Sequence 16317, A	C 963	48	1.3	371	4	US-09-621-976-16048	Sequence 16048, A
C 892	48	1.3	232	4	US-09-621-976-16317	Sequence 16317, A	C 964	48	1.3	396	4	US-09-640-173-16	Sequence 16, Appl
C 893	48	1.3	233	4	US-09-621-976-10675	Sequence 10675, A	C 965	48	1.3	396	4	US-09-713-550-16	Sequence 16, Appl
C 894	48	1.3	233	4	US-09-621-976-16559	Sequence 16559, A	C 966	48	1.3	396	4	US-09-825-294-16	Sequence 16, Appl
C 895	48	1.3	234	4	US-09-621-976-16557	Sequence 16557, A	C 967	48	1.3	396	4	US-09-970-966-16	Sequence 16, Appl
C 896	48	1.3	235	4	US-09-621-976-9455	Sequence 9455, Ap	C 968	48	1.3	399	4	US-09-621-976-9484	Sequence 9484, Ap
C 897	48	1.3	235	4	US-09-621-976-16550	Sequence 16550, A	C 969	48	1.3	406	4	US-09-621-976-15107	Sequence 15107, A
C 898	48	1.3	239	4	US-09-621-976-16632	Sequence 16632, A	C 970	48	1.3	427	4	US-09-461-325-107	Sequence 107, App
C 899	48	1.3	240	4	US-09-621-976-1324	Sequence 1324, Ap	C 971	48	1.3	427	4	US-10-012-542-107	Sequence 107, App
C 900	48	1.3	242	4	US-09-621-976-16320	Sequence 16320, A	C 972	48	1.3	427	4	US-10-115-123-107	Sequence 107, App
C 901	48	1.3	242	4	US-09-621-976-16324	Sequence 16324, A	C 973	48	1.3	441	4	US-09-601-537-10	Sequence 10, Appl
C 902	48	1.3	244	4	US-09-621-976-484	Sequence 484, App	C 974	48	1.3	443	4	US-09-621-976-17631	Sequence 17631, A
C 903	48	1.3	246	4	US-09-621-976-13617	Sequence 13617, A	C 975	48	1.3	443	4	US-09-936-885A-1	Sequence 1, Appl
							C 976	48	1.3	467	2	US-08-841-349-18	Sequence 18, Appl



977	48	1.3	467	4	US-09-431-184A-18	Sequence 18, Appl	c1050	48	1.3	773	3	US-09-149-476-20	Sequence 20, Appl
978	48	1.3	470	3	US-09-020-956-102	Sequence 102, App	c1051	48	1.3	780	2	US-08-540-804-36	Sequence 36, Appl
979	48	1.3	470	3	US-09-030-607-102	Sequence 102, App	c1052	48	1.3	780	3	US-08-590-399-36	Sequence 36, Appl
980	48	1.3	470	3	US-09-433-313-102	Sequence 102, App	1053	48	1.3	789	3	US-09-020-956-32	Sequence 32, Appl
981	48	1.3	470	3	US-09-352-616A-102	Sequence 102, App	1054	48	1.3	789	3	US-09-030-607-32	Sequence 32, Appl
982	48	1.3	470	3	US-09-232-149A-102	Sequence 102, App	1055	48	1.3	789	3	US-09-439-313-32	Sequence 32, Appl
983	48	1.3	470	4	US-09-159-812-102	Sequence 102, App	1056	48	1.3	789	3	US-09-352-616A-32	Sequence 32, Appl
984	48	1.3	470	4	US-09-636-215-102	Sequence 102, App	1057	48	1.3	789	3	US-09-232-149A-32	Sequence 32, Appl
985	48	1.3	470	4	US-09-685-166A-102	Sequence 102, App	1058	48	1.3	789	4	US-09-159-812-32	Sequence 32, Appl
986	48	1.3	470	4	US-09-115-453-102	Sequence 102, App	1059	48	1.3	789	4	US-09-636-215-32	Sequence 32, Appl
987	48	1.3	470	4	US-09-688-489-102	Sequence 102, App	1060	48	1.3	789	4	US-09-685-166A-32	Sequence 32, Appl
988	48	1.3	470	4	US-09-679-426-102	Sequence 102, App	1061	48	1.3	789	4	US-09-115-453-32	Sequence 32, Appl
989	48	1.3	470	4	US-09-759-143-102	Sequence 102, App	1062	48	1.3	789	4	US-09-688-489-32	Sequence 32, Appl
990	48	1.3	470	4	US-09-651-236-102	Sequence 102, App	1063	48	1.3	789	4	US-09-679-426-32	Sequence 32, Appl
c 991	48	1.3	491	4	US-09-311-021-191	Sequence 191, App	1064	48	1.3	789	4	US-09-759-143-32	Sequence 32, Appl
c 992	48	1.3	508	4	US-09-621-976-17886	Sequence 17886, A	1065	48	1.3	789	4	US-09-651-236-32	Sequence 32, Appl
993	48	1.3	509	3	US-09-030-607-202	Sequence 202, App	c1066	48	1.3	803	4	US-09-800-729-60	Sequence 60, Appl
994	48	1.3	509	3	US-09-433-313-202	Sequence 202, App	c1067	48	1.3	835	4	US-09-311-021-71	Sequence 71, Appl
995	48	1.3	509	3	US-09-352-616A-202	Sequence 202, App	c1068	48	1.3	857	1	US-08-308-883-1	Sequence 1, Appl
996	48	1.3	509	3	US-09-232-149A-202	Sequence 202, App	c1069	48	1.3	857	1	US-08-730-163-1	Sequence 1, Appl
997	48	1.3	509	4	US-09-159-812-202	Sequence 202, App	c1070	48	1.3	857	3	US-08-256-799-1	Sequence 1, Appl
998	48	1.3	509	4	US-09-636-215-202	Sequence 202, App	c1071	48	1.3	857	3	US-08-462-437-1	Sequence 1, Appl
999	48	1.3	509	4	US-09-685-166A-202	Sequence 202, App	c1072	48	1.3	872	3	US-09-248-335-63	Sequence 63, Appl
1000	48	1.3	509	4	US-09-115-453-202	Sequence 202, App	c1073	48	1.3	873	3	US-09-475-316A-20	Sequence 20, Appl
1001	48	1.3	509	4	US-09-688-489-202	Sequence 202, App	c1074	48	1.3	873	4	US-09-704-640-20	Sequence 20, Appl
1002	48	1.3	509	4	US-09-679-426-202	Sequence 202, App	c1075	48	1.3	879	1	US-08-158-682A-1	Sequence 1, Appl
1003	48	1.3	509	4	US-09-759-143-202	Sequence 202, App	c1076	48	1.3	879	1	US-08-015-203-1	Sequence 1, Appl
1004	48	1.3	509	4	US-09-651-236-202	Sequence 202, App	c1077	48	1.3	882	2	US-08-909-965C-9	Sequence 9, Appl
c1005	48	1.3	536	2	US-08-341-568-1	Sequence 1, Appl	c1078	48	1.3	882	4	US-09-311-021-107	Sequence 107, App
c1006	48	1.3	536	2	US-08-911-020-1	Sequence 1, Appl	c1079	48	1.3	888	3	US-09-188-930-13	Sequence 13, Appl
c1007	48	1.3	550	4	US-09-010-147B-5	Sequence 5, Appl	c1080	48	1.3	940	2	US-09-312-283C-13	Sequence 13, Appl
c1008	48	1.3	552	4	US-09-461-325-111	Sequence 111, App	c1081	48	1.3	941	4	US-09-205-258-186	Sequence 186, App
c1009	48	1.3	552	4	US-10-012-542-111	Sequence 111, App	c1082	48	1.3	949	4	US-09-489-847-35	Sequence 35, Appl
c1010	48	1.3	552	4	US-10-115-123-111	Sequence 111, App	c1083	48	1.3	960	3	US-09-248-335-57	Sequence 57, Appl
c1011	48	1.3	558	4	US-09-043-861-3	Sequence 3, Appl	c1084	48	1.3	972	1	US-07-935-934-1	Sequence 1, Appl
c1012	48	1.3	563	4	US-09-621-976-19183	Sequence 5, Appl	c1085	48	1.3	972	1	US-08-325-743-1	Sequence 1, Appl
c1013	48	1.3	572	3	US-09-343-653-5	Sequence 5, Appl	c1086	48	1.3	972	3	US-09-549-831-5	Sequence 5, Appl
c1014	48	1.3	578	3	US-09-602-877A-95	Sequence 95, Appl	c1087	48	1.3	972	3	US-08-504-459-13	Sequence 13, Appl
c1015	48	1.3	588	4	US-09-205-258-64	Sequence 64, Appl	c1088	48	1.3	985	4	US-09-322-409-25	Sequence 25, Appl
c1016	48	1.3	593	4	US-09-904-615-59	Sequence 59, Appl	c1089	48	1.3	985	4	US-09-322-409-27	Sequence 27, Appl
c1017	48	1.3	600	4	US-09-774-639-44	Sequence 44, Appl	1090	48	1.3	985	4	US-09-451-527-25	Sequence 25, Appl
c1018	48	1.3	601	4	US-09-949-016-64894	Sequence 64894, A	c1091	48	1.3	985	4	US-09-451-527-25	Sequence 27, Appl
c1019	48	1.3	601	4	US-09-949-016-64895	Sequence 64895, A	1092	48	1.3	985	4	US-09-451-527-27	Sequence 27, Appl
c1020	48	1.3	601	4	US-09-949-016-85308	Sequence 85308, A	c1093	48	1.3	990	4	US-09-800-729-79	Sequence 79, Appl
c1021	48	1.3	607	4	US-09-809-545A-19	Sequence 19, Appl	c1094	48	1.3	1008	4	US-09-780-641-1	Sequence 1, Appl
c1022	48	1.3	614	4	US-09-902-540-1318	Sequence 1318, Ap	c1095	48	1.3	1013	4	US-09-322-409-6	Sequence 6, Appl
c1023	48	1.3	619	4	US-09-489-847-58	Sequence 58, Appl	1096	48	1.3	1013	4	US-09-322-409-8	Sequence 8, Appl
c1024	48	1.3	624	1	US-09-270-767-13424	Sequence 13424, A	1097	48	1.3	1013	4	US-09-451-527-6	Sequence 6, Appl
c1025	48	1.3	630	1	US-08-185-414E-1	Sequence 1, Appl	1098	48	1.3	1013	4	US-09-451-527-8	Sequence 8, Appl
c1026	48	1.3	635	1	US-08-455-633A-35	Sequence 35, Appl	1099	48	1.3	1020	4	US-09-328-475C-43	Sequence 43, Appl
c1027	48	1.3	635	2	US-08-456-460C-35	Sequence 35, Appl	c1100	48	1.3	1023	1	US-08-252-966B-16	Sequence 16, Appl
c1028	48	1.3	635	5	PCT-US94-05334-35	Sequence 35, Appl	c1101	48	1.3	1037	4	US-09-489-847-112	Sequence 112, App
c1029	48	1.3	636	4	US-09-594-506-27	Sequence 27, Appl	c1102	48	1.3	1039	4	US-09-464-535-23	Sequence 23, Appl
c1030	48	1.3	636	4	US-09-482-273-49	Sequence 49, Appl	c1103	48	1.3	1046	1	US-08-361-487B-4	Sequence 4, Appl
c1031	48	1.3	639	4	US-09-904-615-66	Sequence 66, Appl	c1104	48	1.3	1046	1	US-08-484-332C-4	Sequence 4, Appl
c1032	48	1.3	664	4	US-09-620-405B-465	Sequence 465, App	c1105	48	1.3	1050	4	US-09-482-273-58	Sequence 58, Appl
c1033	48	1.3	674	4	US-09-433-828B-465	Sequence 465, App	c1106	48	1.3	1062	4	US-09-796-766-3	Sequence 3, Appl
c1034	48	1.3	674	4	US-09-604-287A-465	Sequence 465, App	c1107	48	1.3	1069	4	US-09-205-258-74	Sequence 74, Appl
c1035	48	1.3	674	4	US-09-834-759-465	Sequence 465, App	c1108	48	1.3	1098	3	US-09-248-335-35	Sequence 35, Appl
c1036	48	1.3	674	4	US-09-590-751A-465	Sequence 465, App	c1109	48	1.3	1129	3	US-09-227-357-40	Sequence 40, Appl
c1037	48	1.3	674	4	US-09-551-621-465	Sequence 465, App	c1110	48	1.3	1143	3	US-09-143-476-119	Sequence 119, App
c1038	48	1.3	687	4	US-09-774-639-106	Sequence 106, App	c1111	48	1.3	1144	4	US-09-904-615-20	Sequence 20, Appl
c1039	48	1.3	687	4	US-09-774-639-106	Sequence 106, App	c1112	48	1.3	1147	1	US-08-665-716-1	Sequence 1, Appl
c1040	48	1.3	688	6	5498694-3	Patent No. 5498694	c1113	48	1.3	1151	3	US-09-270-767-12633	Sequence 12633, A
c1041	48	1.3	688	6	5498694-3	Patent No. 5498694	c1114	48	1.3	1151	3	US-09-149-476-41	Sequence 41, Appl
c1042	48	1.3	708	4	US-09-270-767-13081	Sequence 13081, A	c1115	48	1.3	1181	3	US-09-149-476-310	Sequence 310, App
c1043	48	1.3	730	3	US-09-270-767-14600	Sequence 14600, A	c1116	48	1.3	1184	4	US-09-489-847-76	Sequence 76, Appl
c1044	48	1.3	732	3	US-09-149-476-66	Sequence 66, Appl	c1117	48	1.3	1196	4	US-09-065-040-2	Sequence 2, Appl
c1045	48	1.3	734	1	US-09-949-016-413	Sequence 413, App	c1118	48	1.3	1206	3	US-09-465-558-53	Sequence 53, Appl
c1046	48	1.3	742	1	US-07-847-010-12	Sequence 12, Appl	c1119	48	1.3	1210	3	US-09-443-041A-29	Sequence 29, Appl
1047	48	1.3	756	4	US-09-614-912-93	Sequence 93, Appl	c1120	48	1.3	1210	4	US-09-244-805-45	Sequence 45, Appl
c1048	48	1.3	759	4	US-09-465-559-5	Sequence 5, Appl	c1121	48	1.3	1210	4	US-09-720-318A-3	Sequence 3, Appl
c1049	48	1.3	769	4	US-09-513-775B-5	Sequence 5, Appl	c1122	48	1.3	1212	3	US-09-149-476-186	Sequence 186, App

c1123	48	1.3	1214	4	US-09-780-717-28	Sequence 28, Appl	c1196	48	1.3	1534	4	US-08-988-197-6	Sequence 6, Appl
c1124	48	1.3	1215	4	US-09-646-693-1	Sequence 1, Appl	c1197	48	1.3	1534	4	US-10-385-072-6	Sequence 6, Appl
c1125	48	1.3	1230	4	US-09-244-805-6	Sequence 6, Appl	c1198	48	1.3	1538	4	US-09-205-258-193	Sequence 193, App
c1126	48	1.3	1248	4	US-09-489-847-101	Sequence 101, App	c1199	48	1.3	1544	4	US-09-187-999-14	Sequence 14, Appl
c1127	48	1.3	1273	4	US-09-270-767-14731	Sequence 14731, A	c1200	48	1.3	1545	4	US-09-559-023-1	Sequence 1, Appl
c1128	48	1.3	1279	3	US-09-248-335-25	Sequence 25, Appl	c1201	48	1.3	1559	4	US-09-489-847-42	Sequence 42, Appl
c1129	48	1.3	1296	4	US-09-461-325-29	Sequence 29, Appl	c1202	48	1.3	1560	4	US-09-500-495A-5	Sequence 5, Appl
c1130	48	1.3	1296	4	US-10-012-542-29	Sequence 29, Appl	c1203	48	1.3	1576	1	US-08-157-101A-6	Sequence 6, Appl
c1131	48	1.3	1296	4	US-10-115-123-29	Sequence 29, Appl	c1204	48	1.3	1602	1	US-08-530-950-3	Sequence 3, Appl
c1132	48	1.3	1297	4	US-09-800-729-80	Sequence 80, Appl	c1205	48	1.3	1602	1	US-08-888-429A-3	Sequence 3, Appl
c1133	48	1.3	1302	4	US-09-322-409-91	Sequence 91, Appl	c1206	48	1.3	1602	3	US-09-149-879-3	Sequence 3, Appl
c1134	48	1.3	1302	4	US-09-322-409-91	Sequence 91, Appl	c1207	48	1.3	1602	4	US-09-057-009-3	Sequence 3, Appl
c1135	48	1.3	1302	4	US-09-451-527-91	Sequence 91, Appl	c1208	48	1.3	1602	4	US-09-593-653-3	Sequence 3, Appl
c1136	48	1.3	1302	4	US-09-451-527-93	Sequence 93, Appl	c1209	48	1.3	1605	3	US-09-149-476-187	Sequence 187, App
c1137	48	1.3	1307	2	US-08-960-022-17	Sequence 17, Appl	c1210	48	1.3	1606	4	US-09-820-004-1	Sequence 1, Appl
c1138	48	1.3	1307	4	US-09-641-612-3	Sequence 3, Appl	c1211	48	1.3	1619	4	US-09-522-714-11	Sequence 11, Appl
c1139	48	1.3	1308	4	US-10-151-832-1	Sequence 1, Appl	c1212	48	1.3	1636	4	US-09-578-194-6	Sequence 6, Appl
c1140	48	1.3	1319	2	US-08-504-459-7	Sequence 7, Appl	c1213	48	1.3	1637	4	US-09-205-258-178	Sequence 178, App
c1141	48	1.3	1325	1	US-08-306-691B-51	Sequence 51, Appl	c1214	48	1.3	1639	2	US-08-737-524B-1	Sequence 1, Appl
c1142	48	1.3	1325	2	US-08-464-517-1	Sequence 1, Appl	c1215	48	1.3	1651	4	US-09-800-729-41	Sequence 41, Appl
c1143	48	1.3	1325	2	US-08-246-361A-1	Sequence 1, Appl	c1216	48	1.3	1653	3	US-09-345-469-2	Sequence 2, Appl
c1144	48	1.3	1325	3	US-08-463-772-1	Sequence 1, Appl	c1217	48	1.3	1663	3	US-09-822-862-1	Sequence 1, Appl
c1145	48	1.3	1325	5	PCT-US93-05000-1	Sequence 1, Appl	c1218	48	1.3	1683	3	US-09-347-803-11	Sequence 11, Appl
c1146	48	1.3	1332	3	US-09-333-423-1	Sequence 1, Appl	c1219	48	1.3	1692	4	US-09-821-803A-5	Sequence 5, Appl
c1147	48	1.3	1342	4	US-09-489-847-89	Sequence 89, Appl	c1220	48	1.3	1705	4	US-09-205-258-216	Sequence 216, App
c1148	48	1.3	1358	4	US-09-614-221A-1	Sequence 1, Appl	c1221	48	1.3	1708	4	US-09-859-053-31	Sequence 31, Appl
c1149	48	1.3	1358	4	US-09-949-016-463	Sequence 463, App	c1222	48	1.3	1721	5	PCT-US96-00994-3	Sequence 4, Appl
c1150	48	1.3	1359	3	US-09-387-574-11	Sequence 11, Appl	c1223	48	1.3	1725	4	US-09-668-097A-21	Sequence 21, Appl
c1151	48	1.3	1359	3	US-09-668-096-11	Sequence 11, Appl	c1224	48	1.3	1738	4	US-09-918-909A-27	Sequence 27, Appl
c1152	48	1.3	1386	2	US-08-897-340-1	Sequence 1, Appl	c1225	48	1.3	1740	4	US-09-709-103-45	Sequence 45, Appl
c1153	48	1.3	1386	3	US-09-252-329-1	Sequence 1, Appl	c1226	48	1.3	1746	4	US-09-439-410A-45	Sequence 45, App
c1154	48	1.3	1393	1	US-07-602-824A-1	Sequence 1, Appl	c1227	48	1.3	1746	4	US-09-485-529-57	Sequence 57, App
c1155	48	1.3	1393	1	US-07-983-451-1	Sequence 1, Appl	c1228	48	1.3	1768	4	US-09-485-529-13	Sequence 13, Appl
c1156	48	1.3	1393	1	US-08-261-577-6	Sequence 6, Appl	c1229	48	1.3	1780	3	US-09-202-548B-5	Sequence 5, Appl
c1157	48	1.3	1395	2	US-08-553-367A-1	Sequence 1, Appl	c1230	48	1.3	1780	4	US-09-942-858-5	Sequence 5, Appl
c1158	48	1.3	1395	3	US-09-295-306-1	Sequence 1, Appl	c1231	48	1.3	1780	4	US-10-461-180-5	Sequence 5, Appl
c1159	48	1.3	1395	3	US-09-734-719-1	Sequence 1, Appl	c1232	48	1.3	1790	4	US-09-866-028-31	Sequence 31, Appl
c1160	48	1.3	1405	4	US-09-244-111-9	Sequence 9, Appl	c1233	48	1.3	1790	3	US-09-797-907-31	Sequence 31, Appl
c1161	48	1.3	1412	4	US-09-614-912-197	Sequence 197, App	c1234	48	1.3	1798	3	US-09-944-456-1	Sequence 1, Appl
c1162	48	1.3	1441	3	US-08-821-994-63	Sequence 63, Appl	c1235	48	1.3	1804	2	US-08-504-459-5	Sequence 5, Appl
c1163	48	1.3	1443	4	US-09-904-615-21	Sequence 21, Appl	c1236	48	1.3	1810	4	US-09-800-729-73	Sequence 73, Appl
c1164	48	1.3	1443	3	US-09-697-367-19	Sequence 19, Appl	c1237	48	1.3	1811	4	US-09-800-729-77	Sequence 77, Appl
c1165	48	1.3	1445	3	US-09-814-951A-1	Sequence 1, Appl	c1238	48	1.3	1813	3	US-09-071-224-3	Sequence 3, Appl
c1166	48	1.3	1445	4	US-09-918-909A-19	Sequence 19, Appl	c1239	48	1.3	1827	4	US-09-720-318A-9	Sequence 9, Appl
c1167	48	1.3	1447	3	US-09-443-041A-27	Sequence 27, Appl	c1240	48	1.3	1829	4	US-09-885-723-4	Sequence 4, Appl
c1168	48	1.3	1459	4	US-09-537-654-3	Sequence 3, Appl	c1241	48	1.3	1844	4	US-10-003-332-7	Sequence 7, Appl
c1169	48	1.3	1478	4	US-09-216-333B-7	Sequence 7, Appl	c1242	48	1.3	1864	3	US-09-149-476-130	Sequence 130, App
c1170	48	1.3	1486	4	US-09-461-325-73	Sequence 73, Appl	c1243	48	1.3	1865	3	US-09-370-253-5	Sequence 5, Appl
c1171	48	1.3	1486	4	US-10-012-542-73	Sequence 73, Appl	c1244	48	1.3	1867	4	US-09-482-273-81	Sequence 81, Appl
c1172	48	1.3	1486	4	US-10-115-123-73	Sequence 73, Appl	c1245	48	1.3	1868	3	US-09-739-455-1	Sequence 1, Appl
c1173	48	1.3	1493	1	US-08-340-820-24	Sequence 24, Appl	c1246	48	1.3	1872	3	US-09-291-922-27	Sequence 27, Appl
c1174	48	1.3	1493	1	US-08-593-535-24	Sequence 24, Appl	c1247	48	1.3	1878	3	US-09-732-025-1	Sequence 1, Appl
c1175	48	1.3	1493	6	5340934-5	Sequence 6, Appl	c1248	48	1.3	1882	3	US-09-370-253-1	Sequence 1, Appl
c1176	48	1.3	1493	6	5340934-5	Sequence 6, Appl	c1249	48	1.3	1882	3	US-09-419-679-3	Sequence 3, Appl
c1177	48	1.3	1503	4	US-09-907-794A-220	Sequence 220, App	c1250	48	1.3	1895	1	US-09-444-336-7	Sequence 7, Appl
c1178	48	1.3	1503	4	US-09-905-125A-220	Sequence 220, App	c1251	48	1.3	1897	3	US-08-184-632-1	Sequence 1, Appl
c1179	48	1.3	1503	4	US-09-907-775A-220	Sequence 220, App	c1252	48	1.3	1925	4	US-09-148-545-128	Sequence 128, App
c1180	48	1.3	1503	4	US-09-906-700-220	Sequence 220, App	c1253	48	1.3	1927	3	US-09-336-536-66	Sequence 66, Appl
c1181	48	1.3	1503	4	US-09-903-603A-220	Sequence 220, App	c1254	48	1.3	1929	3	US-09-146-950-1	Sequence 1, Appl
c1182	48	1.3	1503	4	US-09-904-920A-220	Sequence 220, App	c1255	48	1.3	1933	4	US-09-920-759-3	Sequence 3, Appl
c1183	48	1.3	1503	4	US-09-904-960A-220	Sequence 220, App	c1256	48	1.3	1958	3	US-08-665-034A-3	Sequence 3, Appl
c1184	48	1.3	1503	4	US-09-905-361A-220	Sequence 220, App	c1257	48	1.3	1981	4	US-09-720-317A-3	Sequence 3, Appl
c1185	48	1.3	1503	4	US-09-906-618-220	Sequence 220, App	c1258	48	1.3	1985	4	US-09-907-774A-212	Sequence 212, App
c1186	48	1.3	1512	2	US-08-909-965C-8	Sequence 8, Appl	c1259	48	1.3	1985	4	US-09-905-125A-212	Sequence 212, App
c1187	48	1.3	1525	3	US-09-157-603-4	Sequence 4, Appl	c1260	48	1.3	1985	4	US-09-902-775A-212	Sequence 212, App
c1188	48	1.3	1525	3	US-09-587-436-4	Sequence 4, Appl	c1261	48	1.3	1985	4	US-09-906-700-212	Sequence 212, App
c1189	48	1.3	1525	3	US-08-927-165A-4	Sequence 4, Appl	c1262	48	1.3	1985	4	US-09-903-603A-212	Sequence 212, App
c1190	48	1.3	1525	4	US-09-461-325-110	Sequence 110, App	c1263	48	1.3	1985	4	US-09-904-920A-212	Sequence 212, App
c1191	48	1.3	1525	4	US-10-012-542-110	Sequence 110, App	c1264	48	1.3	1985	4	US-09-909-054-212	Sequence 212, App
c1192	48	1.3	1525	4	US-10-115-123-110	Sequence 110, App	c1265	48	1.3	1985	4	US-09-905-381A-212	Sequence 212, App
c1193	48	1.3	1527	4	US-09-244-111-7	Sequence 7, Appl	c1266	48	1.3	1985	4	US-09-906-618-212	Sequence 212, App
c1194	48	1.3	1530	4	US-09-811-361-19	Sequence 19, Appl	c1267	48	1.3	1993	4	US-09-889-463A-13	Sequence 13, Appl
c1195	48	1.3	1534	1	US-08-300-903A-6	Sequence 6, Appl	c1268	48	1.3	2010	1	US-07-864-475A-4	Sequence 4, Appl



c1269	48	1.3	2010	2	US-08-468-249A-4	Sequence 4, Appl	c1342	48	1.3	2539	4	US-10-144-198-21	Sequence 21, Appl
c1270	48	1.3	2017	4	US-09-690-454-45	Sequence 45, Appl	c1343	48	1.3	2540	4	US-09-949-016-431	Sequence 431, Appl
c1271	48	1.3	2025	4	US-09-149-476-316	Sequence 316, Appl	c1344	48	1.3	2567	3	US-08-993-260-4	Sequence 4, Appl
c1272	48	1.3	2028	3	US-09-211-930-12	Sequence 12, Appl	c1345	48	1.3	2604	2	US-08-630-118A-3	Sequence 3, Appl
c1273	48	1.3	2028	3	US-09-340-993-12	Sequence 12, Appl	c1346	48	1.3	2604	2	US-08-838-399-3	Sequence 3, Appl
c1274	48	1.3	2028	3	US-09-468-442-12	Sequence 12, Appl	c1347	48	1.3	2604	3	US-08-235-839-3	Sequence 3, Appl
c1275	48	1.3	2045	3	US-09-153-060-22	Sequence 22, Appl	c1348	48	1.3	2604	3	US-09-327-035-3	Sequence 3, Appl
c1276	48	1.3	2082	2	US-08-785-310A-2	Sequence 2, Appl	c1349	48	1.3	2608	4	US-09-904-035-16	Sequence 16, Appl
c1277	48	1.3	2091	3	US-09-813-818-1	Sequence 1, Appl	c1350	48	1.3	2610	3	US-09-545-814-1	Sequence 1, Appl
c1278	48	1.3	2091	4	US-10-199-333-1	Sequence 10, Appl	c1351	48	1.3	2610	3	US-09-545-814-3	Sequence 3, Appl
c1279	48	1.3	2096	3	US-09-008-481A-10	Sequence 10, Appl	c1352	48	1.3	2628	1	US-08-143-219-1	Sequence 1, Appl
c1280	48	1.3	2096	3	US-09-195-666A-16	Sequence 16, Appl	c1353	48	1.3	2634	3	US-09-463-238-3	Sequence 3, Appl
c1281	48	1.3	2096	3	US-09-309-592-10	Sequence 10, Appl	c1354	48	1.3	2648	3	US-09-417-455-6	Sequence 6, Appl
c1282	48	1.3	2096	3	US-09-633-705-16	Sequence 16, Appl	c1355	48	1.3	2648	3	US-09-348-942-6	Sequence 6, Appl
c1283	48	1.3	2096	3	US-09-634-858A-16	Sequence 16, Appl	c1356	48	1.3	2648	3	US-09-457-626-6	Sequence 6, Appl
c1284	48	1.3	2096	4	US-08-863-927C-16	Sequence 16, Appl	c1357	48	1.3	2648	4	US-09-576-008-6	Sequence 6, Appl
c1285	48	1.3	2114	1	US-07-803-622E-6	Sequence 6, Appl	c1358	48	1.3	2665	3	US-08-971-089-5	Sequence 5, Appl
c1286	48	1.3	2158	1	US-07-602-608-1	Sequence 1, Appl	c1359	48	1.3	2668	3	US-09-370-838-156	Sequence 156, Appl
c1287	48	1.3	2158	1	US-08-261-578-1	Sequence 1, Appl	c1360	48	1.3	2668	4	US-09-854-133-156	Sequence 156, Appl
c1288	48	1.3	2182	4	US-09-214-619-3	Sequence 3, Appl	c1361	48	1.3	2674	3	US-09-817-180-1	Sequence 1, Appl
c1289	48	1.3	2182	4	US-09-555-820A-11	Sequence 11, Appl	c1362	48	1.3	2674	4	US-10-003-295-1	Sequence 1, Appl
c1290	48	1.3	2184	3	US-08-953-918C-1	Sequence 1, Appl	c1363	48	1.3	2674	4	US-10-066-130-19	Sequence 19, Appl
c1291	48	1.3	2184	3	US-08-697-766A-1	Sequence 1, Appl	c1364	48	1.3	2677	4	US-09-733-643B-1	Sequence 1, Appl
c1292	48	1.3	2186	3	US-09-360-545-66	Sequence 66, Appl	c1365	48	1.3	2695	4	US-09-706-197-3	Sequence 3, Appl
c1293	48	1.3	2202	3	US-09-465-558-59	Sequence 59, Appl	c1366	48	1.3	2718	4	US-09-667-135-1	Sequence 1, Appl
c1294	48	1.3	2218	4	US-09-016-434-1157	Sequence 1157, Appl	c1367	48	1.3	2771	4	US-10-066-130-18	Sequence 18, Appl
c1295	48	1.3	2218	4	US-10-329-668-7	Sequence 7, Appl	c1368	48	1.3	2797	4	US-09-482-273-74	Sequence 74, Appl
c1296	48	1.3	2233	1	US-08-496-631-1	Sequence 1, Appl	c1369	48	1.3	2806	3	US-09-653-839-9	Sequence 9, Appl
c1297	48	1.3	2246	3	US-09-363-708-3	Sequence 3, Appl	c1370	48	1.3	2806	4	US-10-202-619-27	Sequence 27, Appl
c1298	48	1.3	2246	4	US-09-083-587-3	Sequence 3, Appl	c1371	48	1.3	2808	4	US-09-917-254-29	Sequence 29, Appl
c1299	48	1.3	2262	4	US-09-311-021-171	Sequence 171, Appl	c1372	48	1.3	2822	4	US-09-907-794A-48	Sequence 48, Appl
c1300	48	1.3	2269	3	US-09-394-645-1	Sequence 1, Appl	c1373	48	1.3	2822	4	US-09-905-125A-48	Sequence 48, Appl
c1301	48	1.3	2269	3	US-09-243-560B-1	Sequence 1, Appl	c1374	48	1.3	2822	4	US-09-902-775A-48	Sequence 48, Appl
c1302	48	1.3	2285	2	US-08-967-101-136	Sequence 136, Appl	c1375	48	1.3	2822	4	US-09-905-700-48	Sequence 48, Appl
c1303	48	1.3	2285	2	US-08-592-541-136	Sequence 136, Appl	c1376	48	1.3	2822	4	US-09-903-603A-48	Sequence 48, Appl
c1304	48	1.3	2285	3	US-09-124-698-136	Sequence 136, Appl	c1377	48	1.3	2822	4	US-09-904-920A-48	Sequence 48, Appl
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## ALIGNMENTS

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RESULT 1
US-09-799-451-571
; Sequence 571, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Reivan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pf_fl_genes version 2.0
; SEQ ID NO 571
; LENGTH: 2240
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1779)
US-09-799-451-571

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Best Local Similarity 99.9%; Pred. No. 2.8e-309;
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Db 1315 CCTGCTGAGCAGCATCTGGCAAGTCTCTGTGAGTTAGTCTCCCTCGTTCAGAT 1374
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## RESULT 2

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; Sequence 817, Application US/09799451
; Patent No. 6783969
;
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.

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; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunging
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_Fl_genes Version 2.0
; SEQ ID NO 817
; LENGTH: 2223
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(2149)
; US-09-799-451-817

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Best local Similarity 100.0%; Pred. No. 1.6e-55;
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### RESULT 3

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; Sequence 144142, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144142
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US-09-949-016-144142

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QY 2241 AATA 2244
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; Sequence 144200, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
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; PRIOR FILING DATE: 2000-09-08
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144200
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-144200

Query Match      1.8%; Score 64; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2181 CCTGAGGTCAGGAATTCAGACACCGCTGGCCAAACATGCGCAAAACCCCATCTCTACTAAA 2240
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Db 165 CCTGAGGTCAGGAATTCAGACACCGCTGGCCAAACATGCGCAAAACCCCATCTCTACTAAA 224
    |||||
QY 2241 AATA 2244
    |||||
Db 225 AATA 228

RESULT 5
US-09-949-016-144258
; Sequence 144258, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144258
; LENGTH: 601
; TYPE: DNA
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; ORGANISM: Human
US-09-949-016-144258

Query Match      1.8%; Score 64; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2181 CCTGAGGTCAGGAATTCAGACACCGCTGGCCAAACATGCGCAAAACCCCATCTCTACTAAA 2240
    |||||
Db 165 CCTGAGGTCAGGAATTCAGACACCGCTGGCCAAACATGCGCAAAACCCCATCTCTACTAAA 224
    |||||
QY 2241 AATA 2244
    |||||
Db 225 AATA 228

RESULT 6
US-09-949-016-144316
; Sequence 144316, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144316
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-144316

Query Match      1.8%; Score 64; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2181 CCTGAGGTCAGGAATTCAGACACCGCTGGCCAAACATGCGCAAAACCCCATCTCTACTAAA 2240
    |||||
Db 165 CCTGAGGTCAGGAATTCAGACACCGCTGGCCAAACATGCGCAAAACCCCATCTCTACTAAA 224
    |||||
QY 2241 AATA 2244
    |||||
Db 225 AATA 228

RESULT 7
US-09-949-016-15817
; Sequence 15817, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 15817  
; LENGTH: 53394  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(53394)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15817

Query Match 1.8%; Score 64; DB 4; Length 53394;  
Best Local Similarity 100.0%; Pred. No. 5.2e-12;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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|||||  
Db 45991 CCTGAGGTCAGGAATTCAGACCCAGCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 46050  
  
QY 2241 AATA 2244  
|||||  
Db 46051 AATA 46054

RESULT 8  
US-09-949-016-15818  
; Sequence 15818, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15818  
; LENGTH: 53394  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(53394)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15818

Query Match 1.8%; Score 64; DB 4; Length 53394;  
Best Local Similarity 100.0%; Pred. No. 5.2e-12;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2181 CCTGAGGTCAGGAATTCAGACCCAGCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 2240  
|||||  
Db 45991 CCTGAGGTCAGGAATTCAGACCCAGCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 46050  
  
QY 2241 AATA 2244  
|||||  
Db 46051 AATA 46054

RESULT 9  
US-09-949-016-15819  
; Sequence 15819, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15819  
; LENGTH: 53394  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(53394)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15819

Query Match 1.8%; Score 64; DB 4; Length 53394;  
Best Local Similarity 100.0%; Pred. No. 5.2e-12;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2181 CCTGAGGTCAGGAATTCAGACCCAGCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 2240  
|||||  
Db 45991 CCTGAGGTCAGGAATTCAGACCCAGCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 46050  
  
QY 2241 AATA 2244  
|||||  
Db 46051 AATA 46054

RESULT 10  
US-09-949-016-15820  
; Sequence 15820, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15820  
; LENGTH: 53394  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(53394)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15820

Query Match 1.8%; Score 64; DB 4; Length 53394;  
Best Local Similarity 100.0%; Pred. No. 5.2e-12;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2181 CCTGAGGTCAGGAATTCAGACCCAGCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 2240  
|||||  
Db 45991 CCTGAGGTCAGGAATTCAGACCCAGCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 46050  
  
QY 2241 AATA 2244  
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Db 46051 AATA 46054

RESULT 11  
US-09-949-016-15602/c  
; Sequence 15602, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15602  
; LENGTH: 134890  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15602

Query Match 1.7%; Score 62; DB 4; Length 134890;  
Best Local Similarity 100.0%; Pred. No. 1.9e-11; Indels 0; Gaps 0;  
Matches 62; Conservative 0; Mismatches 0;  
Qy 2183 TCAGTCTAGGAATTCAGACACGCTGGCCACATGCGCAAAACCCCTCTCTACTAAAAA 2242  
Db 32159 TCAGTCTAGGAATTCAGACACGCTGGCCACATGCGCAAAACCCCTCTCTACTAAAAA 32100  
Qy 2243 TA 2244  
Db 32099 TA 32098

RESULT 12  
US-09-372-422A-23/c  
; Sequence 23, Application US/09372422A  
; Patent No. 6313375  
; GENERAL INFORMATION:  
; APPLICANT: Rudolf Jung  
; APPLICANT: Francois Barrieu  
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof  
; FILE REFERENCE: 0919  
; CURRENT APPLICATION NUMBER: US/09/372,422A  
; CURRENT FILING DATE: 1999-08-11  
; PRIOR APPLICATION NUMBER: US 60/098,692  
; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 23  
; LENGTH: 1193  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (88)...(838)  
US-09-372-422A-23

Query Match 1.6%; Score 59; DB 3; Length 1193;  
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Matches 59; Conservative 0; Mismatches 0;  
Qy 2583 GCGGCGCCGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2641  
Db 1193 GCGGCGCCGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1135

RESULT 13  
US-09-949-016-12928/c  
; Sequence 12928, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12928  
; LENGTH: 194537  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(194537)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12928

Query Match 1.6%; Score 59; DB 4; Length 194537;  
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Matches 59; Conservative 0; Mismatches 0;  
Qy 2195 TTCAGACACGCTGGCCACATGCGCAAAACCCCTCTCTACTAAAAAATTA 2253  
Db 16281 TTCAGACACGCTGGCCACATGCGCAAAACCCCTCTCTACTAAAAAATTA 16223

RESULT 14  
US-09-949-016-12740/c  
; Sequence 12740, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12740  
; LENGTH: 201529  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(201529)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12740

Query Match 1.6%; Score 59; DB 4; Length 201529;  
Best Local Similarity 100.0%; Pred. No. 1.6e-10; Indels 0; Gaps 0;  
Matches 59; Conservative 0; Mismatches 0;  
Qy 2195 TTCAGACACGCTGGCCACATGCGCAAAACCCCTCTCTACTAAAAAATTA 2253



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- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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68	995	27.8	2240	17	US-10-302-172-571
C 69	274	7.7	464	10	US-09-918-995-29372
C 70	201	5.6	2223	17	US-10-302-172-817
C 71	173	4.8	177	9	US-09-880-107-3886
72	152	4.2	441	17	US-10-242-355-187
73	82	2.3	1157	18	US-10-425-115-174016
74	79	2.2	403	18	US-10-425-115-155989
C 75	79	2.2	483	9	US-09-783-590-6515
C 76	76	2.1	2938	18	US-10-425-115-9664
77	74	2.1	1483	18	US-10-425-115-17547

Sequence 110917, A	1950	2.1	74	18	US-10-425-115-110917
Sequence 13888, A	5396	1.8	65	14	US-10-198-846-13888
Sequence 141959, A	1190	1.7	61	18	US-10-425-115-141959
Sequence 80981, A	1772	1.7	61	18	US-10-425-115-80981
Sequence 4953, Ap	60	1.7	60	10	US-09-908-975-4953
Sequence 23466, A	60	1.7	60	10	US-09-908-975-23466
Sequence 6405, Ap	397	1.7	60	9	US-09-960-352-6405
Sequence 100376, A	493	1.7	60	18	US-10-425-115-100376
Sequence 3, Appl1	1408	1.7	60	9	US-09-745-605-3
Sequence 46816, A	1824	1.7	60	18	US-10-425-115-46816
Sequence 13051, A	246	1.6	59	18	US-10-437-963-13051
Sequence 9292, A	291	1.6	59	17	US-10-424-599-9292
Sequence 23886, A	307	1.6	59	18	US-10-425-115-23886
Sequence 69622, A	338	1.6	59	18	US-10-425-115-69622
Sequence 6394, Ap	358	1.6	59	18	US-10-425-115-6394
Sequence 53982, A	363	1.6	59	18	US-10-424-599-21016
Sequence 21016, A	363	1.6	59	18	US-10-425-115-95279
Sequence 95279, A	375	1.6	59	18	US-10-424-599-48966
Sequence 48966, A	377	1.6	59	17	US-10-424-599-48966
Sequence 13424, A	378	1.6	59	18	US-10-425-115-13424
Sequence 109809, A	382	1.6	59	18	US-10-425-115-109809
Sequence 182112, A	382	1.6	59	18	US-10-425-115-182112
Sequence 40806, A	389	1.6	59	18	US-10-425-115-40806
Sequence 90745, A	392	1.6	59	17	US-10-424-599-90745
Sequence 89348, A	401	1.6	59	18	US-10-425-115-89348
Sequence 67437, A	421	1.6	59	18	US-10-437-963-67437
Sequence 36699, A	437	1.6	59	17	US-10-424-599-36699
Sequence 131478, A	446	1.6	59	17	US-10-424-599-131478
Sequence 18960, A	461	1.6	59	18	US-10-767-701-18960
Sequence 80899, A	462	1.6	59	18	US-10-425-115-80899
Sequence 74761, A	464	1.6	59	17	US-10-424-599-74761
Sequence 156487, A	477	1.6	59	18	US-10-425-115-156487
Sequence 36374, A	481	1.6	59	18	US-10-425-115-36374
Sequence 48287, A	510	1.6	59	17	US-10-424-599-48287
Sequence 73854, A	510	1.6	59	18	US-10-425-115-73854
Sequence 14414, A	569	1.6	59	18	US-10-425-115-14414
Sequence 182620, A	640	1.6	59	18	US-10-425-115-182620
Sequence 42846, A	643	1.6	59	18	US-10-425-115-42846
Sequence 60549, A	837	1.6	59	18	US-10-425-115-60549
Sequence 105683, A	1076	1.6	59	18	US-10-425-115-105683
Sequence 754, App	2063	1.6	59	18	US-10-066-543-754
Sequence 1308, App	81	1.6	58	14	US-10-066-543-1308
Sequence 589, App	81	1.6	58	14	US-10-066-543-589
Sequence 849, App	89	1.6	58	14	US-10-066-543-849
Sequence 5046, Ap	92	1.6	58	14	US-10-066-543-5046
Sequence 339, App	93	1.6	58	14	US-10-066-543-339
Sequence 906, App	97	1.6	58	14	US-10-066-543-906
Sequence 895, App	100	1.6	58	14	US-10-066-543-895
Sequence 890, App	101	1.6	58	14	US-10-066-543-890
Sequence 142, App	102	1.6	58	14	US-10-066-543-142
Sequence 876, App	102	1.6	58	14	US-10-066-543-876
Sequence 878, App	103	1.6	58	14	US-10-066-543-878
Sequence 879, App	103	1.6	58	14	US-10-066-543-879
Sequence 880, App	103	1.6	58	14	US-10-066-543-880
Sequence 537, App	103	1.6	58	14	US-10-066-543-537
Sequence 875, App	103	1.6	58	14	US-10-066-543-875
Sequence 1307, Ap	103	1.6	58	14	US-10-066-543-1307
Sequence 865, App	104	1.6	58	14	US-10-066-543-865
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Sequence 7296, Ap	111	1.6	58	14	US-10-066-543-7296
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152	58	1.6	113	9	US-09-924-035A-535	Sequence 535, App	225	58	1.6	330	11	US-09-322-293-42	Sequence 42, Appl
153	58	1.6	114	9	US-09-770-696-756	Sequence 756, App	226	58	1.6	335	18	US-10-425-115-159362	Sequence 159362, App
154	58	1.6	114	9	US-09-770-696-757	Sequence 757, App	227	58	1.6	337	9	US-09-960-352-6976	Sequence 6976, App
155	58	1.6	114	9	US-09-924-035A-747	Sequence 747, App	228	58	1.6	342	17	US-10-424-599-130104	Sequence 130104, App
156	58	1.6	114	14	US-10-066-543-717	Sequence 717, App	c 229	58	1.6	350	9	US-09-960-352-11730	Sequence 11730, A
157	58	1.6	115	9	US-09-770-696-747	Sequence 747, App	230	58	1.6	358	9	US-09-960-352-14598	Sequence 14598, A
158	58	1.6	115	9	US-09-924-035A-258	Sequence 258, App	231	58	1.6	358	14	US-10-198-846-9603	Sequence 9603, App
159	58	1.6	116	9	US-09-770-696-732	Sequence 732, App	232	58	1.6	358	17	US-10-424-599-47581	Sequence 47581, A
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161	58	1.6	116	9	US-09-924-035A-466	Sequence 466, App	c 234	58	1.6	370	9	US-09-960-352-6169	Sequence 6169, App
162	58	1.6	116	14	US-10-066-543-761	Sequence 761, App	235	58	1.6	382	9	US-09-960-352-3209	Sequence 3209, App
163	58	1.6	117	14	US-10-066-543-731	Sequence 731, App	236	58	1.6	382	18	US-10-425-115-112847	Sequence 112847, App
164	58	1.6	118	9	US-09-770-696-706	Sequence 706, App	237	58	1.6	385	9	US-09-770-791-99	Sequence 99, Appl
165	58	1.6	118	9	US-09-770-696-708	Sequence 708, App	238	58	1.6	392	9	US-09-960-352-13003	Sequence 13003, A
166	58	1.6	118	9	US-09-924-035A-542	Sequence 542, App	239	58	1.6	394	9	US-09-960-352-7714	Sequence 7714, App
167	58	1.6	118	14	US-10-066-543-1097	Sequence 1097, App	240	58	1.6	401	9	US-09-983-965-3184	Sequence 3184, App
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182	58	1.6	128	9	US-09-924-035A-805	Sequence 805, App	255	58	1.6	464	17	US-10-424-599-125657	Sequence 125657, App
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184	58	1.6	130	14	US-10-066-543-779	Sequence 779, App	257	58	1.6	484	17	US-10-424-599-20282	Sequence 20282, A
185	58	1.6	134	9	US-09-770-696-596	Sequence 596, App	258	58	1.6	500	18	US-10-425-115-166906	Sequence 166906, A
186	58	1.6	135	14	US-10-066-543-1213	Sequence 1213, App	259	58	1.6	505	17	US-10-424-599-58933	Sequence 58933, A
187	58	1.6	136	9	US-09-960-352-7557	Sequence 7557, App	260	58	1.6	508	17	US-10-424-599-58933	Sequence 58933, A
188	58	1.6	141	14	US-10-066-543-969	Sequence 969, App	261	58	1.6	508	17	US-10-424-599-58933	Sequence 58933, A
189	58	1.6	145	14	US-10-066-543-1004	Sequence 1004, App	262	58	1.6	554	17	US-10-332-859-123	Sequence 123, App
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191	58	1.6	152	9	US-09-960-352-6995	Sequence 6995, App	264	58	1.6	570	17	US-10-424-599-69934	Sequence 69934, A
192	58	1.6	181	9	US-09-960-352-1124	Sequence 1124, App	265	58	1.6	581	17	US-10-231-417-62	Sequence 62, Appl
193	58	1.6	181	9	US-09-960-352-1301	Sequence 1301, App	c 266	58	1.6	589	16	US-10-198-846-8340	Sequence 8340, App
194	58	1.6	186	9	US-09-924-035A-789	Sequence 789, App	267	58	1.6	592	14	US-10-198-846-8817	Sequence 8817, App
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196	58	1.6	203	9	US-09-960-352-3742	Sequence 3742, App	c 269	58	1.6	631	14	US-10-106-698-4889	Sequence 489, App
197	58	1.6	203	9	US-09-960-352-14992	Sequence 14992, A	270	58	1.6	637	15	US-10-106-698-4889	Sequence 489, App
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200	58	1.6	219	9	US-09-960-352-4946	Sequence 4946, App	c 273	58	1.6	735	9	US-09-867-701-10180	Sequence 10180, A
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202	58	1.6	223	9	US-09-960-352-667	Sequence 667, App	c 275	58	1.6	786	9	US-09-925-302-133	Sequence 133, App
203	58	1.6	228	9	US-09-960-352-10334	Sequence 10334, App	276	58	1.6	806	17	US-10-424-599-40588	Sequence 40588, A
204	58	1.6	232	18	US-10-425-115-113844	Sequence 113844, A	c 277	58	1.6	836	18	US-10-739-930-1587	Sequence 1587, App
205	58	1.6	236	9	US-09-960-352-12183	Sequence 12183, A	278	58	1.6	858	9	US-09-770-445-613	Sequence 613, App
206	58	1.6	239	9	US-09-960-352-13139	Sequence 13139, A	c 279	58	1.6	863	17	US-10-426-776-37	Sequence 37, Appl
207	58	1.6	241	9	US-09-960-352-12974	Sequence 12974, A	c 280	58	1.6	871	18	US-10-739-930-1470	Sequence 1470, App
208	58	1.6	242	9	US-09-960-352-3217	Sequence 3217, App	c 281	58	1.6	905	18	US-10-481-652-12	Sequence 12, Appl
209	58	1.6	247	17	US-10-424-599-88829	Sequence 88829, A	c 282	58	1.6	923	17	US-10-374-780A-1047	Sequence 1047, App
210	58	1.6	271	18	US-10-425-115-125721	Sequence 125721, App	c 283	58	1.6	923	17	US-10-412-699B-1298	Sequence 1298, App
211	58	1.6	272	9	US-09-960-352-649	Sequence 649, App	c 284	58	1.6	973	18	US-10-739-930-1578	Sequence 1578, App
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215	58	1.6	291	9	US-09-960-352-1243	Sequence 1243, App	c 288	58	1.6	1023	16	US-10-315-431-38	Sequence 3, Appl
216	58	1.6	296	9	US-09-960-352-3048	Sequence 3048, App	c 289	58	1.6	1023	18	US-10-680-673-3	Sequence 3, Appl
217	58	1.6	301	9	US-09-924-035A-351	Sequence 351, App	c 290	58	1.6	1023	18	US-10-854-485-38	Sequence 1631, App
218	58	1.6	305	18	US-10-425-115-162253	Sequence 162253, App	c 291	58	1.6	1037	18	US-10-739-930-1631	Sequence 38, Appl
219	58	1.6	309	18	US-10-425-115-122772	Sequence 122772, App	c 292	58	1.6	1048	17	US-10-351-334-38	Sequence 16, Appl
220	58	1.6	310	9	US-09-867-701-10189	Sequence 10189, A	c 293	58	1.6	1057	17	US-10-632-983-16	Sequence 124, App
221	58	1.6	312	9	US-09-960-352-6315	Sequence 6315, App	c 294	58	1.6	1064	10	US-09-974-879-124	Sequence 126, App
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C 299	1.6	1070	14	US-10-176-847-183	Sequence 83, Appl	C 372	58	1.6	2713	16	US-10-436-523-34	Sequence 34, Appl
C 300	1.6	1083	9	US-09-764-853-373	Sequence 373, App	C 373	58	1.6	2738	17	US-10-426-776-32	Sequence 32, Appl
C 301	1.6	1083	14	US-10-091-438-17	Sequence 17, Appl	C 374	58	1.6	2778	14	US-10-176-847-75	Sequence 75, Appl
C 302	1.6	1083	14	US-10-091-438-83	Sequence 83, Appl	C 375	58	1.6	2779	18	US-10-425-115-177717	Sequence 177717, Appl
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C 304	1.6	1156	17	US-09-925-299-14	Sequence 14, Appl	C 377	58	1.6	2875	17	US-10-184-648-9	Sequence 9, Appl
C 305	1.6	1156	17	US-10-264-049-544	Sequence 544, App	C 378	58	1.6	2964	13	US-09-766-511B-1	Sequence 1, Appl
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C 354	1.6	2242	18	US-10-357-930-22588	Sequence 22588, A	C 427	57	1.6	1023	17	US-10-412-699B-1465	Sequence 1465, App
C 355	1.6	2242	18	US-10-357-930-28429	Sequence 28429, A	C 428	57	1.6	1046	9	US-09-925-237-307	Sequence 307, App
C 356	1.6	2252	17	US-10-374-780A-1488	Sequence 1488, App	C 429	57	1.6	1102	18	US-10-425-115-15192	Sequence 15192, A
C 357	1.6	2262	17	US-10-412-699B-1576	Sequence 1576, App	C 430	57	1.6	1162	11	US-09-764-875-163	Sequence 163, App
C 358	1.6	2266	17	US-10-264-049-471	Sequence 471, App	C 431	57	1.6	1194	15	US-10-106-698-1692	Sequence 1692, App
C 359	1.6	2274	14	US-10-097-065-113	Sequence 113, App	C 432	57	1.6	1198	9	US-09-789-561-19	Sequence 19, Appl
C 360	1.6	2274	17	US-10-372-876-113	Sequence 113, App	C 433	57	1.6	1198	18	US-10-883-936-19	Sequence 1378, App
C 361	1.6	2292	11	US-09-764-875-321	Sequence 321, App	C 434	57	1.6	1306	18	US-10-739-930-1378	Sequence 1378, App
C 362	1.6	2294	17	US-10-264-049-818	Sequence 818, App	C 435	57	1.6	1621	9	US-09-739-907-14	Sequence 14, Appl
C 363	1.6	2357	15	US-10-106-698-2037	Sequence 2037, App	C 436	57	1.6	1621	11	US-09-938-671-14	Sequence 14, Appl
C 364	1.6	2369	17	US-10-635-822-13	Sequence 13, Appl	C 437	57	1.6	1621	19	US-10-935-098-14	Sequence 5454, App
C 365	1.6	2419	17	US-10-310-154-151	Sequence 151, App	C 438	57	1.6	1782	18	US-10-425-115-5454	Sequence 97293, A
C 366	1.6	2591	18	US-10-357-930-21265	Sequence 21265, A	C 439	57	1.6	1968	17	US-10-424-599-97293	Sequence 20, Appl
C 367	1.6	2591	18	US-10-357-930-27107	Sequence 27107, A	C 440	57	1.6	2235	15	US-10-318-780-20	Sequence 51, Appl
C 368	1.6	2713	16	US-10-436-523-1	Sequence 1, Appl	C 441	57	1.6	2581	14	US-10-062-548-51	Sequence 51, Appl
C 369	1.6	2713	16	US-10-436-523-31	Sequence 31, Appl	C 442	57	1.6	2581	19	US-10-918-446-51	Sequence 51, Appl

C 443	57	1.6	2584	17	US-10-632-983-47	Sequence 47, Appl	c 516	56	1.6	895	18	US-10-767-701-9396	Sequence 9396, Ap
C 444	57	1.6	3160	13	US-10-098-841-273	Sequence 273, Appl	517	56	1.6	907	18	US-10-481-652-11	Sequence 11, Appl
C 445	56	1.6	72	9	US-09-919-580-221	Sequence 221, Appl	c 518	56	1.6	931	10	US-09-984-276-31	Sequence 31, Appl
C 446	56	1.6	73	9	US-09-919-580-542	Sequence 542, Appl	c 519	56	1.6	931	10	US-09-984-271-31	Sequence 31, Appl
C 447	56	1.6	74	9	US-09-919-580-262	Sequence 262, Appl	c 520	56	1.6	938	18	US-10-425-115-70736	Sequence 70736, A
C 448	56	1.6	74	9	US-09-919-580-394	Sequence 394, Appl	c 521	56	1.6	980	15	US-10-425-115-70736	Sequence 26, Appl
C 449	56	1.6	74	18	US-10-021-323-9257	Sequence 9257, Ap	c 522	56	1.6	1039	18	US-10-799-747-26	Sequence 141566,
C 450	56	1.6	77	9	US-09-919-580-1325	Sequence 135, Appl	c 523	56	1.6	1039	18	US-10-739-930-1331	Sequence 1331, Ap
C 451	56	1.6	79	9	US-09-919-580-206	Sequence 206, Appl	c 524	56	1.6	1070	17	US-10-424-599-141566	Sequence 141566,
C 452	56	1.6	81	9	US-09-919-580-749	Sequence 749, Appl	c 525	56	1.6	1080	18	US-10-425-115-107267	Sequence 107267,
C 453	56	1.6	82	9	US-09-919-580-220	Sequence 220, Appl	c 526	56	1.6	1085	18	US-10-425-115-136900	Sequence 136900,
C 454	56	1.6	82	9	US-09-919-580-278	Sequence 278, Appl	c 527	56	1.6	1138	9	US-09-800-729-44	Sequence 44, Appl
C 455	56	1.6	90	9	US-09-919-580-157	Sequence 157, Appl	c 528	56	1.6	1342	18	US-10-425-115-150282	Sequence 44, Appl
C 456	56	1.6	95	9	US-09-919-580-246	Sequence 246, Appl	c 529	56	1.6	1362	15	US-10-050-882-44	Sequence 37, Appl
C 457	56	1.6	100	9	US-09-919-580-428	Sequence 428, Appl	c 530	56	1.6	1367	16	US-10-411-224-37	Sequence 37, Appl
C 458	56	1.6	105	14	US-10-066-543-872	Sequence 872, Appl	c 531	56	1.6	1367	17	US-10-047-021-37	Sequence 20, Appl
C 459	56	1.6	113	9	US-09-983-965-4693	Sequence 4693, Ap	c 532	56	1.6	1407	17	US-10-426-776-20	Sequence 104777,
C 460	56	1.6	117	9	US-09-919-580-762	Sequence 762, Appl	c 533	56	1.6	1408	18	US-10-425-115-104777	Sequence 24, Appl
C 461	56	1.6	128	14	US-10-066-543-1216	Sequence 1216, Ap	c 534	56	1.6	1421	16	US-10-411-224-24	Sequence 24, Appl
C 462	56	1.6	154	9	US-09-919-580-152	Sequence 152, Appl	c 535	56	1.6	1421	17	US-10-047-021-24	Sequence 193, App
C 463	56	1.6	160	9	US-09-960-352-11058	Sequence 11058, A	c 536	56	1.6	1524	9	US-09-925-302-193	Sequence 153, App
C 464	56	1.6	161	9	US-09-919-580-243	Sequence 243, Appl	c 537	56	1.6	1524	10	US-09-925-302-193	Sequence 227, App
C 465	56	1.6	208	17	US-10-424-599-123367	Sequence 123367,	c 538	56	1.6	1526	17	US-10-364-237-227	Sequence 8255, A
C 466	56	1.6	244	18	US-10-425-115-88230	Sequence 88230, A	c 539	56	1.6	1548	18	US-10-425-115-88255	Sequence 138108,
C 467	56	1.6	255	18	US-10-425-115-25874	Sequence 25874, A	c 540	56	1.6	1554	18	US-10-425-115-138108	Sequence 581, App
C 468	56	1.6	279	17	US-10-424-599-83996	Sequence 83996, A	c 541	56	1.6	1574	9	US-09-925-301-581	Sequence 134, App
C 469	56	1.6	286	9	US-09-960-352-8161	Sequence 8161, Ap	c 542	56	1.6	1657	9	US-09-925-301-134	Sequence 144, App
C 470	56	1.6	338	18	US-10-437-963-57609	Sequence 57609, A	c 543	56	1.6	1694	9	US-09-925-299-144	Sequence 144, App
C 471	56	1.6	353	18	US-10-425-115-113949	Sequence 113949,	c 544	56	1.6	1694	10	US-09-925-299-144	Sequence 115253,
C 472	56	1.6	366	18	US-10-425-115-130732	Sequence 130732,	c 545	56	1.6	1694	18	US-10-425-115-115253	Sequence 102, App
C 473	56	1.6	367	17	US-10-424-599-65070	Sequence 65070, A	c 546	56	1.6	1722	10	US-09-984-276-102	Sequence 102, App
C 474	56	1.6	370	18	US-10-437-963-26300	Sequence 26300, A	c 547	56	1.6	1722	10	US-09-984-271-102	Sequence 1239, Ap
C 475	56	1.6	383	17	US-10-424-599-46064	Sequence 46064, A	c 548	56	1.6	1724	17	US-10-364-237-1217	Sequence 61177, A
C 476	56	1.6	398	17	US-10-424-599-13756	Sequence 13756, A	c 549	56	1.6	1732	17	US-10-424-599-61177	Sequence 108, App
C 477	56	1.6	401	17	US-10-424-599-58129	Sequence 58129, A	c 550	56	1.6	1779	10	US-09-892-877-108	Sequence 108, App
C 478	56	1.6	408	9	US-09-960-352-11233	Sequence 11233, A	c 551	56	1.6	1779	10	US-09-948-783-109	Sequence 109, App
C 479	56	1.6	411	17	US-10-425-115-16531	Sequence 16531, A	c 552	56	1.6	1791	18	US-10-425-115-48559	Sequence 48559, A
C 480	56	1.6	417	18	US-10-424-599-117777	Sequence 117777,	c 553	56	1.6	1825	9	US-09-922-261-75	Sequence 75, Appl
C 481	56	1.6	424	9	US-09-960-352-13484	Sequence 13484, A	c 554	56	1.6	1825	17	US-10-364-237-1324	Sequence 1324, Ap
C 482	56	1.6	437	9	US-09-924-035A-152	Sequence 152, Appl	c 555	56	1.6	1977	17	US-10-364-237-1217	Sequence 1217, Ap
C 483	56	1.6	438	18	US-10-425-115-70695	Sequence 70695, A	c 556	56	1.6	2108	18	US-10-425-115-14255	Sequence 14255, A
C 484	56	1.6	456	18	US-10-425-115-59159	Sequence 59159, A	c 557	56	1.6	2539	18	US-10-425-115-14255	Sequence 140288,
C 485	56	1.6	464	18	US-10-437-963-19054	Sequence 19054, A	c 558	56	1.6	2755	17	US-10-264-049-222	Sequence 222, App
C 486	56	1.6	467	18	US-10-437-963-598	Sequence 598, Appl	c 559	56	1.6	3144	9	US-09-925-302-191	Sequence 191, App
C 487	56	1.6	467	18	US-10-437-963-598	Sequence 598, Appl	c 560	56	1.6	3144	10	US-09-814-353-20006	Sequence 131, App
C 488	56	1.6	467	18	US-10-425-115-89331	Sequence 89331, A	c 561	56	1.6	4773	10	US-09-814-353-20006	Sequence 20006, A
C 489	56	1.6	485	18	US-10-357-930-55641	Sequence 55641, A	c 562	55	1.5	94	14	US-10-066-543-1258	Sequence 1258, Ap
C 490	56	1.6	487	9	US-09-729-835-22	Sequence 22, Appl	c 563	55	1.5	96	14	US-10-066-543-713	Sequence 713, App
C 491	56	1.6	506	17	US-10-373-809-22	Sequence 22, Appl	c 564	55	1.5	110	14	US-10-066-543-342	Sequence 342, App
C 492	56	1.6	521	18	US-10-424-599-56636	Sequence 56636, A	c 565	55	1.5	138	9	US-09-983-965-207	Sequence 207, App
C 493	56	1.6	521	18	US-10-425-115-111585	Sequence 111585,	c 566	55	1.5	172	9	US-09-815-343-1505	Sequence 1505, Ap
C 494	56	1.6	522	18	US-10-425-115-123105	Sequence 123105,	c 567	55	1.5	172	17	US-10-097-105-1505	Sequence 1505, Ap
C 495	56	1.6	531	17	US-10-424-599-81285	Sequence 81285, A	c 568	55	1.5	210	9	US-09-960-352-3981	Sequence 3981, Ap
C 496	56	1.6	541	17	US-10-424-599-35290	Sequence 35290, A	c 569	55	1.5	252	18	US-10-425-115-100475	Sequence 100475,
C 497	56	1.6	554	17	US-10-424-599-97944	Sequence 97944, A	c 570	55	1.5	257	9	US-09-960-352-8890	Sequence 8890, App
C 498	56	1.6	554	18	US-10-021-323-5547	Sequence 5547, Ap	c 571	55	1.5	277	9	US-09-924-035A-585	Sequence 585, App
C 499	56	1.6	558	18	US-10-425-115-37527	Sequence 37527, A	c 572	55	1.5	278	18	US-10-425-115-105175	Sequence 105175,
C 500	56	1.6	565	18	US-10-425-115-18764	Sequence 18764, A	c 573	55	1.5	321	9	US-09-960-352-13013	Sequence 13013, A
C 501	56	1.6	565	18	US-10-425-115-37807	Sequence 37807, A	c 574	55	1.5	328	18	US-10-425-115-144615	Sequence 144615,
C 502	56	1.6	569	18	US-10-425-115-31618	Sequence 31618, A	c 575	55	1.5	344	18	US-10-425-115-68510	Sequence 68510, A
C 503	56	1.6	569	17	US-10-424-599-34774	Sequence 34774, A	c 576	55	1.5	355	9	US-09-960-352-2945	Sequence 2945, Ap
C 504	56	1.6	571	18	US-10-425-115-69390	Sequence 89390, A	c 577	55	1.5	359	9	US-09-770-791-558	Sequence 558, App
C 505	56	1.6	575	18	US-10-425-115-70286	Sequence 70286, A	c 578	55	1.5	360	18	US-10-425-115-154595	Sequence 154595,
C 506	56	1.6	579	18	US-10-425-115-44286	Sequence 44286, A	c 579	55	1.5	365	17	US-10-424-599-120990	Sequence 120990,
C 507	56	1.6	585	18	US-10-425-115-175362	Sequence 175362,	c 580	55	1.5	381	10	US-09-918-995-8255	Sequence 8255, Ap
C 508	56	1.6	587	18	US-10-021-323-15513	Sequence 15513,	c 581	55	1.5	382	18	US-10-767-701-16889	Sequence 16889, A
C 509	56	1.6	601	18	US-10-437-963-39474	Sequence 39474, A	c 582	55	1.5	392	18	US-10-425-115-13019	Sequence 13019, A
C 510	56	1.6	639	18	US-10-482-985-10	Sequence 10, Appl	c 583	55	1.5	393	18	US-10-425-115-122487	Sequence 122487,
C 511	56	1.6	659	18	US-10-425-115-45561	Sequence 45561, A	c 584	55	1.5	402	18	US-10-437-963-34549	Sequence 34549, A
C 512	56	1.6	669	17	US-10-424-599-141641	Sequence 141641,	c 585	55	1.5	426	18	US-10-425-115-54531	Sequence 54531, A
C 513	56	1.6	735	18	US-10-425-115-62884	Sequence 62884, A	c 586	55	1.5	439	9	US-09-764-869-332	Sequence 332, App
C 514	56	1.6	824	14	US-10-144-929-29	Sequence 29, Appl	c 587	55	1.5	439	14	US-10-091-504-332	Sequence 332, App
C 515	56	1.6	824	17	US-10-144-929-29	Sequence 29, Appl	c 588	55	1.5	439	17	US-10-227-577-332	Sequence 332, App

589	55	1.5	441	17	US-10-424-599-31092	Sequence 31092, A	c 662	54	1.5	354	18	US-10-425-115-26048	Sequence 26048, A
590	55	1.5	502	18	US-10-425-115-137010	Sequence 137010, A	c 663	54	1.5	360	9	US-09-770-791-532	Sequence 532, App
591	55	1.5	509	18	US-10-437-963-845010	Sequence 84501, A	c 664	54	1.5	367	18	US-10-425-115-49226	Sequence 49226, A
592	55	1.5	518	18	US-10-437-963-23217	Sequence 23217, A	c 665	54	1.5	369	18	US-10-425-115-52629	Sequence 52629, A
593	55	1.5	535	18	US-10-425-115-6513	Sequence 6513, App	c 666	54	1.5	380	18	US-10-425-115-60437	Sequence 60437, A
594	55	1.5	551	18	US-10-425-115-154555	Sequence 154555, A	c 667	54	1.5	381	18	US-10-425-115-78509	Sequence 78509, A
595	55	1.5	559	18	US-10-425-115-18763	Sequence 18763, A	c 668	54	1.5	382	18	US-10-425-115-78509	Sequence 78509, A
596	55	1.5	559	18	US-10-425-115-155836	Sequence 155836, A	c 669	54	1.5	384	18	US-10-425-115-180943	Sequence 180943, A
597	55	1.5	568	18	US-10-021-323-12971	Sequence 12971, A	c 670	54	1.5	385	9	US-09-924-035A-848	Sequence 848, App
598	55	1.5	568	18	US-10-021-323-8302	Sequence 8302, App	c 671	54	1.5	390	17	US-10-424-599-3459	Sequence 3459, App
599	55	1.5	579	18	US-10-021-323-17839	Sequence 17839, A	c 672	54	1.5	393	18	US-10-437-963-100408	Sequence 100408, A
600	55	1.5	598	17	US-10-424-599-89182	Sequence 89182, A	c 673	54	1.5	398	17	US-10-424-599-73667	Sequence 73667, A
601	55	1.5	603	18	US-10-021-323-5966	Sequence 5966, App	c 674	54	1.5	407	18	US-10-021-323-9680	Sequence 9680, App
602	55	1.5	604	14	US-10-144-929-15	Sequence 15, App	c 675	54	1.5	408	18	US-10-437-963-19491	Sequence 19491, A
603	55	1.5	604	17	US-10-144-929-15	Sequence 15, App	c 676	54	1.5	410	9	US-09-960-352-8969	Sequence 8969, App
604	55	1.5	621	18	US-10-425-115-82625	Sequence 82625, A	c 677	54	1.5	412	18	US-10-425-115-84156	Sequence 84156, A
605	55	1.5	638	18	US-10-425-115-12248	Sequence 12248, A	c 678	54	1.5	417	10	US-09-918-995-6724	Sequence 6724, App
606	55	1.5	756	18	US-10-425-115-51642	Sequence 51642, A	c 679	54	1.5	421	18	US-10-425-115-43004	Sequence 43004, A
607	55	1.5	832	10	US-09-774-639-57	Sequence 57, App	c 680	54	1.5	426	9	US-09-924-035A-817	Sequence 817, App
608	55	1.5	832	10	US-09-969-730-18	Sequence 18, App	c 681	54	1.5	428	17	US-10-424-599-15564	Sequence 15564, A
609	55	1.5	832	17	US-10-621-363-18	Sequence 18, App	c 682	54	1.5	432	17	US-10-424-599-107176	Sequence 107176, A
610	55	1.5	834	18	US-10-739-930-1368	Sequence 1368, App	c 683	54	1.5	432	18	US-10-425-115-167620	Sequence 167620, A
611	55	1.5	878	18	US-10-425-115-173677	Sequence 173677, A	c 684	54	1.5	440	18	US-10-425-115-22621	Sequence 22621, A
612	55	1.5	880	18	US-10-425-115-8129	Sequence 8129, App	c 685	54	1.5	448	17	US-10-424-599-6035	Sequence 6035, App
613	55	1.5	974	18	US-10-337-930-25629	Sequence 25629, A	c 686	54	1.5	450	17	US-10-424-599-108900	Sequence 108900, A
614	55	1.5	1001	18	US-09-986-480-93	Sequence 93, App	c 687	54	1.5	472	18	US-10-425-115-20833	Sequence 20833, A
615	55	1.5	1027	18	US-10-739-930-1883	Sequence 1883, App	c 688	54	1.5	472	18	US-10-425-115-40048	Sequence 40048, A
616	55	1.5	1049	17	US-10-425-115-131033	Sequence 131033, A	c 689	54	1.5	477	18	US-10-437-963-15271	Sequence 15271, A
617	55	1.5	1129	17	US-10-264-237-1241	Sequence 1241, App	c 690	54	1.5	478	18	US-10-425-115-23077	Sequence 23077, A
618	55	1.5	1142	10	US-09-397-945-88	Sequence 88, App	c 691	54	1.5	482	18	US-10-437-963-68155	Sequence 68155, A
619	55	1.5	1259	17	US-10-653-595-88	Sequence 88, App	c 692	54	1.5	484	10	US-09-918-995-11820	Sequence 11820, A
620	55	1.5	1259	17	US-10-264-049-886	Sequence 886, App	c 693	54	1.5	487	18	US-10-021-323-8739	Sequence 8739, App
621	55	1.5	1265	18	US-10-425-115-150426	Sequence 150426, A	c 694	54	1.5	487	18	US-10-767-795-6225	Sequence 6225, App
622	55	1.5	1355	18	US-10-425-115-125985	Sequence 125985, A	c 695	54	1.5	499	18	US-10-425-115-88302	Sequence 88302, A
623	55	1.5	1392	18	US-10-425-115-107438	Sequence 107438, A	c 696	54	1.5	510	10	US-09-814-353-18805	Sequence 18805, A
624	55	1.5	1418	18	US-10-425-115-110834	Sequence 110834, A	c 697	54	1.5	514	18	US-10-021-323-7651	Sequence 7651, App
625	55	1.5	1459	18	US-10-425-115-124308	Sequence 124308, A	c 698	54	1.5	522	18	US-10-425-115-129269	Sequence 129269, A
626	55	1.5	1473	9	US-09-796-753-47	Sequence 47, App	c 699	54	1.5	523	18	US-10-425-115-13607	Sequence 13607, A
627	55	1.5	1539	9	US-09-925-300-447	Sequence 447, App	c 700	54	1.5	523	18	US-10-425-115-44359	Sequence 44359, A
628	55	1.5	1794	18	US-10-425-115-76840	Sequence 76840, A	c 701	54	1.5	531	18	US-10-425-115-181362	Sequence 181362, A
629	55	1.5	1796	18	US-10-425-115-74502	Sequence 74502, A	c 702	54	1.5	535	17	US-10-424-599-117295	Sequence 117295, A
630	55	1.5	1945	18	US-10-425-115-65906	Sequence 65906, A	c 703	54	1.5	540	18	US-10-425-115-123478	Sequence 123478, A
631	55	1.5	2197	18	US-10-723-860-4898	Sequence 4898, App	c 704	54	1.5	545	18	US-10-437-963-89099	Sequence 89099, A
632	55	1.5	2224	17	US-10-424-599-10608	Sequence 10608, A	c 705	54	1.5	550	9	US-09-764-887-91	Sequence 91, App
633	55	1.5	2438	17	US-10-264-049-796	Sequence 796, App	c 706	54	1.5	550	14	US-10-073-961-91	Sequence 91, App
634	55	1.5	2888	17	US-10-443-622-33	Sequence 33, App	c 707	54	1.5	554	18	US-10-425-115-27542	Sequence 27542, A
635	55	1.5	2895	10	US-09-759-130B-271	Sequence 271, App	c 708	54	1.5	555	18	US-10-425-115-171087	Sequence 171087, A
636	55	1.5	2895	14	US-10-189-123-1	Sequence 1, App	c 709	54	1.5	556	17	US-10-424-599-74285	Sequence 74285, A
637	55	1.5	2895	16	US-10-188-495-1	Sequence 1, App	c 710	54	1.5	562	17	US-10-425-115-41747	Sequence 41747, A
638	55	1.5	3036	17	US-10-741-790-271	Sequence 271, App	c 711	54	1.5	562	17	US-10-424-599-87969	Sequence 87969, A
639	55	1.5	3036	17	US-10-264-049-931	Sequence 931, App	c 712	54	1.5	563	18	US-10-425-115-6781	Sequence 6781, App
640	55	1.5	3037	14	US-10-050-704-46	Sequence 46, App	c 713	54	1.5	563	18	US-10-425-115-110109	Sequence 110109, A
641	55	1.5	3037	18	US-10-788-512-46	Sequence 46, App	c 714	54	1.5	585	18	US-10-425-115-1869	Sequence 1869, App
642	55	1.5	3058	17	US-10-424-599-13614	Sequence 13614, A	c 715	54	1.5	588	18	US-10-021-323-8041	Sequence 8041, App
643	55	1.5	3234	18	US-10-425-115-74703	Sequence 74703, A	c 716	54	1.5	605	18	US-10-425-115-148026	Sequence 148026, A
644	55	1.5	3585	18	US-10-437-963-13180	Sequence 13180, A	c 717	54	1.5	635	17	US-10-424-599-70780	Sequence 70780, A
645	55	1.5	6023	17	US-10-138-588-51	Sequence 51, App	c 718	54	1.5	638	9	US-09-925-301-630	Sequence 630, App
646	55	1.5	7001	18	US-10-437-963-98673	Sequence 98673, A	c 719	54	1.5	652	18	US-10-425-115-74276	Sequence 74276, A
647	54	1.5	66	14	US-10-066-543-585	Sequence 585, App	c 720	54	1.5	653	17	US-10-424-599-46097	Sequence 46097, A
648	54	1.5	180	18	US-10-021-323-2502	Sequence 2502, App	c 721	54	1.5	682	18	US-10-425-115-157131	Sequence 157131, A
649	54	1.5	193	18	US-10-425-115-37812	Sequence 37812, A	c 722	54	1.5	684	18	US-10-425-115-118289	Sequence 118289, A
650	54	1.5	203	9	US-09-960-352-5438	Sequence 5438, App	c 723	54	1.5	752	18	US-10-767-795-2049	Sequence 2049, App
651	54	1.5	215	18	US-10-425-115-123101	Sequence 123101, A	c 724	54	1.5	772	18	US-10-425-115-152740	Sequence 152740, A
652	54	1.5	221	18	US-10-357-930-59145	Sequence 59145, A	c 725	54	1.5	796	17	US-10-333-184-311	Sequence 311, App
653	54	1.5	226	18	US-10-021-323-15685	Sequence 15685, A	c 726	54	1.5	812	18	US-10-425-115-97406	Sequence 97406, A
654	54	1.5	242	18	US-10-425-115-47703	Sequence 47703, A	c 727	54	1.5	848	14	US-10-198-846-8654	Sequence 8654, App
655	54	1.5	260	17	US-10-424-599-13375	Sequence 13375, A	c 728	54	1.5	848	16	US-10-231-417-55	Sequence 55, App
656	54	1.5	279	18	US-10-425-115-17712	Sequence 17712, A	c 729	54	1.5	854	13	US-10-001-887-25	Sequence 25, App
657	54	1.5	308	18	US-10-425-115-142042	Sequence 142042, A	c 730	54	1.5	854	19	US-10-958-863-25	Sequence 25, App
658	54	1.5	336	18	US-10-425-115-11658	Sequence 11658, A	c 731	54	1.5	866	18	US-10-425-115-76851	Sequence 76851, A
659	54	1.5	344	18	US-10-425-115-85675	Sequence 85675, A	c 732	54	1.5	883	17	US-10-264-049-416	Sequence 416, App
660	54	1.5	345	18	US-10-425-115-66223	Sequence 66223, A	c 733	54	1.5	927	18	US-10-739-930-1431	Sequence 1431, App
661	54	1.5	347	18	US-10-425-115-20886	Sequence 20886, A	c 734	54	1.5	928	18	US-10-425-115-5274	Sequence 5274, App

C 735	54	1.5	942	17	US-10-424-599-91119	Sequence 91119, A	808	53	1.5	263	18	US-10-425-115-174630	Sequence 174630,
C 736	54	1.5	978	18	US-10-767-795-4358	Sequence 4358, Ap	809	53	1.5	264	9	US-09-867-701-10185	Sequence 10185, A
C 737	54	1.5	993	18	US-10-739-930-1579	Sequence 1579, Ap	810	53	1.5	265	18	US-10-437-963-4817	Sequence 4817, Ap
C 738	54	1.5	1007	18	US-10-425-115-53453	Sequence 53453, A	C 811	53	1.5	266	18	US-10-425-115-88938	Sequence 88938, A
C 739	54	1.5	1046	18	US-10-425-115-80457	Sequence 80457, A	C 812	53	1.5	269	17	US-10-424-599-134367	Sequence 134367,
C 740	54	1.5	1060	9	US-09-925-299-43	Sequence 43, Appl	C 813	53	1.5	269	18	US-10-357-930-7483	Sequence 7483, Ap
C 741	54	1.5	1060	10	US-09-925-299-43	Sequence 43, Appl	C 814	53	1.5	275	9	US-09-919-580-75	Sequence 75, Appl
C 742	54	1.5	1081	18	US-10-425-115-155277	Sequence 155277, A	C 815	53	1.5	275	18	US-10-425-115-180214	Sequence 180214,
C 743	54	1.5	1123	18	US-10-739-930-3770	Sequence 3770, Ap	C 816	53	1.5	281	10	US-09-814-353-17383	Sequence 17383, A
C 744	54	1.5	1150	17	US-10-424-599-121759	Sequence 121759, Ap	C 817	53	1.5	281	18	US-10-357-930-17394	Sequence 35994, A
C 745	54	1.5	1194	18	US-10-744-572-13	Sequence 13, Appl	C 818	53	1.5	283	18	US-10-357-930-61322	Sequence 61322, A
C 746	54	1.5	1221	18	US-10-739-930-1833	Sequence 1833, Ap	C 819	53	1.5	285	18	US-10-425-115-34607	Sequence 34607, A
C 747	54	1.5	1269	15	US-10-180-375-135	Sequence 135, App	C 820	53	1.5	286	17	US-10-424-599-134048	Sequence 134048,
C 748	54	1.5	1298	17	US-10-183-687-265	Sequence 265, App	C 821	53	1.5	290	18	US-10-437-963-51258	Sequence 51258, A
C 749	54	1.5	1369	18	US-10-425-115-81395	Sequence 81395, A	C 822	53	1.5	295	9	US-09-764-846-33	Sequence 33, Appl
C 750	54	1.5	1408	18	US-10-425-115-28249	Sequence 28249, A	C 823	53	1.5	295	14	US-10-091-483-33	Sequence 33, Appl
C 751	54	1.5	1723	14	US-10-012-542-98	Sequence 98, Appl	C 824	53	1.5	296	10	US-09-814-353-5940	Sequence 5940, Ap
C 752	54	1.5	1723	14	US-10-115-123-98	Sequence 98, Appl	C 825	53	1.5	296	10	US-09-814-353-12220	Sequence 12220, A
C 753	54	1.5	1774	18	US-10-425-115-117350	Sequence 117350, A	C 826	53	1.5	296	18	US-10-425-115-98517	Sequence 98517, A
C 754	54	1.5	1797	17	US-10-424-599-41191	Sequence 41191, A	C 827	53	1.5	298	17	US-10-424-599-120040	Sequence 120040,
C 755	54	1.5	1847	17	US-10-264-049-820	Sequence 820, App	C 828	53	1.5	303	18	US-10-437-963-51951	Sequence 51951, A
C 756	54	1.5	1931	10	US-09-813-153-78	Sequence 78, Appl	C 829	53	1.5	304	9	US-09-764-846-109	Sequence 109, App
C 757	54	1.5	1932	10	US-09-813-153-78	Sequence 78, Appl	C 830	53	1.5	304	14	US-10-091-483-109	Sequence 109, App
C 758	54	1.5	2017	17	US-10-424-599-108607	Sequence 108607, A	C 831	53	1.5	304	17	US-10-424-599-133280	Sequence 133280,
C 759	54	1.5	2029	18	US-10-437-963-91052	Sequence 91052, A	C 832	53	1.5	305	17	US-10-424-599-94601	Sequence 94601, A
C 760	54	1.5	2053	18	US-10-425-115-142365	Sequence 142365, A	C 833	53	1.5	310	17	US-10-424-599-69405	Sequence 69405, A
C 761	54	1.5	2058	17	US-10-424-599-63979	Sequence 63979, A	C 834	53	1.5	311	18	US-10-425-115-82662	Sequence 82662, A
C 762	54	1.5	2150	18	US-10-881-088-37	Sequence 37, Appl	C 835	53	1.5	312	18	US-10-425-115-125299	Sequence 125299,
C 763	54	1.5	2254	17	US-10-424-599-3803	Sequence 3803, Ap	C 836	53	1.5	313	9	US-09-960-352-2670	Sequence 2670, Ap
C 764	54	1.5	2386	18	US-10-739-930-1418	Sequence 1418, Ap	C 837	53	1.5	317	18	US-10-357-930-15166	Sequence 15166, A
C 765	54	1.5	2506	18	US-10-425-115-95015	Sequence 95015, A	C 838	53	1.5	318	10	US-09-814-353-6389	Sequence 6389, Ap
C 766	54	1.5	2728	18	US-10-425-115-57309	Sequence 57309, A	C 839	53	1.5	318	10	US-09-814-353-12666	Sequence 12666, A
C 767	54	1.5	2753	18	US-10-437-963-78534	Sequence 78534, A	C 840	53	1.5	318	18	US-10-425-115-25520	Sequence 25520, A
C 768	54	1.5	2756	9	US-09-925-301-351	Sequence 351, App	C 841	53	1.5	318	18	US-10-425-115-26677	Sequence 26677, A
C 769	54	1.5	3006	9	US-09-962-678-1	Sequence 1, Appl	C 842	53	1.5	320	17	US-10-424-599-22672	Sequence 22672, A
C 770	54	1.5	3066	17	US-10-184-648-38	Sequence 38, Appl	C 843	53	1.5	321	18	US-10-425-115-169025	Sequence 169025,
C 771	54	1.5	3552	10	US-09-814-353-19891	Sequence 19891, A	C 844	53	1.5	321	18	US-10-425-115-37134	Sequence 37134, A
C 772	54	1.5	3552	14	US-10-198-846-11479	Sequence 11479, A	C 845	53	1.5	323	18	US-10-357-930-61015	Sequence 61015, A
C 773	54	1.5	3552	18	US-10-357-930-21448	Sequence 21448, A	C 846	53	1.5	324	17	US-10-424-599-131074	Sequence 131074,
C 774	54	1.5	3552	18	US-10-357-930-27289	Sequence 27289, A	C 847	53	1.5	327	18	US-10-425-115-130293	Sequence 130293,
C 775	53	1.5	58	9	US-09-919-580-703	Sequence 703, App	C 848	53	1.5	328	10	US-09-814-353-17578	Sequence 17578, A
C 776	53	1.5	60	9	US-09-919-580-419	Sequence 419, App	C 849	53	1.5	331	17	US-10-125-968-928	Sequence 928, App
C 777	53	1.5	74	14	US-10-066-543-1108	Sequence 1108, Ap	C 850	53	1.5	332	10	US-09-814-353-5594	Sequence 5594, Ap
C 778	53	1.5	90	9	US-09-919-580-217	Sequence 217, App	C 851	53	1.5	332	10	US-09-814-353-11881	Sequence 11881, A
C 779	53	1.5	90	14	US-10-066-543-328	Sequence 328, App	C 852	53	1.5	336	10	US-09-814-353-4742	Sequence 4742, Ap
C 780	53	1.5	107	14	US-10-066-543-1787	Sequence 1787, Ap	C 853	53	1.5	336	10	US-09-814-353-11039	Sequence 11039, A
C 781	53	1.5	125	18	US-10-466-894-229	Sequence 229, App	C 854	53	1.5	337	9	US-09-770-791-889	Sequence 889, App
C 782	53	1.5	144	13	US-10-114-893-208	Sequence 208, App	C 855	53	1.5	337	18	US-10-357-930-60892	Sequence 60892, A
C 783	53	1.5	160	18	US-10-466-894-269	Sequence 269, App	C 856	53	1.5	337	18	US-10-131-827-8601	Sequence 8601, Ap
C 784	53	1.5	175	9	US-09-983-965-2999	Sequence 2999, Ap	C 857	53	1.5	338	18	US-10-425-115-22891	Sequence 22891, A
C 785	53	1.5	197	17	US-10-264-049-1247	Sequence 1247, Ap	C 858	53	1.5	339	18	US-10-357-930-49015	Sequence 49015, A
C 786	53	1.5	202	9	US-09-960-352-9114	Sequence 9114, Ap	C 859	53	1.5	339	18	US-10-425-115-80751	Sequence 80751, A
C 787	53	1.5	204	18	US-10-357-930-19212	Sequence 19212, A	C 860	53	1.5	339	18	US-10-425-115-126017	Sequence 126017, A
C 788	53	1.5	211	18	US-10-357-930-14987	Sequence 14987, A	C 861	53	1.5	340	18	US-10-425-115-3498	Sequence 3498, Ap
C 789	53	1.5	214	17	US-10-242-535A-15838	Sequence 15838, A	C 862	53	1.5	340	18	US-10-425-115-88133	Sequence 88133, A
C 790	53	1.5	214	17	US-10-085-783A-15838	Sequence 15838, A	C 863	53	1.5	341	18	US-10-425-115-14920	Sequence 14920, A
C 791	53	1.5	219	18	US-10-357-930-60860	Sequence 60860, A	C 864	53	1.5	342	18	US-10-425-115-53693	Sequence 53693, A
C 792	53	1.5	221	17	US-10-424-599-11732	Sequence 11732, A	C 865	53	1.5	343	18	US-10-425-115-49757	Sequence 49757, A
C 793	53	1.5	222	10	US-09-814-353-18350	Sequence 18350, A	C 866	53	1.5	343	18	US-10-357-930-60962	Sequence 60962, A
C 794	53	1.5	224	18	US-10-425-115-87153	Sequence 87153, A	C 867	53	1.5	344	17	US-10-424-599-97275	Sequence 97275, A
C 795	53	1.5	225	17	US-10-242-535A-46212	Sequence 46212, A	C 868	53	1.5	344	18	US-10-021-323-1846	Sequence 1846, Ap
C 796	53	1.5	225	17	US-10-085-783A-46212	Sequence 46212, A	C 869	53	1.5	346	10	US-09-814-353-17676	Sequence 17676, A
C 797	53	1.5	226	18	US-10-357-930-5818	Sequence 5818, Ap	C 870	53	1.5	347	9	US-09-960-352-3771	Sequence 3771, Ap
C 798	53	1.5	233	18	US-10-425-115-70230	Sequence 70230, A	C 871	53	1.5	350	10	US-09-814-353-5753	Sequence 5753, Ap
C 799	53	1.5	234	10	US-09-814-353-4810	Sequence 4810, Ap	C 872	53	1.5	350	10	US-09-814-353-12036	Sequence 12036, A
C 800	53	1.5	234	10	US-09-814-353-11107	Sequence 11107, A	C 873	53	1.5	350	17	US-10-424-599-41239	Sequence 41239, A
C 801	53	1.5	235	18	US-10-357-930-60948	Sequence 60948, A	C 874	53	1.5	351	10	US-09-814-353-48899	Sequence 48899, Ap
C 802	53	1.5	240	10	US-09-814-353-12780	Sequence 12780, A	C 875	53	1.5	351	10	US-09-814-353-11194	Sequence 11194, A
C 803	53	1.5	241	10	US-09-814-353-5827	Sequence 5827, Ap	C 876	53	1.5	351	17	US-10-424-599-115233	Sequence 115233,
C 804	53	1.5	248	18	US-10-357-930-60895	Sequence 60895, A	C 877	53	1.5	352	18	US-10-357-930-56917	Sequence 56917, A
C 805	53	1.5	255	17	US-10-424-599-56737	Sequence 56737, A	C 878	53	1.5	352	18	US-10-357-930-60876	Sequence 60876, A
C 806	53	1.5	256	18	US-10-425-115-167530	Sequence 167530, A	C 879	53	1.5	354	18	US-10-425-115-53496	Sequence 53496, A
C 807	53	1.5	262	18	US-10-425-115-130837	Sequence 130837, A	C 880	53	1.5	358	10	US-09-814-353-6302	Sequence 6302, Ap

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882	53	1.5	358	18	US-10-437-963-28060	Sequence 28060, A	955	53	1.5	418	18	US-10-425-115-148868	Sequence 148868, A
c 883	53	1.5	359	18	US-10-437-963-78882	Sequence 78882, A	956	53	1.5	419	17	US-10-424-599-8	Sequence 8, Appl
884	53	1.5	359	18	US-10-437-963-46653	Sequence 46653, A	957	53	1.5	420	18	US-10-425-115-102918	Sequence 102918, A
885	53	1.5	360	17	US-10-424-599-113609	Sequence 113609, A	958	53	1.5	420	18	US-10-357-930-56852	Sequence 56852, A
886	53	1.5	361	9	US-09-867-701-8566	Sequence 8566, Ap	959	53	1.5	421	18	US-10-425-115-61692	Sequence 61692, A
887	53	1.5	361	17	US-10-424-599-14016	Sequence 14016, A	960	53	1.5	422	17	US-10-424-599-82450	Sequence 82450, A
c 888	53	1.5	362	17	US-10-424-599-65278	Sequence 65278, A	961	53	1.5	422	17	US-10-424-599-82450	Sequence 82450, A
c 889	53	1.5	362	18	US-10-425-115-181680	Sequence 181680, A	962	53	1.5	422	18	US-10-425-115-113602	Sequence 113602, A
890	53	1.5	367	18	US-10-425-115-85200	Sequence 85200, A	963	53	1.5	423	18	US-10-425-115-178328	Sequence 178328, A
c 891	53	1.5	367	18	US-10-357-930-54992	Sequence 54992, A	964	53	1.5	423	18	US-10-425-115-172264	Sequence 172264, A
892	53	1.5	369	18	US-10-437-963-40696	Sequence 40696, A	965	53	1.5	424	18	US-10-437-963-32593	Sequence 32593, A
893	53	1.5	371	18	US-10-425-115-88000	Sequence 88000, A	966	53	1.5	426	18	US-10-357-930-38081	Sequence 38081, A
894	53	1.5	371	18	US-10-425-115-88000	Sequence 88000, A	967	53	1.5	426	18	US-10-357-930-38081	Sequence 38081, A
895	53	1.5	373	18	US-10-021-323-5700	Sequence 5700, Ap	968	53	1.5	426	18	US-10-357-930-38081	Sequence 38081, A
c 896	53	1.5	373	18	US-10-021-323-5700	Sequence 5700, Ap	969	53	1.5	426	18	US-10-357-930-38081	Sequence 38081, A
897	53	1.5	375	18	US-09-814-353-12535	Sequence 12535, A	970	53	1.5	429	18	US-10-437-963-18973	Sequence 18973, A
898	53	1.5	375	18	US-09-814-353-18474	Sequence 18474, A	971	53	1.5	429	18	US-10-425-115-67241	Sequence 67241, A
c 899	53	1.5	376	17	US-10-424-599-141998	Sequence 141998, A	972	53	1.5	430	14	US-10-078-090-87	Sequence 87, Appl
c 900	53	1.5	378	17	US-10-424-599-105378	Sequence 105378, A	973	53	1.5	430	17	US-10-424-599-98110	Sequence 98110, A
901	53	1.5	379	17	US-10-424-599-43341	Sequence 43341, A	974	53	1.5	430	17	US-10-437-963-19293	Sequence 19293, A
902	53	1.5	380	10	US-09-814-353-17491	Sequence 17491, A	975	53	1.5	432	18	US-10-425-115-52588	Sequence 52588, A
903	53	1.5	383	10	US-09-814-353-18006	Sequence 18006, A	976	53	1.5	432	18	US-10-425-115-52588	Sequence 52588, A
904	53	1.5	383	18	US-10-357-930-34078	Sequence 34078, A	977	53	1.5	433	10	US-09-814-353-4798	Sequence 4798, Ap
905	53	1.5	383	18	US-10-357-930-42946	Sequence 42946, A	978	53	1.5	433	10	US-09-814-353-11095	Sequence 11095, A
906	53	1.5	384	10	US-09-814-353-18604	Sequence 18604, A	979	53	1.5	433	10	US-09-814-353-18420	Sequence 18420, A
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908	53	1.5	385	10	US-09-814-353-19050	Sequence 19050, A	981	53	1.5	434	18	US-09-814-353-17917	Sequence 17917, A
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925	53	1.5	396	15	US-09-970-966-10	Sequence 966, Ap	998	53	1.5	441	18	US-10-425-115-78734	Sequence 78734, A
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1187	53	1.5	536	18	US-10-425-115-161900	Sequence 161900, A	1260	53	1.5	570	10	US-09-814-353-12090	Sequence 12090, A
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1193	53	1.5	538	18	US-10-021-323-16995	Sequence 16995, A	1266	53	1.5	574	18	US-10-425-115-113952	Sequence 113952, A
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1198	53	1.5	539	18	US-10-425-115-10243	Sequence 10243, A	1271	53	1.5	578	18	US-10-021-323-7928	Sequence 7928, App
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1361	53	1.5	667	18	US-10-425-115-137182	Sequence 137182, A	c1434	53	1.5	1096	9	US-09-764-864-363	Sequence 363, App
1362	53	1.5	668	18	US-10-425-115-52791	Sequence 52791, A	c1435	53	1.5	1107	18	US-10-739-930-5240	Sequence 5240, Ap
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c1379	53	1.5	704	9	US-09-770-149-243	Sequence 243, App	c1452	53	1.5	1368	18	US-10-023-896-18	Sequence 18, Appl
1380	53	1.5	705	10	US-09-814-353-5022	Sequence 5022, Ap	1453	53	1.5	1369	14	US-10-715-872-132	Sequence 132, App
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1384	53	1.5	709	18	US-10-425-115-122726	Sequence 122726, A	c1457	53	1.5	1442	17	US-10-264-049-405	Sequence 405, App
1385	53	1.5	714	17	US-10-424-599-30576	Sequence 30576, A	c1458	53	1.5	1445	17	US-10-451-093-17	Sequence 23775, A
1386	53	1.5	716	18	US-10-425-115-79860	Sequence 79860, A	c1459	53	1.5	1457	18	US-10-437-963-23775	Sequence 4277, Ap
1387	53	1.5	721	18	US-10-425-115-10985	Sequence 10985, A	c1460	53	1.5	1506	18	US-10-437-963-40658	Sequence 40658, A
1388	53	1.5	723	10	US-09-814-353-4726	Sequence 4726, Ap	c1461	53	1.5	1521	18	US-10-425-115-120340	Sequence 120340,
1389	53	1.5	723	10	US-09-814-353-11024	Sequence 11024, A	c1462	53	1.5	1553	18	US-10-425-115-158775	Sequence 158775,
1390	53	1.5	723	18	US-10-425-115-274	Sequence 274, App	c1463	53	1.5	1575	18	US-10-425-115-159910	Sequence 159910,
c1391	53	1.5	723	18	US-10-425-115-106484	Sequence 106484, A	c1464	53	1.5	1585	17	US-10-374-780A-1747	Sequence 1747, Ap
										1591	17	US-10-191-803-135	Sequence 135, App

cl1465	53	1.5	1591	17	US-10-152-319A-1755	Sequence 1755, Ap
cl1466	53	1.5	1654	18	US-10-425-115-169117	Sequence 169117, A
cl1467	53	1.5	1669	18	US-10-437-963-93881	Sequence 93881, A
cl1468	53	1.5	1763	19	US-10-819-860-3	Sequence 3, Appli
cl1469	53	1.5	1811	17	US-10-424-599-59218	Sequence 59218, A
cl1470	53	1.5	1812	10	US-09-37A-046A-63	Sequence 63, Appl
cl1471	53	1.5	1812	17	US-10-616-263-63	Sequence 63, Appl
cl1472	53	1.5	1816	17	US-10-723-860-7371	Sequence 7371, Ap
cl1473	53	1.5	1827	15	US-10-176-306-16	Sequence 16, Appl
cl1474	53	1.5	1882	9	US-09-925-298-301	Sequence 301, App
cl1475	53	1.5	1882	14	US-10-102-806-301	Sequence 301, App
cl1476	53	1.5	1882	17	US-10-310-154-338	Sequence 338, App
cl1477	53	1.5	1919	18	US-10-437-963-4720	Sequence 4720, Ap
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cl1479	53	1.5	1944	17	US-10-424-599-94481	Sequence 94481, A
cl1480	53	1.5	1975	17	US-10-264-237-1379	Sequence 1379, Ap
cl1481	53	1.5	1975	18	US-10-425-115-35489	Sequence 35489, A
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cl1483	53	1.5	1977	10	US-09-983-802-83	Sequence 83, Appl
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cl1488	53	1.5	2052	18	US-10-425-115-137886	Sequence 137886, A
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cl1499	53	1.5	2317	17	US-10-264-237-1331	Sequence 1331, Ap
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Search completed: March 29, 2005, 10:05:26  
Job time : 5595 secs

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Run on: March 28, 2005, 19:45:32 ; Search time 10141 Seconds

(without alignments)  
13437.539 Million cell updates/sec

Title: US-10-015-388A-53

Perfect score: 3580

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Scoring table: <OHIGO\_NUC

Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Database :

EST:\*

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3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gsa1:\*

9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
C	1	663	18.5	903	5	BQ213573 AGENCOURT
C	2	656	18.3	899	5	BU552398 AGENCOURT
C	3	652	18.2	1014	4	BM469318 AGENCOURT
C	4	559	15.6	572	2	BF058311 7k29d11.x
C	5	550	15.4	692	5	BU688759 AGENCOURT
C	6	540	15.1	646	8	AQ472645 CITBI-EI
C	7	536	15.0	927	5	BU542994 AGENCOURT
C	8	527	14.7	527	2	AW815410 QVO-ST021
C	9	519	14.5	527	2	BF940597 nae24a05
C	10	515	14.4	908	4	BM459709 AGENCOURT
C	11	500	14.0	500	4	BM702052 UI-E-CQ1
C	12	497	13.9	996	5	BU552474 AGENCOURT
C	13	468	13.1	527	2	BE675211 7f04e08.x
C	14	464	13.0	523	2	BE646425 7e86e12.x
C	15	456	12.7	526	1	AI992191 wt75g03.x
C	16	441	12.3	628	6	CD367538 UI-H-FTL
C	17	437	12.2	500	2	BF732972 nae17f09
C	18	436	12.2	541	5	BQ082104 K-EST0054
C	19	432	12.1	506	1	AI122852 qb01b09.s
C	20	427	11.9	478	1	AI760894 wi09g08.x
C	21	427	11.9	974	5	BQ891683 AGENCOURT
C	22	425	11.9	991	1	AA203602 2x59f07.r
C	23	403	11.3	612	2	BE159384 MRO-HT040
C	24	393	11.0	494	1	AA625133 af70b02.r

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99	77	2.2	703	7	C0877355	BovGen_05	c 172	60	1.7	228	4	BI676144	BI676144	dai90a06.																																																																																																																																																																																																																																																																																																																																																																												
100	77	2.2	801	7	C0389483	AGENCOURT	c 173	60	1.7	250	4	C0889606	C0889606	BovGen_17																																																																																																																																																																																																																																																																																																																																																																												
101	77	2.2	921	5	B0520844	AGENCOURT	c 174	60	1.7	264	4	CK423942	AUF_ipSppt	CK423942																																																																																																																																																																																																																																																																																																																																																																												
102	76	2.1	516	7	C0893525	BovGen_21	c 175	60	1.7	279	4	BI443418	dai31d09.	BI443418																																																																																																																																																																																																																																																																																																																																																																												
103	76	2.1	578	7	CF547196	AGENCOURT	176	60	1.7	502	6	CD679487	hql1e06.y	CD679487																																																																																																																																																																																																																																																																																																																																																																												
104	75	2.1	263	1	AI275175	qw08d05.x	177	60	1.7	534	7	C0889459	BovGen_17	C0889459																																																																																																																																																																																																																																																																																																																																																																												
105	75	2.1	271	5	BQ800126	BovGen_18	178	60	1.7	560	7	CF873229	tr1c004xx	CF873229																																																																																																																																																																																																																																																																																																																																																																												
106	75	2.1	305	7	CR745362	CR745362	179	60	1.7	562	7	CF886129	tr1c0085xn	CF886129																																																																																																																																																																																																																																																																																																																																																																												
107	75	2.1	359	4	BG222312	na74h04.	180	60	1.7	571	7	CF873697	tr1c005xg	CF873697																																																																																																																																																																																																																																																																																																																																																																												
108	75	2.1	431	5	BX845583	BX845583	181	60	1.7	577	7	CF875579	tr1c008xj	CF875579																																																																																																																																																																																																																																																																																																																																																																												
109	75	2.1	463	7	C0874821	BovGen_03	182	60	1.7	577	7	CF876254	tr1c010xm	CF876254																																																																																																																																																																																																																																																																																																																																																																												
110	75	2.1	545	7	C0886964	BovGen_15	183	60	1.7	580	7	CF882655	tr1c0031xd	CF882655																																																																																																																																																																																																																																																																																																																																																																												
111	75	2.1	565	7	C0890319	BovGen_18	184	60	1.7	581	7	CF875955	tr1c009xc	CF875955																																																																																																																																																																																																																																																																																																																																																																												
112	75	2.1	606	7	C0894286	BovGen_22	185	60	1.7	584	7	CF876645	tr1c011xi	CF876645																																																																																																																																																																																																																																																																																																																																																																												
113	75	2.1	933	7	CK194878	FGAS00331	c 186	60	1.7	597	4	BG896920	HOA59-1-B	BG896920																																																																																																																																																																																																																																																																																																																																																																												
114	75	2.1	1099	4	BM467696	AGENCOURT	187	60	1.7	658	4	BF968907	602270874	BF968907																																																																																																																																																																																																																																																																																																																																																																												
115	75	2.1	1385	3	AY103744	Zea may	188	60	1.7	675	7	C0891521	BovGen_19	C0891521																																																																																																																																																																																																																																																																																																																																																																												
116	74	2.1	220	6	CB474275	jns02_A12	c 189	60	1.7	686	7	C0894553	BovGen_22	C0894553																																																																																																																																																																																																																																																																																																																																																																												
117	74	2.1	469	7	C0890709	BovGen_19	c 190	60	1.7	718	7	CK172899	EST762219	CK172899																																																																																																																																																																																																																																																																																																																																																																												
118	74	2.1	667	6	CA076217	SCMCAM110	191	60	1.7	801	7	CV120758	AGENCOURT	CV120758																																																																																																																																																																																																																																																																																																																																																																												
119	74	2.1	678	7	C0894416	BovGen_22	192	60	1.7	817	7	CK172900	EST762220	CK172900																																																																																																																																																																																																																																																																																																																																																																												
120	73	2.0	514	6	CD723758	oj26b09.y	193	60	1.7	846	7	CK194390	FGAS00281	CK194390																																																																																																																																																																																																																																																																																																																																																																												
121	72	2.0	743	7	C0878776	BovGen_07	194	60	1.7	859	5	BUI70431	AGENCOURT	BUI70431																																																																																																																																																																																																																																																																																																																																																																												
122	72	2.0	751	7	CF285041	AGENCOURT	195	60	1.7	870	7	CF885064	tr1c077xe	CF885064																																																																																																																																																																																																																																																																																																																																																																												
123	71	2.0	163	1	AI289747	qv91e07.x	196	60	1.7	883	7	CF885106	tr1c0077x1	CF885106																																																																																																																																																																																																																																																																																																																																																																												
124	71	2.0	551	7	CK431019	oj56h10.y	197	60	1.7	886	7	CK199049	FGAS00754	CK199049																																																																																																																																																																																																																																																																																																																																																																												
125	71	2.0	635	7	C0878096	BovGen_06	198	60	1.7	894	7	CF885605	tr1c082x1	CF885605																																																																																																																																																																																																																																																																																																																																																																												
126	71	2.0	903	5	BUI72251	AGENCOURT	199	60	1.7	908	7	CF885585	tr1c082xc	CF885585																																																																																																																																																																																																																																																																																																																																																																												
127	70	2.0	184	4	BM192204	dai21g08.	200	60	1.7	910	7	CF886357	tr1c086xx	CF886357																																																																																																																																																																																																																																																																																																																																																																												
128	70	2.0	301	6	CA263211	SCPLB203	201	60	1.7	929	7	CF885679	tr1c082xh	CF885679																																																																																																																																																																																																																																																																																																																																																																												
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130	69	1.9	551	7	CK431019	oj56h10.y	203	60	1.7	946	6	CA987707	AGENCOURT	CA987707																																																																																																																																																																																																																																																																																																																																																																												
131	68	1.9	520	7	CK235878	SB0100240	204	60	1.7	990	7	CF873636	tr1c005xg	CF873636																																																																																																																																																																																																																																																																																																																																																																												
132	67	1.9	314	7	C0874293	BovGen_02	205	60	1.7	1083	5	BM905598	AGENCOURT	BM905598																																																																																																																																																																																																																																																																																																																																																																												
133	67	1.9	495	5	BQ238068	TaE05008H	206	59	1.6	139	2	BF812963	MR2-C1018	BF812963																																																																																																																																																																																																																																																																																																																																																																												
134	67	1.9	673	7	C0887800	BovGen_16	207	59	1.6	158	4	BM632157	170006875	BM632157																																																																																																																																																																																																																																																																																																																																																																												
135	67	1.9	695	7	C0878226	BovGen_06	208	59	1.6	165	1	AI469764	tm20f02.x	AI469764																																																																																																																																																																																																																																																																																																																																																																												
136	67	1.9	853	7	C0007895	EST796230	209	59	1.6	325	1	AI801589	to91d07.x	AI801589																																																																																																																																																																																																																																																																																																																																																																												
137	67	1.9	1057	5	B0506841	AGENCOURT	210	59	1.6	358	4	BG781092	SEADMC001	BG781092																																																																																																																																																																																																																																																																																																																																																																												
138	66	1.8	187	1	AU284592	XU284592	211	59	1.6	360	1	AI440261	tj01d06.x	AI440261																																																																																																																																																																																																																																																																																																																																																																												
139	66	1.8	249	2	AW197139	xb16c02.x	212	59	1.6	385	1	AI334804	qw24n01.x	AI334804																																																																																																																																																																																																																																																																																																																																																																												
140	65	1.8	236	5	BQ732209	AGENCOURT	213	59	1.6	399	1	AI954200	wx94a02.x	AI954200																																																																																																																																																																																																																																																																																																																																																																												
141	65	1.8	422	1	AI358581	qx60d02.x	c 214	59	1.6	469	7	CF874064	tr1c035xe	CF874064																																																																																																																																																																																																																																																																																																																																																																												
142	65	1.8	596	4	BM569567	ih96h01.x	c 215	59	1.6	474	7	CN717811	E0753B09-	CN717811																																																																																																																																																																																																																																																																																																																																																																												
143	65	1.8	732	7	C0879622	BovGen_07	c 216	59	1.6	612	5	BQ389802	NISC_mq09	BQ389802																																																																																																																																																																																																																																																																																																																																																																												
144	64	1.8	618	2	AW324530	AB027_Eas	c 217	59	1.6	675	6	CA123657	SCSFLR203	CA123657																																																																																																																																																																																																																																																																																																																																																																												
145	64	1.8	898	5	BQ230783	AGENCOURT	c 218	59	1.6	719	7	C0882395	BovGen_10	C0882395																																																																																																																																																																																																																																																																																																																																																																												
146	63	1.8	130	4	BG167830	602339983	c 219	59	1.6	721	7	C0887461	BovGen_15	C0887461																																																																																																																																																																																																																																																																																																																																																																												
147	63	1.8	257	1	AI888022	wn12b06.x	c 220	59	1.6	726	7	C0877944	BovGen_06	C0877944																																																																																																																																																																																																																																																																																																																																																																												
148	63	1.8	294	4	CN271810	170006003	c 221	59	1.6	738	7	C0879400	BovGen_07	C0879400																																																																																																																																																																																																																																																																																																																																																																												
149	63	1.8	374	1	AJ687174	AJ687174	c 222	59	1.6	772	4	BG114985	602315847	BG114985																																																																																																																																																																																																																																																																																																																																																																												
150	63	1.8	490	2	BF191917	242931_MA	c 223	59	1.6	785	6	CB903607	tr1c035xe	CB903607																																																																																																																																																																																																																																																																																																																																																																												
151	63	1.8	493	5	BQ387802	NISC_mm25	c 224	59	1.6	822	7	CK193166	FGAS000158	CK193166																																																																																																																																																																																																																																																																																																																																																																												
152	63	1.8	558	7	C0880948	BovGen_09	c 225	59	1.6	837	7	CK193117	FGAS000153	CK193117																																																																																																																																																																																																																																																																																																																																																																												
153	63	1.8	659	7	C0875161	BovGen_03	c 226	59	1.6	890	7	CK797460	AGENCOURT	CK797460																																																																																																																																																																																																																																																																																																																																																																												
154	63	1.8	660	7	C0896277	BovGen_24	c 227	59	1.6	955	7	CK805318	AGENCOURT	CK805318																																																																																																																																																																																																																																																																																																																																																																												
155	62	1.7	189	7	CF8881722	tr1c085xc	c 228	59	1.6	1071	5	BM907452	AGENCOURT	BM907452																																																																																																																																																																																																																																																																																																																																																																												
156	62	1.7	434	7	C0889127	BovGen_17	c 229	59	1.6	1497	2	BF788820	602110529	BF788820																																																																																																																																																																																																																																																																																																																																																																												
157	62	1.7	621	7	C0885415	BovGen_13	c 230	58	1.6	63	1	AI371229	qw77h05.x	AI371229																																																																																																																																																																																																																																																																																																																																																																												
158	62	1.7	656	6	CA239050	SCBFL507	c 231	58	1.6	65	1	AI282249	qv92f06.x	AI282249																																																																																																																																																																																																																																																																																																																																																																												
159	62	1.7	656	7	C0526531	3530_1_17	c 232	58	1.6	65	1	AI698352	tx63f09.x	AI698352																																																																																																																																																																																																																																																																																																																																																																												
160	62	1.7	758	6	CB908372	tr1c085xc	c 233	58	1.6	69	1	AI358271	qw19g12.x	AI358271																																																																																																																																																																																																																																																																																																																																																																												
161	62	1.7	881	5	BQ735806	AGENCOURT	c 234	58	1.6	70	1	AI225248	qx12d07.x	AI225248																																																																																																																																																																																																																																																																																																																																																																												
162	62	1.7	925	5	BQ945533	AGENCOURT	c 235	58	1.6	71	1	AI867068	tz45h12.x	AI867068																																																																																																																																																																																																																																																																																																																																																																												
163	62	1.7	955	7	CK805318	AGENCOURT	c 236	58	1.6	71	1	AI952433	wx73f09.x	AI952433																																																																																																																																																																																																																																																																																																																																																																												
164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164	61	1.7	164

244	58	1.6	80	1	AI521571	to64h04.x	317	58	1.6	120	1	AI590043	AI590043	tr75c04.x
245	58	1.6	80	1	AI561168	tr75d07.x	318	58	1.6	120	1	AI872423	AI872423	wm58g09.x
246	58	1.6	80	1	AI828597	w142g01.x	319	58	1.6	120	1	AI923989	AI923989	wn73a09.x
247	58	1.6	81	1	AI285419	qt83a06.x	320	58	1.6	121	1	AI582932	AI582932	ts07g04.x
248	58	1.6	81	1	AI559957	tr77c07.x	321	58	1.6	121	1	AI887775	AI887775	wm18f04.x
249	58	1.6	81	2	AW089557	xd20b11.x	322	58	1.6	125	1	AI538850	AI538850	tp74e02.x
250	58	1.6	82	1	AI885949	wn06g06.x	323	58	1.6	127	1	AI500523	AI500523	tn92g08.x
251	58	1.6	83	1	AI878201	fc58f08.y	324	58	1.6	128	1	AI801325	AI801325	to87g09.x
252	58	1.6	83	7	CF643428	D90_C09_F	325	58	1.6	128	1	AI866691	AI866691	wn10c06.x
253	58	1.6	85	1	AI539707	tp77b02.x	326	58	1.6	129	1	AI815232	AI815232	wk72f10.x
254	58	1.6	85	1	AI702065	tr20h10.x	327	58	1.6	130	7	CF641337	CF641337	D38_E07_F
255	58	1.6	87	1	AI431238	ar56a12.x	328	58	1.6	132	1	AI866465	AI866465	tz48a12.x
256	58	1.6	87	1	AI539781	cp77f12.x	329	58	1.6	133	2	BE883591	BE883591	601508064
257	58	1.6	87	5	BQ392175	NISC_mq23	330	58	1.6	134	1	AI045724	AI045724	DKFxp434D
258	58	1.6	88	2	AW151979	xf71c01.x	331	58	1.6	135	4	BM639526	BM639526	170006875
259	58	1.6	89	1	AI887499	wn06c05.x	332	58	1.6	137	1	AI500659	AI500659	tn93g08.x
260	58	1.6	90	1	AI539260	tp64d08.x	333	58	1.6	137	1	AI815239	AI815239	wk72g07.x
261	58	1.6	90	1	AI828574	w142d08.x	334	58	1.6	138	1	AI804505	AI804505	tp60b03.x
262	58	1.6	92	1	AI242736	qt86d12.x	335	58	1.6	138	5	BQ392169	BQ392169	NISC_mq23
263	58	1.6	93	1	AI431316	ar55b10.x	336	58	1.6	140	1	AA087985	AA087985	mo39e12.x
264	58	1.6	93	1	AI610557	tp41b11.x	337	58	1.6	142	4	BM628708	BM628708	170006874
265	58	1.6	93	1	AI860003	wm22f10.x	338	58	1.6	143	1	AI494201	AI494201	ti09e06.x
266	58	1.6	94	1	AI567971	tr86e11.x	339	58	1.6	144	1	AI537677	AI537677	tp34d01.x
267	58	1.6	94	1	AI866786	tz53b05.x	340	58	1.6	144	5	BQ638107	BQ638107	hd18e10.y
268	58	1.6	96	1	AI440238	tj01a04.x	341	58	1.6	145	1	AI440260	AI440260	tj01d05.x
269	58	1.6	98	1	AI431307	ar55a11.x	342	58	1.6	145	7	CN414669	CN414669	170006004
270	58	1.6	98	1	AI440252	tj01c03.x	343	58	1.6	149	1	AI432644	AI432644	ti22a02.x
271	58	1.6	99	1	AI491710	tn94d05.x	344	58	1.6	151	2	BE897632	BE897632	601432481
272	58	1.6	99	1	AI371228	qv77h03.x	345	58	1.6	152	2	BF301996	BF301996	602032834
273	58	1.6	99	1	AI581033	ti94d04.x	346	58	1.6	152	2	AW151132	AW151132	xg33g07.x
274	58	1.6	100	1	AI355779	qt94d10.x	347	58	1.6	152	4	BM612283	BM612283	170006871
275	58	1.6	100	1	AI623736	tr83f07.x	348	58	1.6	154	1	AI539771	AI539771	tp77e11.x
276	58	1.6	101	1	AI889147	wm46c06.x	349	58	1.6	159	2	AI511136	AI511136	xg33h03.x
277	58	1.6	101	1	AI436429	ti09a04.x	350	58	1.6	162	4	BQ252929	BQ252929	602365530
278	58	1.6	101	1	AI859591	wm22e05.x	351	58	1.6	163	4	BQ289279	BQ289279	602384287
279	58	1.6	102	1	AI285439	qt83d04.x	352	58	1.6	163	5	BQ387472	BQ387472	NISC_mn24
280	58	1.6	102	1	AI877953	fc55f03.y	353	58	1.6	163	5	BQ637071	BQ637071	he05c09.y
281	58	1.6	102	7	CO373230	MJR013A02	354	58	1.6	164	1	AI554821	AI554821	tp73g04.x
282	58	1.6	103	1	AI888118	wm52b09.x	355	58	1.6	164	1	AI561170	AI561170	tr73d10.x
283	58	1.6	103	5	BU167500	AGENCOURT	356	58	1.6	165	1	AI690946	AI690946	tr73e09.x
284	58	1.6	104	1	AI284513	qt88g01.x	357	58	1.6	166	1	AI648567	AI648567	tz54g06.x
285	58	1.6	104	1	AI434248	ti33d01.x	358	58	1.6	166	5	BQ639348	BQ639348	he14d05.y
286	58	1.6	104	1	AI500714	tn94b05.x	359	58	1.6	167	1	AI433157	AI433157	ti32b12.x
287	58	1.6	105	1	AI888661	wn34b03.x	360	58	1.6	173	4	BM620920	BM620920	170006874
288	58	1.6	106	1	AI434242	ti33c05.x	361	58	1.6	176	7	CO890294	CO890294	BovGen_18
289	58	1.6	106	1	AI805769	tr89h05.x	362	58	1.6	177	4	BQ294490	BQ294490	602391813
290	58	1.6	107	1	AI866469	tz43b05.x	363	58	1.6	178	4	BM494829	BM494829	lpc3br1_4
291	58	1.6	108	1	AI434256	ti33d09.x	364	58	1.6	178	5	BQ391656	BQ391656	NISC_mq20
292	58	1.6	109	1	AI633493	th62g08.x	365	58	1.6	179	4	BQ029667	BQ029667	602296662
293	58	1.6	110	1	AI866573	tz51b10.x	366	58	1.6	179	5	BQ390838	BQ390838	NISC_mq15
294	58	1.6	111	1	AI927233	wn24a06.x	367	58	1.6	184	4	BM594107	BM594107	170006874
295	58	1.6	112	1	AI440263	tj01d10.x	368	58	1.6	185	4	BG110517	BG110517	602378945
296	58	1.6	112	1	AI538885	tp74h10.x	369	58	1.6	186	1	AI371243	AI371243	qv78h02.x
297	58	1.6	112	1	AI889168	wm46e11.x	370	58	1.6	182	6	CA340216	CA340216	NISC_ly12
298	58	1.6	112	5	BQ387826	NISC_mn26	371	58	1.6	183	4	BG113493	BG113493	602283943
299	58	1.6	113	1	AI284509	qt88f05.x	372	58	1.6	186	5	BQ239222	BQ239222	TaE05035F
300	58	1.6	113	1	AI539800	tp77h10.x	373	58	1.6	186	4	BM631584	BM631584	170006875
301	58	1.6	113	1	AI582912	tr07e06.x	374	58	1.6	185	4	BG110517	BG110517	602378945
302	58	1.6	113	2	AW172723	xj02e12.x	375	58	1.6	185	7	CF319467	CF319467	HD--09_P1
303	58	1.6	114	1	AI285417	qt83a02.x	376	58	1.6	186	1	AI371243	AI371243	qv78h02.x
304	58	1.6	114	1	AI500662	tn93h02.x	377	58	1.6	186	5	BQ239222	BQ239222	TaE05035F
305	58	1.6	114	2	AW151974	xf71b01.x	378	58	1.6	189	5	BQ400307	BQ400307	NISC_mq08
306	58	1.6	115	1	AI521560	to64g03.x	379	58	1.6	190	4	BQ292880	BQ292880	602389512
307	58	1.6	115	1	AI889189	wm46h09.x	380	58	1.6	191	4	BQ294808	BQ294808	602391631
308	58	1.6	115	7	CO883195	BovGen_11	381	58	1.6	191	7	CO892085	CO892085	BovGen_20
309	58	1.6	117	1	AI289791	qw12c03.x	382	58	1.6	192	5	BQ761011	BQ761011	EBR004_SQ
310	58	1.6	117	1	AI926593	wo48b03.x	383	58	1.6	193	4	AI031194	AI031194	8D4M_Xeno
311	58	1.6	117	2	BF811804	MR2-CI018	384	58	1.6	194	4	BG257535	BG257535	602377685
312	58	1.6	117	2	AW151138	xg33h06.x	385	58	1.6	195	1	AU060359	AU060359	AU060359
313	58	1.6	118	1	AI445237	tr88b09.x	386	58	1.6	195	5	BQ389262	BQ389262	NISC_mq06
314	58	1.6	118	1	AI491776	tn94h08.x	387	58	1.6	196	1	AL039390	AL039390	DKFxp434J
315	58	1.6	119	1	AI500706	tn94a06.x	388	58	1.6	196	2	BF795712	BF795712	602259590
316	58	1.6	120	1	AI284517	qt88g07.x	389	58	1.6	196	7	CO893749	CO893749	BovGen_22



330	58	1.6	197	2	BF796402	BF796402	602260040	463	58	1.6	319	5	BQ525547	BQ525547	NISC_nol1
331	58	1.6	200	1	A1274759	A1274759	qv66e09.x	464	58	1.6	323	4	BM116311	BM116311	L0834B04-
332	58	1.6	200	1	AW858522	AW858522	CM3-CT034	465	58	1.6	324	4	A1521589	A1521589	to65b08.x
333	58	1.6	201	5	BQ523741	BQ523741	NISC_n123	466	58	1.6	324	4	BM117156	BM117156	L0847A02-
334	58	1.6	202	4	BQ391612	BQ391612	602417868	467	58	1.6	325	5	BQ525099	BQ525099	NISC_n008
335	58	1.6	202	4	BM641556	BM641556	170006873	468	58	1.6	326	4	BM117385	BM117385	L0850E11-
336	58	1.6	203	5	BQ399198	BQ399198	NISC_mp02	c 469	58	1.6	326	7	CF874010	CF874010	tr1c035xc
337	58	1.6	206	4	B1437582	B1437582	ic81a01.y	470	58	1.6	328	7	CF722703	CF722703	B04_LKF00
338	58	1.6	207	1	A1433976	A1433976	ti12c12.x	471	58	1.6	328	7	CF722703	CF722703	B04_LKF00
339	58	1.6	207	4	BM579757	BM579757	170006872	472	58	1.6	330	7	CF639408	CF639408	D15_C12_F
340	58	1.6	207	5	BQ399361	BQ399361	NISC_mp03	c 473	58	1.6	330	7	CF639408	CF639408	D15_C12_F
341	58	1.6	209	7	CK420226	CK420226	AUF_IpTrk	c 474	58	1.6	333	7	CF866168	CF866168	tr1c005xe
342	58	1.6	214	4	BM636166	BM636166	170006875	475	58	1.6	334	1	A1537273	A1537273	tp07a04.x
343	58	1.6	217	6	CD678870	CD678870	hq01d06.x	476	58	1.6	335	5	BQ388737	BQ388737	NISC_mq03
344	58	1.6	217	7	CK622030	CK622030	ml31g04.y	477	58	1.6	336	1	A1537191	A1537191	tp01d05.x
345	58	1.6	218	5	BQ392177	BQ392177	NISC_mq23	478	58	1.6	336	5	BQ400952	BQ400952	NISC_mpl2
346	58	1.6	220	4	BM506521	BM506521	1144n08.y	479	58	1.6	337	2	AW151970	AW151970	xf71a07.x
347	58	1.6	223	4	BM610799	BM610799	170006871	480	58	1.6	337	5	BQ392456	BQ392456	NISC_mq24
348	58	1.6	224	1	A1539863	A1539863	tp65h06.x	481	58	1.6	338	5	CF645623	CF645623	K3B_E12_F
349	58	1.6	224	1	A1582910	A1582910	ts07e04.x	482	58	1.6	338	7	CF872097	CF872097	tr1c029xo
350	58	1.6	225	1	A1366900	A1366900	qv94f07.x	c 483	58	1.6	338	7	CF872097	CF872097	tr1c029xo
351	58	1.6	227	1	AJ770217	AJ770217	AJ770217	484	58	1.6	340	1	A1371265	A1371265	qv79h09.x
352	58	1.6	231	7	CK429584	CK429584	oj38e11.y	485	58	1.6	340	1	A136456	A136456	ti09c12.x
353	58	1.6	234	1	A1366910	A1366910	qv94g09.x	486	58	1.6	341	1	AL046681	AL046681	DKF2p434B
354	58	1.6	239	5	BQ390209	BQ390209	NISC_mq11	487	58	1.6	343	1	AL039287	AL039287	DKF2p434B
355	58	1.6	240	5	BQ265962	BQ265962	NISC_ff10	c 488	58	1.6	346	4	BQ059804	BQ059804	naf44a04.x
356	58	1.6	241	1	A1561177	A1561177	tg37e11.x	489	58	1.6	347	1	A1963846	A1963846	wr67g08.x
357	58	1.6	244	5	BQ392210	BQ392210	NISC_mq23	490	58	1.6	347	5	BQ392745	BQ392745	NISC_mq26
358	58	1.6	249	4	BM593925	BM593925	170006874	c 491	58	1.6	347	7	CK119356	CK119356	213b14.p1
359	58	1.6	253	4	BM637390	BM637390	170006875	492	58	1.6	349	1	A1567940	A1567940	q86a12.x
360	58	1.6	253	7	CF722747	CF722747	F10_LKF00	493	58	1.6	349	5	BQ520314	BQ520314	NISC_n104
361	58	1.6	255	1	AL047611	AL047611	DKF2p586H	494	58	1.6	349	6	CD723632	CD723632	oj24f02.y
362	58	1.6	257	4	BG113712	BG113712	602284230	495	58	1.6	350	5	BQ390727	BQ390727	NISC_mq14
363	58	1.6	259	1	A1582926	A1582926	ts07f10.x	496	58	1.6	350	5	BQ397046	BQ397046	NISC_mq25
364	58	1.6	264	7	CO881096	CO881096	BovGen_09	497	58	1.6	351	1	A1610357	A1610357	tp18g10.x
365	58	1.6	265	7	CK275140	CK275140	170006000	498	58	1.6	351	5	BQ526633	BQ526633	NISC_nol7
366	58	1.6	265	7	CO889401	CO889401	BovGen_17	499	58	1.6	353	4	BG178532	BG178532	602328358
367	58	1.6	269	5	BQ392506	BQ392506	NISC_mq24	500	58	1.6	354	1	A1817244	A1817244	wk21e09.x
368	58	1.6	273	7	CF651927	CF651927	23-L02052	501	58	1.6	357	4	BG180295	BG180295	602331131
369	58	1.6	276	5	BQ389379	BQ389379	NISC_mq07	502	58	1.6	358	4	BF968504	BF968504	602271283
370	58	1.6	277	4	BM644186	BM644186	170006873	c 503	58	1.6	360	7	CF640472	CF640472	D27_G03_F
371	58	1.6	278	1	A1521566	A1521566	to64g10.x	c 504	58	1.6	361	1	A1612913	A1612913	tx07g06.x
372	58	1.6	278	1	BG785787	BG785787	SEAUMC005	c 505	58	1.6	361	7	CF874123	CF874123	tr1c035x1
373	58	1.6	279	5	BQ392248	BQ392248	NISC_mq23	506	58	1.6	367	5	BQ525045	BQ525045	NISC_n008
374	58	1.6	281	1	A1499463	A1499463	tn95f08.x	507	58	1.6	368	5	BQ520417	BQ520417	NISC_n104
375	58	1.6	283	4	BG163646	BG163646	602338823	508	58	1.6	368	7	CK273721	CK273721	170006000
376	58	1.6	283	5	BQ391743	BQ391743	NISC_mq20	509	58	1.6	371	1	A1476694	A1476694	tm18b06.x
377	58	1.6	284	5	BQ392194	BQ392194	NISC_mq23	c 510	58	1.6	371	7	CK273721	CK273721	170006000
378	58	1.6	285	1	AL047152	AL047152	DKF2p586E	511	58	1.6	372	1	A1285826	A1285826	qu81n06.x
379	58	1.6	286	1	A1355126	A1355126	qt75c04.x	512	58	1.6	375	5	BG780328	BG780328	SEAUMC000
380	58	1.6	290	4	B1119510	B1119510	AR18A_Po	c 513	58	1.6	376	4	BQ391608	BQ391608	NISC_mq19
381	58	1.6	291	1	AL045166	AL045166	DKF2p434A	514	58	1.6	377	1	A1863014	A1863014	wm45c09.x
382	58	1.6	291	4	B1186556	B1186556	AR04LD09P	515	58	1.6	377	5	BQ390108	BQ390108	NISC_mq11
383	58	1.6	294	7	CF640192	CF640192	D24_E03_F	c 516	58	1.6	377	7	CF881912	CF881912	tr1c085xn
384	58	1.6	295	1	A1354981	A1354981	qt78c12.x	517	58	1.6	378	5	BQ392652	BQ392652	NISC_mq25
385	58	1.6	296	1	A1610362	A1610362	tp18h07.x	518	58	1.6	378	5	BQ395906	BQ395906	NISC_mq17
386	58	1.6	297	2	BF720448	BF720448	mab54d10	519	58	1.6	380	1	A1355765	A1355765	qt94f06.x
387	58	1.6	297	7	CO392256	CO392256	NISC_mq23	520	58	1.6	380	1	A1521594	A1521594	to65c12.x
388	58	1.6	297	7	CO879901	CO879901	BovGen_08	521	58	1.6	382	1	A1499512	A1499512	to02d06.x
389	58	1.6	298	4	BM123506	BM123506	L0526C06-	522	58	1.6	382	5	BQ524726	BQ524726	NISC_n006
390	58	1.6	304	5	BQ265956	BQ265956	NISC_ff10	523	58	1.6	385	5	BQ520372	BQ520372	NISC_n104
391	58	1.6	305	5	BQ265996	BQ265996	NISC_ff10	524	58	1.6	388	6	CB259870	CB259870	16-B9603-
392	58	1.6	305	5	BQ377746	BQ377746	AGENCOURT	525	58	1.6	389	1	A1588360	A1588360	fb99g09.x
393	58	1.6	309	5	EX517975	EX517975	EX517975	526	58	1.6	390	5	BQ386279	BQ386279	NISC_mn17
394	58	1.6	310	1	A1440239	A1440239	tj01a06.x	527	58	1.6	391	1	A1889133	A1889133	wm45e03.x
395	58	1.6	310	1	A1567961	A1567961	tg86d08.x	528	58	1.6	391	5	BQ520378	BQ520378	NISC_n104
396	58	1.6	310	1	AA285478	AA285478	VC33f02.f	529	58	1.6	392	1	A1538881	A1538881	tp74h05.x
397	58	1.6	311	1	A1521596	A1521596	to65d02.x	530	58	1.6	393	1	A1805774	A1805774	tx89h10.x
398	58	1.6	311	7	CO893754	CO893754	BovGen_22	531	58	1.6	393	5	BQ389292	BQ389292	NISC_mq06
399	58	1.6	312	1	A1436438	A1436438	ti09b04.x	532	58	1.6	393	5	BQ524850	BQ524850	NISC_n007
400	58	1.6	312	2	BF727352	BF727352	by20c12.y	533	58	1.6	393	5	BQ525032	BQ525032	NISC_n008
401	58	1.6	317	5	BQ400927	BQ400927	NISC_mpl2	534	58	1.6	396	5	BQ519847	BQ519847	NISC_n101
402	58	1.6	318	5	BQ389767	BQ389767	NISC_mq09	c 535	58	1.6	397	4	BG924268	BG924268	HNC26-1-B

536	58	1.6	398	5	BQ524540	NISC no05	BQ524540	NISC no05	609	58	1.6	449	5	BQ390822	NISC mq15
537	58	1.6	398	5	BX847873	BX847873	BX847873	BX847873	610	58	1.6	449	7	CO885887	Bovden_14
538	58	1.6	399	5	BQ520127	NISC nl03	BQ520127	NISC nl03	611	58	1.6	450	5	BQ389233	NISC mq06
539	58	1.6	401	5	BQ524751	NISC no06	BQ524751	NISC no06	612	58	1.6	450	5	BQ399241	NISC nl07
540	58	1.6	401	7	CK120781	206c02.p1	CK120781	206c02.p1	613	58	1.6	450	5	BQ522595	NISC nl17
541	58	1.6	402	1	A1927252	wn24c09.x	A1927252	wn24c09.x	614	58	1.6	451	5	BQ525103	NISC no08
542	58	1.6	402	5	BQ526842	NISC no18	BQ526842	NISC no18	615	58	1.6	451	5	BQ525017	Q197a06.x
543	58	1.6	403	1	A1499508	co02d01.x	A1499508	co02d01.x	616	58	1.6	454	1	AL079910	KRFp586A
544	58	1.6	403	1	A1885920	wm76c04.x	A1885920	wm76c04.x	617	58	1.6	456	5	BQ524518	NISC no05
545	58	1.6	403	5	BQ383743	NISC nm02	BQ383743	NISC nm02	618	58	1.6	457	1	AI955441	wt14e10.x
546	58	1.6	405	7	CK620773	ml16d03.y	CK620773	ml16d03.y	619	58	1.6	457	5	BQ400416	NISC mp09
547	58	1.6	406	5	BQ390779	NISC mq15	BQ390779	NISC mq15	620	58	1.6	457	7	CO896683	BovGen_25
548	58	1.6	408	4	BQ528925	HNC10-1-F	BQ528925	HNC10-1-F	621	58	1.6	458	5	BQ389693	NISC mq09
549	58	1.6	409	1	A1499483	to02a08.x	A1499483	to02a08.x	622	58	1.6	459	1	AI431321	ar55c04.x
550	58	1.6	410	5	BQ387607	NISC nm24	BQ387607	NISC nm24	623	58	1.6	459	1	AI434255	t133d08.x
551	58	1.6	410	5	BQ523105	NISC nl20	BQ523105	NISC nl20	624	58	1.6	459	4	BW117975	L085H01-
552	58	1.6	410	7	CF577499	AGENCOURT	CF577499	AGENCOURT	625	58	1.6	459	5	BQ392701	NISC mq26
553	58	1.6	411	7	CF641990	D46_E08_F	CF641990	D46_E08_F	626	58	1.6	459	5	BQ393509	NISC ng03
554	58	1.6	413	1	A1500658	tn3507.x	A1500658	tn3507.x	627	58	1.6	459	5	BQ520846	NISC nl07
555	58	1.6	413	5	BQ389879	NISC mq10	BQ389879	NISC mq10	628	58	1.6	461	4	BW117198	L0847F03-
556	58	1.6	413	5	BQ524857	NISC no07	BQ524857	NISC no07	629	58	1.6	462	5	BQ389446	NISC mq07
557	58	1.6	414	4	BQ898312	HOA39-1-A	BQ898312	HOA39-1-A	630	58	1.6	463	5	BQ525578	NISC ng01
558	58	1.6	414	5	BQ399519	NISC mp04	BQ399519	NISC mp04	631	58	1.6	463	6	CD721864	oJ2d12.y
559	58	1.6	415	5	BX844259	BX844259	BX844259	BX844259	632	58	1.6	465	1	AI610402	tp18a10.x
560	58	1.6	417	1	AI432653	t122b04.x	AI432653	t122b04.x	633	58	1.6	465	6	CB044392	NISC gc04
561	58	1.6	417	4	BQ924847	HNC4-1-F8	BQ924847	HNC4-1-F8	634	58	1.6	466	5	BQ388149	NISC mn27
562	58	1.6	417	5	BQ400532	NISC mp09	BQ400532	NISC mp09	635	58	1.6	468	4	BW115559	L0831H09-
563	58	1.6	418	5	BQ519962	NISC nl02	BQ519962	NISC nl02	636	58	1.6	468	5	BQ392544	NISC mq25
564	58	1.6	418	5	BQ391548	NISC mq19	BQ391548	NISC mq19	637	58	1.6	468	5	BQ395820	NISC ng17
565	58	1.6	418	5	BQ400406	NISC mp09	BQ400406	NISC mp09	638	58	1.6	468	5	BQ399226	NISC mq02
566	58	1.6	418	5	BQ520326	NISC nl04	BQ520326	NISC nl04	639	58	1.6	469	4	BQ286991	602382881
567	58	1.6	419	2	AW229306	uo09a03.y	AW229306	uo09a03.y	640	58	1.6	469	6	CA334673	NISC l811
568	58	1.6	419	5	BQ525525	NISC ng25	BQ525525	NISC ng25	641	58	1.6	470	1	AI521551	to64e12.x
569	58	1.6	420	5	BQ397024	NISC ng12	BQ397024	NISC ng12	642	58	1.6	470	5	BQ521062	NISC nl08
570	58	1.6	422	1	A1537925	tp26g12.x	A1537925	tp26g12.x	643	58	1.6	472	5	BQ391529	NISC mq19
571	58	1.6	425	5	BQ520586	NISC nl05	BQ520586	NISC nl05	644	58	1.6	472	5	BQ522890	NISC nl19
572	58	1.6	425	5	BQ520785	NISC nl07	BQ520785	NISC nl07	645	58	1.6	474	5	BQ523196	NISC nl20
573	58	1.6	426	1	A1282268	qu92h08.x	A1282268	qu92h08.x	646	58	1.6	476	5	BQ397256	NISC ng26
574	58	1.6	427	5	BQ336287	NISC ng03	BQ336287	NISC ng03	647	58	1.6	476	5	BQ399811	NISC mp05
575	58	1.6	427	5	BQ388757	NISC mq03	BQ388757	NISC mq03	648	58	1.6	476	5	BQ522205	NISC nl15
576	58	1.6	427	5	BQ395904	NISC ng17	BQ395904	NISC ng17	649	58	1.6	478	5	BQ389285	NISC mq06
577	58	1.6	429	1	AL042787	DXP2p434E	AL042787	DXP2p434E	650	58	1.6	478	5	BQ521567	NISC nl11
578	58	1.6	429	5	BQ389497	NISC mq07	BQ389497	NISC mq07	651	58	1.6	478	5	BQ524478	NISC no05
579	58	1.6	429	5	BQ393388	NISC ng03	BQ393388	NISC ng03	652	58	1.6	478	5	BX525322	BX525322
580	58	1.6	429	5	BQ522980	NISC nl19	BQ522980	NISC nl19	653	58	1.6	480	5	BQ383958	NISC mn04
581	58	1.6	431	1	A1923061	wn24h02.x	AI923061	wn24h02.x	654	58	1.6	480	5	BQ526773	NISC no18
582	58	1.6	431	5	BQ525081	NISC no08	BQ525081	NISC no08	655	58	1.6	481	4	BQ606034	L0908G01-
583	58	1.6	432	1	AI433323	ar55c08.x	AI433323	ar55c08.x	656	58	1.6	481	5	BQ523936	NISC no01
584	58	1.6	432	5	BQ520532	NISC nl05	BQ520532	NISC nl05	657	58	1.6	484	1	AI434223	t133a04.x
585	58	1.6	432	7	CO885766	BovGen_14	CO885766	BovGen_14	658	58	1.6	484	5	BQ389902	NISC mq10
586	58	1.6	433	7	CK620902	ml17h06.y	CK620902	ml17h06.y	659	58	1.6	485	5	BQ520997	NISC nl08
587	58	1.6	434	1	A1357672	qu21b04.x	AI357672	qu21b04.x	660	58	1.6	486	5	BQ387780	NISC mn25
588	58	1.6	435	5	BQ522932	NISC nl19	BQ522932	NISC nl19	661	58	1.6	487	1	AI285432	qt83c04.x
589	58	1.6	436	4	BG114865	602315646	BG114865	602315646	662	58	1.6	487	5	BQ388940	NISC mq04
590	58	1.6	436	5	BQ401004	NISC mp12	BQ401004	NISC mp12	663	58	1.6	488	5	BQ388916	NISC mq04
591	58	1.6	437	1	A1923446	wn85f11.x	AI923446	wn85f11.x	664	58	1.6	489	5	BQ522509	NISC nl17
592	58	1.6	437	5	BQ395916	NISC ng17	BQ395916	NISC ng17	665	58	1.6	490	5	BQ522780	NISC nl18
593	58	1.6	438	5	BQ389812	NISC mq09	BQ389812	NISC mq09	666	58	1.6	490	5	BQ524514	NISC no05
594	58	1.6	438	5	BX515080	NISC nl15	BX515080	NISC nl15	667	58	1.6	491	5	BQ520528	NISC nl05
595	58	1.6	439	5	BQ522280	NISC nl05	BQ522280	NISC nl05	668	58	1.6	491	5	BQ520964	NISC nl08
596	58	1.6	440	5	BQ391695	NISC mq20	BQ391695	NISC mq20	669	58	1.6	492	5	BQ387653	NISC mn25
597	58	1.6	440	5	BQ522645	NISC nl17	BQ522645	NISC nl17	670	58	1.6	492	5	BQ396967	NISC ng25
598	58	1.6	441	5	BQ391237	NISC mq17	BQ391237	NISC mq17	671	58	1.6	493	1	AI697243	qt17f09.x
599	58	1.6	441	5	BQ392753	NISC mq26	BQ392753	NISC mq26	672	58	1.6	493	5	BQ521529	NISC nl11
600	58	1.6	442	5	BQ525620	NISC nl01	BQ525620	NISC nl01	673	58	1.6	493	5	BQ522519	NISC nl17
601	58	1.6	443	5	BQ520151	NISC nl03	BQ520151	NISC nl03	674	58	1.6	493	7	GN485082	hx22f03.y
602	58	1.6	443	5	BQ522776	NISC nl18	BQ522776	NISC nl18	675	58	1.6	494	5	BQ256801	NISC ko06
603	58	1.6	444	5	BQ391745	NISC mq20	BQ391745	NISC mq20	676	58	1.6	494	5	BQ388095	NISC mn27
604	58	1.6	447	1	AL042572	DKF2d434J	AL042572	DKF2d434J	677	58	1.6	494	5	BQ522717	NISC nl18
605	58	1.6	447	2	AW081133	xc25f04.x	AW081133	xc25f04.x	678	58	1.6	494	6	CD677131	ho11f03.y
606	58	1.6	447	4	BQ897194	HOA46-1-A	BQ897194	HOA46-1-A	679	58	1.6	495	5	BQ400644	NISC mp10
607	58	1.6	448	2	AW087954	xb45c10.x	AW087954	xb45c10.x	680	58	1.6	496	4	BQ965898	602829682
608	58	1.6	448	6	CD723606	oJ24c08.y	CD723606	oJ24c08.y	681	58	1.6	497	1	AI610429	tp18d10.x

682	58	1.6	497	5	BQ525592	BQ525592	NISC no11	755	58	1.6	530	1	AL042944	AL042944	DKF2p434L
683	58	1.6	498	5	BQ526857	BQ526857	NISC no18	756	58	1.6	530	5	BQ396970	BQ396970	NISC ng25
684	58	1.6	499	1	AI434222	AI434222	t133a02.x	757	58	1.6	531	4	BM013859	BM013859	603639450
685	58	1.6	499	5	BQ522756	BQ522756	NISC nl18	758	58	1.6	531	5	BQ522393	BQ522393	NISC nl16
686	58	1.6	500	1	AI284515	AI284515	qt8905.x	759	58	1.6	533	1	AL042451	AL042451	DKF2p434D
687	58	1.6	500	1	AI628850	AI628850	ty17c08.x	760	58	1.6	533	5	BQ387422	BQ387422	NISC mn23
688	58	1.6	500	5	BQ388671	BQ388671	NISC mg03	761	58	1.6	534	1	AL042416	AL042416	DKF2p434C
689	58	1.6	500	5	BQ521021	BQ521021	NISC nl08	762	58	1.6	535	5	BQ400600	BQ400600	NISC mp10
690	58	1.6	500	6	CD724212	CD724212	oj31g09.y	763	58	1.6	536	6	CA390852	CA390852	cs115c11
691	58	1.6	501	5	BQ520834	BQ520834	NISC nl07	764	58	1.6	536	7	CF884415	CF884415	tr1c039xf
692	58	1.6	501	5	BQ521575	BQ521575	NISC nl11	765	58	1.6	537	5	BQ389732	BQ389732	NISC mq09
693	58	1.6	501	7	CK414590	CK414590	AUF_IpG11	766	58	1.6	537	5	BQ399474	BQ399474	NISC mp03
694	58	1.6	502	5	BQ400913	BQ400913	NISC mp12	767	58	1.6	537	5	BQ525297	BQ525297	NISC no09
695	58	1.6	503	6	CD723592	CD723592	oj24b04.y	768	58	1.6	538	5	BQ522633	BQ522633	NISC nl17
696	58	1.6	505	1	AI434240	AI434240	t133c01.x	769	58	1.6	538	5	BQ389913	BQ389913	NISC mg10
697	58	1.6	505	1	AI804515	AI804515	tp60c04.x	770	58	1.6	539	5	BQ526582	BQ526582	NISC no17
698	58	1.6	505	5	BQ389788	BQ389788	NISC mq09	771	58	1.6	540	4	BQ528904	BQ528904	HNC57-1-H
699	58	1.6	505	5	BQ520026	BQ520026	NISC nl02	772	58	1.6	541	5	BQ520137	BQ520137	NISC nl03
700	58	1.6	505	5	BQ522647	BQ522647	NISC nl17	773	58	1.6	542	5	BQ390259	BQ390259	NISC mg12
701	58	1.6	505	5	BQ522850	BQ522850	NISC nl18	774	58	1.6	544	4	BQ927920	BQ927920	HNC45-1-E
702	58	1.6	506	5	BQ388704	BQ388704	NISC mg03	775	58	1.6	544	5	BQ391651	BQ391651	NISC mg19
703	58	1.6	506	5	BQ399192	BQ399192	NISC mp02	776	58	1.6	544	5	BQ399337	BQ399337	NISC mg03
704	58	1.6	507	5	BQ388655	BQ388655	NISC mg03	777	58	1.6	545	1	AI687614	AI687614	tp97h10.x
705	58	1.6	507	5	BQ390068	BQ390068	NISC mg11	778	58	1.6	545	5	BQ390214	BQ390214	NISC mg11
706	58	1.6	508	5	BQ391243	BQ391243	NISC mg17	779	58	1.6	545	5	BQ393105	BQ393105	NISC ng01
707	58	1.6	508	5	AI284516	AI284516	qt88g06.x	780	58	1.6	546	1	AI539632	AI539632	tp60e06.x
708	58	1.6	509	1	AI284516	AI284516	qt88g06.x	781	58	1.6	547	5	BQ399284	BQ399284	NISC mp02
709	58	1.6	509	5	BQ383513	BQ383513	NISC no01	782	58	1.6	547	7	CF873233	CF873233	tr1c004xm
710	58	1.6	510	4	BM123229	BM123229	LO521D08-	783	58	1.6	548	4	BQ924789	BQ924789	HNC36-1-G
711	58	1.6	510	5	BQ391681	BQ391681	NISC mg20	784	58	1.6	549	4	BG111831	BG111831	602283430
712	58	1.6	511	5	BQ389929	BQ389929	NISC mg10	785	58	1.6	549	4	BM124796	BM124796	LO545B08-
713	58	1.6	511	5	BQ399969	BQ399969	NISC mp06	786	58	1.6	550	1	AL039494	AL039494	DKF2p434A
714	58	1.6	511	5	BQ520949	BQ520949	NISC nl08	787	58	1.6	550	5	BQ391749	BQ391749	NISC mg20
715	58	1.6	511	7	CO888164	CO888164	BovGen_16	788	58	1.6	550	5	BQ524488	BQ524488	NISC no05
716	58	1.6	512	5	BQ390352	BQ390352	NISC mg12	789	58	1.6	550	5	BQ524570	BQ524570	NISC no05
717	58	1.6	512	5	BQ520038	BQ520038	NISC no18	790	58	1.6	551	4	BQ900028	BQ900028	HNC48-1-G
718	58	1.6	512	5	BQ526846	BQ526846	NISC no18	791	58	1.6	551	5	BQ389493	BQ389493	NISC mg07
719	58	1.6	513	5	BQ521513	BQ521513	NISC nl11	792	58	1.6	551	7	CF883818	CF883818	tr1c035xo
720	58	1.6	514	5	BQ389814	BQ389814	NISC mg09	793	58	1.6	553	1	AJ457500	AJ457500	AD457500
721	58	1.6	514	5	BQ399119	BQ399119	NISC mp01	794	58	1.6	553	5	BQ520659	BQ520659	NISC nl06
722	58	1.6	515	1	AI436458	AI436458	t109d02.x	795	58	1.6	553	7	CF873726	CF873726	tr1c005xp
723	58	1.6	515	5	BQ389421	BQ389421	NISC mg06	796	58	1.6	553	7	CF873586	CF873586	tr1c008xp
724	58	1.6	518	5	BQ387993	BQ387993	NISC mn27	797	58	1.6	554	1	AI889148	AI889148	wm46c07.x
725	58	1.6	519	1	AI433968	AI433968	t112c03.x	798	58	1.6	555	5	BQ390179	BQ390179	NISC mg11
726	58	1.6	519	5	BQ399021	BQ399021	NISC mp01	799	58	1.6	555	5	BQ397268	BQ397268	NISC ng26
727	58	1.6	521	5	BQ389771	BQ389771	NISC mg09	800	58	1.6	556	4	BG869433	BG869433	602789120
728	58	1.6	521	5	BQ522862	BQ522862	NISC nl18	801	58	1.6	556	5	BQ520577	BQ520577	NISC nl05
729	58	1.6	521	7	CO895616	CO895616	BovGen_23	802	58	1.6	556	6	CA189203	CA189203	SCCCLB1C0
730	58	1.6	522	5	BQ390268	BQ390268	NISC mg12	803	58	1.6	557	5	BQ389775	BQ389775	NISC mg09
731	58	1.6	522	7	CK628408	CK628408	ip11h09.y	804	58	1.6	558	5	BQ389894	BQ389894	NISC mg10
732	58	1.6	522	7	BQ522695	BQ522695	NISC nl18	805	58	1.6	558	5	BQ520512	BQ520512	NISC nl05
733	58	1.6	523	5	BQ522695	BQ522695	NISC nl18	806	58	1.6	559	5	BQ388969	BQ388969	NISC mg04
734	58	1.6	523	7	CF865961	CF865961	tr1c004xc	807	58	1.6	559	7	CF873198	CF873198	tr1c004xc
735	58	1.6	524	5	BQ390040	BQ390040	NISC mg11	808	58	1.6	561	1	AL042533	AL042533	DKF2p434I
736	58	1.6	525	4	BM115871	BM115871	LO826F09-	809	58	1.6	561	5	BQ587060	BQ587060	E012351-0
737	58	1.6	525	5	BQ522265	BQ522265	NISC nl15	810	58	1.6	562	1	AL042694	AL042694	DKF2p434P
738	58	1.6	525	5	BQ524568	BQ524568	NISC no05	811	58	1.6	562	7	CF884490	CF884490	tr1c040xf
739	58	1.6	525	6	CB938583	CB938583	IPCGT_x13	812	58	1.6	563	5	BQ522407	BQ522407	NISC nl16
740	58	1.6	526	1	AI469784	AI469784	tm20h06.x	813	58	1.6	563	7	CF882666	CF882666	tr1c031xg
741	58	1.6	526	1	AI476086	AI476086	t197g03.x	814	58	1.6	565	7	CF875106	CF875106	tr1c007xd
742	58	1.6	526	1	AI537187	AI537187	tp01d01.x	815	58	1.6	566	1	AI815233	AI815233	wk74r11.x
743	58	1.6	527	4	BQ529587	BQ529587	602378722	816	58	1.6	566	5	BQ390642	BQ390642	NISC mg14
744	58	1.6	527	1	AI499581	AI499581	to22h12.x	817	58	1.6	567	4	BG898583	BG898583	HOA56-1-E
745	58	1.6	527	2	AW151131	AW151131	xg37g06.x	818	58	1.6	567	7	CO882737	CO882737	BovGen_11
746	58	1.6	527	4	BI3809314	BI3809314	BFLGI_002	819	58	1.6	569	7	CM485219	CM485219	hx24g07.y
747	58	1.6	527	5	BQ387327	BQ387327	NISC mn23	820	58	1.6	570	5	BQ389346	BQ389346	NISC mg07
748	58	1.6	527	5	BQ389790	BQ389790	NISC mg09	821	58	1.6	570	5	BQ520814	BQ520814	NISC nl07
749	58	1.6	528	4	BQ924370	BQ924370	HNC26-1-G	822	58	1.6	570	5	BQ522259	BQ522259	NISC nl15
750	58	1.6	528	5	BQ400410	BQ400410	NISC mp09	823	58	1.6	571	1	AI702063	AI702063	tq20f08.x
751	58	1.6	528	5	BQ519883	BQ519883	NISC nl01	824	58	1.6	571	4	BG900978	BG900978	HOA52-1-C
752	58	1.6	528	6	CA230442	CA230442	SCJFLLC0	825	58	1.6	571	5	BQ524526	BQ524526	NISC no05
753	58	1.6	529	5	BQ390324	BQ390324	NISC mg12	826	58	1.6	572	5	BQ390373	BQ390373	NISC mg12
754	58	1.6	530	1	AI469754	AI469754	tm20e01.x	827	58	1.6	573	1	AI538867	AI538867	tp74g01.x

828	58	1.6	573	2	AW118237	AW118237 xel2b08.x	c 901	58	1.6	633	4	BG899001	BG899001 HOA58-1-B
829	58	1.6	574	1	AI439995	AI439995 t163f08.x	902	58	1.6	633	5	BQ527151	BQ527151 NISC no20
830	58	1.6	575	1	AL042377	AL042377 DKF2p434A	c 903	58	1.6	636	4	BQ26743	BQ26743 HNC63-1-D
831	58	1.6	576	7	CF867055	CF867055 tr1c009xh	904	58	1.6	643	5	BQ389933	BQ389933 NISC mq10
832	58	1.6	577	7	CF882708	CF882708 tr1c031xm	905	58	1.6	646	5	BQ389769	BQ389769 NISC mq09
833	58	1.6	578	5	BQ390388	BQ390388 NISC_mq12	c 906	58	1.6	646	7	CO893125	CO893125 BovGen_21
834	58	1.6	579	5	BQ390338	BQ390338 NISC_mq12	907	58	1.6	648	1	AI872300	AI872300 wms7d05.x
835	58	1.6	580	1	AI687587	AI687587 tp97e07.x	908	58	1.6	648	7	CO884930	CO884930 BovGen_13
836	58	1.6	581	5	BQ384132	BQ384132 NISC mn05	909	58	1.6	650	4	BI855926	BI855926 603383093
837	58	1.6	582	5	BQ390195	BQ390195 NISC_mq11	910	58	1.6	650	4	BI889674	BI889674 2F637-2-0
838	58	1.6	583	5	BQ392711	BQ392711 NISC_mq26	911	58	1.6	651	1	AI554827	AI554827 tp73h04.x
839	58	1.6	584	5	BQ250200	BQ250200 NISC_no08	912	58	1.6	652	5	BQ401053	BQ401053 NISC_mq12
840	58	1.6	585	4	BQ26540	BQ26540 HNC4-1-A9	c 913	58	1.6	654	4	BQ525161	BQ525161 HNC37-1-C
841	58	1.6	586	5	BQ396558	BQ396558 NISC_rq21	914	58	1.6	662	4	BI858668	BI858668 603388946
842	58	1.6	585	1	AI539847	AI539847 tp65e12.x	c 915	58	1.6	662	7	CO887751	CO887751 BovGen_16
843	58	1.6	585	5	BQ389752	BQ389752 NISC_mq09	916	58	1.6	664	7	CO872672	CO872672 BovGen_00
844	58	1.6	585	5	BQ400077	BQ400077 NISC_mq07	917	58	1.6	664	1	AI863357	AI863357 tz47d01.x
845	58	1.6	585	7	CO875413	CO875413 BovGen_03	c 918	58	1.6	665	4	BQ255347	BQ255347 HNC40-1-B
846	58	1.6	586	1	AI690948	AI690948 tq02e11.x	c 919	58	1.6	667	4	BQ927733	BQ927733 HNC44-1-G
847	58	1.6	586	1	AL042853	AL042853 DKF2p434H	920	58	1.6	669	1	AI872310	AI872310 wms7e07.x
848	58	1.6	586	5	BQ400992	BQ400992 NISC_mq12	921	58	1.6	669	2	AW172745	AW172745 xj02h09.x
849	58	1.6	586	5	BQ522485	BQ522485 NISC_n116	c 922	58	1.6	677	4	BQ928514	BQ928514 HNC49-1-A
850	58	1.6	587	5	BQ391116	BQ391116 NISC_mq16	923	58	1.6	679	1	AL042981	AL042981 DKF2p434M
851	58	1.6	588	1	AI521634	AI521634 to65h04.x	c 924	58	1.6	680	7	CO881552	CO881552 BovGen_09
852	58	1.6	588	1	AU301568	AU301568 AU301568	925	58	1.6	683	1	AI446536	AI446536 tj05b10.x
853	58	1.6	589	1	AI521465	AI521465 th61c02.x	926	58	1.6	685	9	AG076896	AG076896 Pan trogl
854	58	1.6	589	5	BQ388694	BQ388694 NISC_mq03	927	58	1.6	688	1	AL042557	AL042557 DKF2p434J
855	58	1.6	589	5	BQ391645	BQ391645 NISC_mq19	928	58	1.6	688	7	CO889662	CO889662 BovGen_17
856	58	1.6	589	5	EX846370	EX846370 EX846370	929	58	1.6	691	4	BF965904	BF965904 602277262
857	58	1.6	589	7	CF886069	CF886069 tr1c085xe	930	58	1.6	692	1	AI538878	AI538878 tp74h01.x
858	58	1.6	590	1	AI828583	AI828583 w142e08.x	931	58	1.6	693	1	AI354998	AI354998 qu16b10.x
859	58	1.6	591	5	BQ390621	BQ390621 NISC_mq14	932	58	1.6	695	1	AI888575	AI888575 wms3b09.x
860	58	1.6	592	4	BQ926032	BQ926032 HNC23-1-B	933	58	1.6	695	4	BG179586	BG179586 602328213
861	58	1.6	592	5	BQ390609	BQ390609 NISC_mq14	934	58	1.6	700	4	BG299059	BG299059 602397761
862	58	1.6	593	5	BQ390665	BQ390665 NISC_mq11	935	58	1.6	701	4	BG111590	BG111590 602282624
863	58	1.6	594	5	BQ929418	BQ929418 HNC50-1-B	936	58	1.6	703	4	BI087461	BI087461 602851091
864	58	1.6	594	5	BQ929418	BQ929418 HNC50-1-B	937	58	1.6	704	1	AI863197	AI863197 tz44e08.x
865	58	1.6	594	5	BQ400399	BQ400399 NISC_mq09	938	58	1.6	704	4	BI554245	BI554245 603235329
866	58	1.6	596	4	BG896174	BG896174 HOA9-1-B1	c 939	58	1.6	705	7	CK118011	CK118011 207k15.p1
867	58	1.6	599	5	BQ384194	BQ384194 NISC_mq05	c 940	58	1.6	709	7	CK120856	CK120856 205m12.p1
868	58	1.6	599	5	EX847993	EX847993 EX847993	941	58	1.6	710	2	BE306712	BE306712 601104130
869	58	1.6	601	4	BF971261	BF971261 602273289	942	58	1.6	712	1	AI567944	AI567944 tq86b08.x
870	58	1.6	602	5	BQ525565	BQ525565 NISC_no11	943	58	1.6	713	1	AI888665	AI888665 tq86e05.x
871	58	1.6	604	4	BG899723	BG899723 HOA39-1-F	944	58	1.6	721	1	AI567968	AI567968 tq86e08.x
872	58	1.6	604	5	BQ522555	BQ522555 NISC_n117	945	58	1.6	725	4	BF968622	BF968622 602271054
873	58	1.6	606	5	BQ389945	BQ389945 NISC_mq10	946	58	1.6	727	1	AI804531	AI804531 tp60d11.x
874	58	1.6	606	5	BQ390348	BQ390348 NISC_mq12	c 947	58	1.6	728	7	CO881106	CO881106 BovGen_09
875	58	1.6	606	7	CK619769	CK619769 mk28b09.y	948	58	1.6	731	1	AL042865	AL042865 DKF2p434H
876	58	1.6	608	5	BQ524165	BQ524165 NISC_no03	949	58	1.6	732	4	BG114012	BG114012 602284496
877	58	1.6	609	1	AI866472	AI866472 tz49b10.x	950	58	1.6	733	7	CF520284	CF520284 AGENCOURT
878	58	1.6	609	6	CA175113	CA175113 SCJFST101	951	58	1.6	735	1	AI567935	AI567935 tq86a04.x
879	58	1.6	610	1	AL042338	AL042338 DKF2p434I	952	58	1.6	737	1	AL043196	AL043196 DKF2p434H
880	58	1.6	610	5	EX849028	EX849028 EX849028	953	58	1.6	739	1	AL042750	AL042750 DKF2p434C
881	58	1.6	610	6	CA264570	CA264570 SCBFLA17	954	58	1.6	741	4	BG251851	BG251851 602364466
882	58	1.6	612	5	BQ391612	BQ391612 NISC_mq19	955	58	1.6	744	4	BI888935	BI888935 2F637-2-0
883	58	1.6	613	1	AL040006	AL040006 DKF2p434M	956	58	1.6	745	4	BG284564	BG284564 602408723
884	58	1.6	614	1	BI868792	BI868792 603391947	957	58	1.6	747	7	CK357136	CK357136 AGENCOURT
885	58	1.6	614	1	AI888317	AI888317 wn31f11.x	958	58	1.6	748	1	AL042515	AL042515 DKF2p434H
886	58	1.6	614	6	CA128240	CA128240 SCJFTR203	c 959	58	1.6	750	6	CB903665	CB903665 tr1c035x1
887	58	1.6	614	7	CF878170	CF878170 tr1c016xm	c 960	58	1.6	753	6	CB903554	CB903554 tr1c035xc
888	58	1.6	616	1	AI288281	AI288281 qv84a03.x	961	58	1.6	754	1	AI805762	AI805762 tx89g09.x
889	58	1.6	617	4	BG927885	BG927885 HNC7-1-D1	962	58	1.6	756	7	CK195662	CK195662 FGAS00410
890	58	1.6	618	4	BG928558	BG928558 HNC68-1-E	c 963	58	1.6	759	6	CB902325	CB902325 tr1c029xc
891	58	1.6	619	4	BG929420	BG929420 HNC50-1-A	964	58	1.6	760	2	BF538723	BF538723 602051061
892	58	1.6	620	7	CF873624	CF873624 tr1c005xd	c 965	58	1.6	761	9	CG847811	CG847811 ZMMHB031
893	58	1.6	621	1	AI887785	AI887785 wms18g07.x	966	58	1.6	763	7	CK198343	CK198343 FGAS00682
894	58	1.6	622	2	AW180982	AW180982 MGA0133x	967	58	1.6	770	7	CF284480	CF284480 AGENCOURT
895	58	1.6	623	4	BG926630	BG926630 HNC62-1-E	968	58	1.6	776	4	BI871663	BI871663 603395562
896	58	1.6	623	7	CF884293	CF884293 tr1c038xg	969	58	1.6	777	4	BI855622	BI855622 603383136
897	58	1.6	629	5	BQ522332	BQ522332 NISC_n116	970	58	1.6	779	4	BG782822	BG782822 SEAUUMC002
898	58	1.6	630	5	BG927301	BG927301 HNC66-1-B	971	58	1.6	780	4	BG165260	BG165260 602344152
899	58	1.6	632	1	AL043021	AL043021 DKF2p434O	972	58	1.6	781	7	CK195756	CK195756 FGAS00419
900	58	1.6	632	7	CO879146	CO879146 BovGen_07	c 973	58	1.6	782	6	CB895899	CB895899 tr1c004xc

974	58	1.6	782	6	CB9898562	1047	58	1.6	826	7	CK196393	CK196393	FGAS00485
c 975	58	1.6	782	4	CB903275	1048	58	1.6	826	7	CK196998	CK196998	FGAS00546
976	58	1.6	785	4	BQ288001	1049	58	1.6	827	7	CK195533	CK195533	FGAS00397
977	58	1.6	786	7	CK479384	1050	58	1.6	827	7	CK196232	CK196232	FGAS00468
c 978	58	1.6	788	7	CF285572	1051	58	1.6	827	7	CK200843	CK200843	FGAS00936
979	58	1.6	791	6	CB986126	1052	58	1.6	827	7	CK200927	CK200927	FGAS00944
c 980	58	1.6	793	1	A1610426	1053	58	1.6	828	7	CK193000	CK193000	FGAS00140
981	58	1.6	794	7	CF147535	1054	58	1.6	828	7	CK193053	CK193053	FGAS00146
982	58	1.6	796	7	CK195721	1055	58	1.6	828	7	CK193648	CK193648	FGAS00206
983	58	1.6	797	7	CO566927	1056	58	1.6	828	7	CK194229	CK194229	FGAS00264
984	58	1.6	800	7	CK196897	1057	58	1.6	828	7	CK194448	CK194448	FGAS00287
c 985	58	1.6	800	7	CK792681	1058	58	1.6	828	7	CK194972	CK194972	FGAS00340
986	58	1.6	801	4	BG782551	1059	58	1.6	828	7	CK196355	CK196355	FGAS00341
987	58	1.6	801	5	BQ434265	1060	58	1.6	828	7	CK196878	CK196878	FGAS00534
988	58	1.6	801	7	CF873386	1061	58	1.6	828	7	CK198145	CK198145	FGAS00662
989	58	1.6	801	7	CF873397	1062	58	1.6	828	7	CK198379	CK198379	FGAS00686
c 990	58	1.6	801	7	CK200310	1063	58	1.6	828	7	CK199532	CK199532	FGAS00803
991	58	1.6	801	7	CK792023	1064	58	1.6	828	7	CK200896	CK200896	FGAS00941
992	58	1.6	802	7	CK196378	1065	58	1.6	829	7	CK195739	CK195739	FGAS00418
993	58	1.6	805	7	CK200304	1066	58	1.6	829	7	CK196423	CK196423	FGAS00488
994	58	1.6	807	1	A1432656	1067	58	1.6	829	7	CK196646	CK196646	FGAS00510
995	58	1.6	807	4	BG393344	1068	58	1.6	829	7	CK199037	CK199037	FGAS00752
996	58	1.6	807	7	CK196289	1069	58	1.6	829	7	CK201011	CK201011	FGAS00952
997	58	1.6	807	7	CK197553	1070	58	1.6	830	7	CK193158	CK193158	FGAS00157
c 998	58	1.6	807	7	CK199534	1071	58	1.6	830	7	CK195617	CK195617	FGAS00405
999	58	1.6	809	7	CB997064	1072	58	1.6	830	7	CK196779	CK196779	FGAS00524
1000	58	1.6	811	6	CK194846	1073	58	1.6	830	7	CK196984	CK196984	FGAS00545
1001	58	1.6	812	7	CF872637	1074	58	1.6	830	7	CK198340	CK198340	FGAS00682
1002	58	1.6	812	7	CK195770	1075	58	1.6	831	7	CK196333	CK196333	FGAS00478
c1003	58	1.6	812	9	CG847981	1076	58	1.6	831	7	CK198286	CK198286	FGAS00677
1004	58	1.6	813	7	CK192880	1077	58	1.6	831	7	CK198776	CK198776	FGAS00726
1005	58	1.6	813	7	CK193688	1078	58	1.6	831	7	CK198924	CK198924	FGAS00741
1006	58	1.6	813	7	CK194268	1079	58	1.6	831	7	CK198938	CK198938	FGAS00742
1007	58	1.6	813	7	CK196966	1080	58	1.6	831	7	CK200278	CK200278	FGAS00878
1008	58	1.6	813	7	CK200167	1081	58	1.6	832	7	CK194439	CK194439	FGAS00286
1009	58	1.6	814	5	BQ227852	1082	58	1.6	832	7	CK196953	CK196953	FGAS00542
1010	58	1.6	814	7	CK200261	1083	58	1.6	832	7	CK198323	CK198323	FGAS00680
1011	58	1.6	814	7	CK200263	1084	58	1.6	832	7	CK200757	CK200757	FGAS00927
1012	58	1.6	814	7	CK200329	1085	58	1.6	833	5	BQ233461	BQ233461	AGENCOURT
1013	58	1.6	815	7	CK200375	1086	58	1.6	833	7	CK195815	CK195815	FGAS00426
1014	58	1.6	816	7	CK196242	1087	58	1.6	833	7	CK196827	CK196827	FGAS00529
1015	58	1.6	816	7	CK197263	1088	58	1.6	833	7	CK197043	CK197043	FGAS00551
1016	58	1.6	816	7	CK200360	1089	58	1.6	833	7	CK199653	CK199653	FGAS00815
1017	58	1.6	817	7	CK196872	1090	58	1.6	833	7	CK199679	CK199679	FGAS00818
1018	58	1.6	817	7	CK199307	1091	58	1.6	834	7	CK192938	CK192938	FGAS00134
1019	58	1.6	818	7	CK194969	1092	58	1.6	834	7	CK193106	CK193106	FGAS00151
1020	58	1.6	818	7	CK198899	1093	58	1.6	834	7	CK197725	CK197725	FGAS00620
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1022	58	1.6	819	7	CK197025	1095	58	1.6	834	7	CK198390	CK198390	FGAS00687
1023	58	1.6	820	7	CK200974	1096	58	1.6	835	7	CK194334	CK194334	FGAS00275
1024	58	1.6	821	7	CK194961	1097	58	1.6	835	7	CK195582	CK195582	FGAS00402
1025	58	1.6	821	7	CK200359	1098	58	1.6	836	7	CK194202	CK194202	FGAS00262
1026	58	1.6	821	7	CK200794	1099	58	1.6	836	7	CK194248	CK194248	FGAS00266
1027	58	1.6	821	7	CK200879	1100	58	1.6	836	7	CK198202	CK198202	FGAS00668
1028	58	1.6	822	4	BG782371	1101	58	1.6	836	7	CK198244	CK198244	FGAS00672
1029	58	1.6	822	7	CK195026	1102	58	1.6	836	7	CK199507	CK199507	FGAS00800
1030	58	1.6	822	7	CK199583	1103	58	1.6	836	7	CK200220	CK200220	FGAS00872
1031	58	1.6	823	7	CK195025	1104	58	1.6	837	7	CK193585	CK193585	FGAS00159
1032	58	1.6	823	7	CK196405	1105	58	1.6	837	7	CK198005	CK198005	FGAS00648
1033	58	1.6	823	7	CK197545	1106	58	1.6	837	7	CK200849	CK200849	FGAS00936
1034	58	1.6	824	7	CK198388	1107	58	1.6	838	7	CK195428	CK195428	FGAS00386
1035	58	1.6	824	7	CK199020	1108	58	1.6	838	7	CK195643	CK195643	FGAS00408
c1036	58	1.6	825	6	CB908623	1109	58	1.6	838	7	CK196262	CK196262	FGAS00471
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1038	58	1.6	825	7	CK193024	1111	58	1.6	838	7	CK196837	CK196837	FGAS00530
1039	58	1.6	825	7	CK194237	1112	58	1.6	838	7	CK197607	CK197607	FGAS00608
1040	58	1.6	825	7	CK196907	1113	58	1.6	839	7	CK198909	CK198909	FGAS00739
1041	58	1.6	825	7	CK197012	1114	58	1.6	839	7	CK193746	CK193746	FGAS00216
1042	58	1.6	825	7	CK199445	1115	58	1.6	839	7	CK194870	CK194870	FGAS00330
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1044	58	1.6	825	7	CK200255	1117	58	1.6	839	7	CK197079	CK197079	FGAS00555
1045	58	1.6	826	7	CK193685	1118	58	1.6	840	5	BQ522683	BQ522683	AGENCOURT
1046	58	1.6	826	7	CK195554	1119	58	1.6	840	7	CK192960	CK192960	FGAS00136

1120	58	1.6	840	7	CK196277	CK196277	FGAS00473	1193	58	1.6	853	7	CK193529	CK193529	FGAS00194
1121	58	1.6	840	7	CK197060	CK197060	FGAS00553	1194	58	1.6	853	7	CK194907	CK194907	FGAS00334
1122	58	1.6	840	7	CK197074	CK197074	FGAS00554	1195	58	1.6	853	7	CK195119	CK195119	FGAS00355
1123	58	1.6	840	7	CK197669	CK197669	FGAS00614	1196	58	1.6	853	7	CK198267	CK198267	FGAS00675
1124	58	1.6	840	7	CK200853	CK200853	FGAS00937	1197	58	1.6	853	7	CK199634	CK199634	FGAS00813
1125	58	1.6	841	7	CK198415	CK198415	FGAS00937	1198	58	1.6	853	7	CK200279	CK200279	FGAS00878
1126	58	1.6	841	7	CK193049	CK193049	FGAS00146	1199	58	1.6	853	7	CK200708	CK200708	FGAS00922
1127	58	1.6	841	7	CK195765	CK195765	FGAS00420	1200	58	1.6	853	7	CK007895	CK007895	EST796230
1128	58	1.6	841	7	CK196266	CK196266	FGAS00471	1201	58	1.6	854	7	CK194464	CK194464	FGAS00289
1129	58	1.6	842	7	CK193110	CK193110	FGAS00152	1202	58	1.6	854	7	CK195033	CK195033	FGAS00347
1130	58	1.6	842	7	CK195745	CK195745	FGAS00418	1203	58	1.6	854	7	CK195063	CK195063	FGAS00350
1131	58	1.6	842	7	CK196318	CK196318	FGAS00477	1204	58	1.6	854	7	CK196223	CK196223	FGAS00467
1132	58	1.6	843	6	CK127447	CK127447	SCCIR3C0	1205	58	1.6	854	7	CK196257	CK196257	FGAS00470
1133	58	1.6	843	7	CK196365	CK196365	FGAS00482	1206	58	1.6	854	7	CK196456	CK196456	FGAS00491
1134	58	1.6	843	7	CK198914	CK198914	FGAS00740	1207	58	1.6	854	7	CK199481	CK199481	FGAS00491
1135	58	1.6	844	7	CK192919	CK192919	FGAS00132	1208	58	1.6	854	7	CK200848	CK200848	FGAS00798
1136	58	1.6	844	7	CK194277	CK194277	FGAS00269	1209	58	1.6	854	7	CK200848	CK200848	FGAS00798
1137	58	1.6	844	7	CK194391	CK194391	FGAS00281	1210	58	1.6	855	7	CK195062	CK195062	FGAS00350
1138	58	1.6	844	7	CK196422	CK196422	FGAS00488	1211	58	1.6	855	7	CK195527	CK195527	FGAS00396
1139	58	1.6	845	7	CK192875	CK192875	FGAS00128	1212	58	1.6	855	7	CK196217	CK196217	FGAS00466
1140	58	1.6	845	7	CK193161	CK193161	FGAS00157	1213	58	1.6	855	7	CK196317	CK196317	FGAS00477
1141	58	1.6	845	7	CK195076	CK195076	FGAS00351	1214	58	1.6	855	7	CK196558	CK196558	FGAS00501
1142	58	1.6	845	7	CK196823	CK196823	FGAS00528	1215	58	1.6	856	7	CK195138	CK195138	FGAS00357
1143	58	1.6	845	7	CK199008	CK199008	FGAS00749	1216	58	1.6	857	4	CK198452	CK198452	602278402
1144	58	1.6	845	7	CK200777	CK200777	FGAS00929	1217	58	1.6	857	7	CK198185	CK198185	FGAS00666
1145	58	1.6	846	7	CK196304	CK196304	FGAS00475	1218	58	1.6	858	7	CK193712	CK193712	FGAS00212
1146	58	1.6	846	7	CK199016	CK199016	FGAS00750	1219	58	1.6	858	7	CK194387	CK194387	FGAS00281
1147	58	1.6	846	7	CK200907	CK200907	FGAS00942	1220	58	1.6	858	7	CK197083	CK197083	FGAS00555
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1149	58	1.6	846	7	CK205064	CK205064	FGAS001360	1222	58	1.6	859	7	CK196358	CK196358	FGAS00481
1150	58	1.6	847	7	CK194370	CK194370	FGAS00279	1223	58	1.6	859	7	CK198166	CK198166	FGAS00664
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1152	58	1.6	847	7	CK199544	CK199544	FGAS00804	1225	58	1.6	860	7	CK194324	CK194324	FGAS00274
1153	58	1.6	847	7	CK199561	CK199561	FGAS00806	1226	58	1.6	860	7	CK198177	CK198177	FGAS00666
1154	58	1.6	847	7	CK199689	CK199689	FGAS00819	1227	58	1.6	861	2	BE895801	BE895801	601432727
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1158	58	1.6	848	4	CK197535	CK197535	602311872	1231	58	1.6	862	7	CK197542	CK197542	FGAS00601
1159	58	1.6	848	7	CK192879	CK192879	FGAS00128	1232	58	1.6	862	7	CK198129	CK198129	FGAS00661
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1161	58	1.6	848	7	CK193796	CK193796	FGAS00221	1234	58	1.6	862	7	CK200737	CK200737	FGAS00925
1162	58	1.6	848	7	CK198136	CK198136	FGAS00661	1235	58	1.6	863	7	CK193790	CK193790	FGAS00230
1163	58	1.6	848	7	CK199711	CK199711	FGAS00821	1236	58	1.6	863	7	CK195645	CK195645	FGAS00408
1164	58	1.6	849	7	CK192884	CK192884	FGAS00129	1237	58	1.6	863	7	CK196201	CK196201	FGAS00464
1165	58	1.6	849	7	CK195094	CK195094	FGAS00353	1238	58	1.6	863	7	CK198188	CK198188	FGAS00667
1166	58	1.6	849	7	CK195905	CK195905	FGAS00537	1239	58	1.6	863	7	CK199036	CK199036	FGAS00752
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1168	58	1.6	849	7	CK198254	CK198254	FGAS00673	1241	58	1.6	864	7	CK197565	CK197565	FGAS00604
1169	58	1.6	849	7	CK199438	CK199438	FGAS00793	1242	58	1.6	864	7	CK198303	CK198303	FGAS00678
1170	58	1.6	849	7	CK199720	CK199720	FGAS00822	1243	58	1.6	864	7	CK198412	CK198412	FGAS00689
1171	58	1.6	849	7	CK200176	CK200176	FGAS00868	1244	58	1.6	865	7	CK193569	CK193569	FGAS00198
1172	58	1.6	849	7	CK200363	CK200363	FGAS00887	1245	58	1.6	865	7	CK196196	CK196196	FGAS00464
1173	58	1.6	850	7	CK196182	CK196182	FGAS00462	1246	58	1.6	865	7	CK196364	CK196364	FGAS00482
1174	58	1.6	850	7	CK196346	CK196346	FGAS00480	1247	58	1.6	865	7	CK196813	CK196813	FGAS00527
1175	58	1.6	850	7	CK196881	CK196881	FGAS00534	1248	58	1.6	865	7	CK197648	CK197648	FGAS00612
1176	58	1.6	850	7	CK198353	CK198353	FGAS00683	1249	58	1.6	865	7	CK198814	CK198814	FGAS00730
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1178	58	1.6	851	7	CK193709	CK193709	FGAS00212	1251	58	1.6	866	7	CK193452	CK193452	FGAS00795
1179	58	1.6	851	7	CK195646	CK195646	FGAS00408	1252	58	1.6	866	7	CK200117	CK200117	FGAS00862
1180	58	1.6	851	7	CK198407	CK198407	FGAS00689	1253	58	1.6	867	7	CK192898	CK192898	FGAS00130
1181	58	1.6	851	7	CK198413	CK198413	FGAS00689	1254	58	1.6	867	7	CK193007	CK193007	FGAS00141
1182	58	1.6	851	7	CK199594	CK199594	FGAS00809	1255	58	1.6	867	7	CK194211	CK194211	FGAS00263
1183	58	1.6	852	7	CK194319	CK194319	FGAS00274	1256	58	1.6	867	7	CK194422	CK194422	FGAS00285
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1185	58	1.6	852	7	CK195112	CK195112	FGAS00355	1258	58	1.6	868	7	CK198243	CK198243	FGAS00672
1186	58	1.6	852	7	CK195558	CK195558	FGAS00399	1259	58	1.6	868	7	CK198316	CK198316	FGAS00680
1187	58	1.6	852	7	CK196381	CK196381	FGAS00483	1260	58	1.6	869	7	CK198922	CK198922	FGAS00741
1188	58	1.6	852	7	CK198402	CK198402	FGAS00688	1261	58	1.6	870	4	BM014441	BM014441	603640204
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 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
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 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC/DC/DTP  
 cDNA Library Preparation: Life Technologies, Inc.  
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 Clone Distribution: MGC clone distribution information can be  
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AUTHORS  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL  
Genome Res. 6 (9), 791-806 (1996)  
MEDLINE  
97044477  
PUBMED  
8889548  
COMMENT  
Contact: McCray, PB  
McCrays Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).

Seq primer: M13 FORWARD  
POLYA=Yes.  
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source  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="UI-CF-EC1-adv-c-23-0-UI"  
/tissue\_type="Lung"  
/dev\_stages="Adult and Fetal"  
/lab\_host="DHI0B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-EC1"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-CF-EC1 is a normalized cDNA library containing the  
following tissue(s): Normal lung from adult and from fetal  
day 64, day 87, week 19 and week 42. The library was  
constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into pT7T3-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is  
AAGTGCCTAC.  
TAG\_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371  
and 380-383  
TAG\_L1B=UI-CF-EC1  
TAG\_SEQ=AAGTGCCTAC"

ORIGIN  
Query Match 15.4%; Score 550; DB 5; Length 692;  
Best Local Similarity 99.7%; Pred. No. 7.2e-191;  
Matches 650; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2659 AAATTCTCCACACAGATGGCTCTGCAATCTGCCACAGCTCTGGGGCGGTGCTGTAGG 2718  
Db 41 AAATTCTCCACACAGATGGCTCTGCAATCTGCCACAGCTCTGGGGCGGTGCTGTAGG 100  
Qy 2719 GAAAGGCGCTGTTTTCCTGAGGGCGGCTGGGCTGTTCATGGCTCCGCGAGCTGCGC 2778  
Db 101 GAAAGGCGCTGTTTTCCTGAGGGCGGCTGGGCTGTTCATGGCTCCGCGAGCTGCGC 160  
Qy 2779 GTGCTTGGCGCCCTGGCGGTGTGTAGCTGCTTCTTGGCGGCGACAGAGCTGCGGGGTCT 2838  
Db 161 GTGCTTGGCGCCCTGGCGGTGTGTAGCTGCTTCTTGGCGGCGACAGAGCTGCGGGGTCT 220  
Qy 2839 GGGGCGACCGGAGCTAAGACAGAGCTCTGTGTGAGGGGTGGAGGCTGTCTTTAAACCG 2898  
Db 221 GGGGCGACCGGAGCTAAGACAGAGCTCTGTGTGAGGGGTGGAGGCTGTCTTTAAACCG 280  
Qy 2899 ACACCTCGAGTGTCTCTGAGATGCTGGGTCCACCTGAGTGGCACGCGGAGCAGCTGTG 2958  
Db 281 ACACCTCGAGTGTCTCTGAGATGCTGGGTCCACCTGAGTGGCACGCGGAGCAGCTGTG 340  
Qy 2959 GCGGCTGCTCTCTCTAGGCGAGTCTGGGAACTAAGCTCGGGCCCTTCTTTGCAAG 3018  
Db 341 GCGGCTGCTCTCTCTAGGCGAGTCTGGGAACTAAGCTCGGGCCCTTCTTTGCAAG 400  
Qy 3019 ACCGAGGATGGGTGGGTGCTGGGAGCTCATGGGGAATGGCTGAGGAGCTACGTGTGAA 3078  
Db 401 ACCGAGGATGGGTGGGTGCTGGGAGCTCATGGGGAATGGCTGAGGAGCTACGTGTGAA 460  
Qy 3079 GAGGCGCGGTTTGTGGCTGCAAGCGGCTTGGAGCGGCTCTCTCTCAGGCTCAGATTTC 3138  
Db 461 AAGGCGCGGTTTGTGGCTGCAAGCGGCTTGGAGCGGCTCTCTCTCAGGCTCAGATTTC 520  
Qy 3139 CTTTTCGCTTAATGAAGAAACATGCGCTCTGGGTCTCAGGGCTATTAGGCTTTGCCCT 3198  
Db 521 CTTTTCGCTTAATGAAGAAACATGCGCTCTGGGTCTCAGGGCTATTAGGCTTTGCCCT 580

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Qy 3199 CAGGAAGTGGCTTGGACGAGGTCATGTTATTTTCAACACTGTCCTCGGAGCTTGGCCT 3258
Db 581 CAGGAAGTGGCTTGGACGAGGTCATGTTATTTTCAACACTGTCCTCGGAGCTTGGCCT 640
Qy 3259 GGGCACGTCATGGAATGCGCCATGTCCTCTGTCGTCGTCGAGCTCGCGGTG 3310
Db 641 GGGCACGTCATGGAATGCGCCATGTCCTCTGTCGTCGTCGAGCTCGCGGTG 692

RESULT 6
AQ472645/c
LOCUS
DEFINITION CITBI-EI-2585H18.TP CITBI-EI Homo sapiens genomic clone 2585H18,
genomic survey sequence.
ACCESSION AQ472645
VERSION AQ472645.1 GI:4651600
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 646)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other GSSs: CITBI-EI-2585H18.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

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    Location/Qualifiers
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            /sex="male"
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            /clone_lib="CITBI-EI"
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Matches 640; Conserved 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1556 AGCCCCACCTGCAGAACCCAGCTTAAGAGCTGTGAGTGTGTGTCAGCAACCGGGCA 1615
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Qy 1616 CTGTGCTGGCCAGAGCTAGGGCTGAGAAAGTGGCCCTGCTTGGGCAATTCACCAAGACC 1675
Db 585 CTGTGCTGGCCAGAGCTAGGGCTGATTAAGTGGCCCTGCTTGGGCAATTCACCAAGACC 526
Qy 1676 CTGAGCCCCCGCTCACAGAGAGGCCCAAGTGGCCCAATGCAGACCTCACTGGTGGGGT 1735
Db 525 CTGAGCCCCCGCTCACAGAGAGGCCCAAGTGGCCCAATGCAGACCTCACTGGTGGGGT 466
Qy 1736 GTAGCTGGGTCTACAGTCAGACTTCTCTCTTAAGGGGTGTCAGTCCCTGGGCATCCACCA 1795
Db 465 GTAGCTGGGTCTACAGTCAGACTTCTCTCTTAAGGGGTGTCAGTCCCTGGGCATCCACCA 406
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Qy 1796 CGCGAATCCTAGAGGAAGGAGAGTTGGCTCATTTGGGATTTATGGCAAGAAAGTCCAGAG 1855
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Qy 1856 ATGCCAGTCCCTGGAGTAGAAGAGGTGGTGGTTTATCTCTTGGATTAATAAGAAATG 1915
Db 345 ATGCCAGTCCCTGGAGTAGAAGAGGTGGTGGTTTATCTCTTGGATTAATAAGAAATG 286
Qy 1916 AGGTGTGTGGGCTTGTCAACACAGAAATTCAAAGCCCTCATTTGCTATCCAGCATCTCTTAA 1975
Db 285 AGGTGTGTGGGCTTGTCAACACAGAAATTCAAAGCCCTCATTTGCTATCCAGCATCTCTTAA 226
Qy 1976 AACTTTGTAGTCTTGGAAATTCATACAGAGAGCAATGACTCTGCTTAACTTATGAAGAA 2035
Db 225 AACTTTGTAGTCTTGGAAATTCATACAGAGAGCAATGACTCTGCTTAACTTATGAAGAA 166
Qy 2036 AGTTAAAACATGAATCTTGGGAGTCTACATTTTCTTATCACAGAGAGCTGAGCTGCCATC 2095
Db 165 AGTTAAAACATGAATCTTGGGAGTCTACATTTTCTTATCACAGAGAGCTGAGCTGCCATC 106
Qy 2096 TCCTTTATAAATGCTTAACACAGAGCGGGTCTGGTGGCTCATGCTGTAAATCCAGCACTT 2155
Db 105 TCCTTTATAAATGCTTAACACAGAGCGGGTCTGGTGGCTCATGCTGTAAATCCAGCACTT 46
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Db 45 TGAGAGGCTCAGGTGCGCGGACTGCGCTGAGGTCAGGAATTC 4

RESULT 7
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LOCUS
DEFINITION AGENCOURT 10338675 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6574977
5', mRNA sequence.
ACCESSION BU542994
VERSION BU542994.1 GI:22853477
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 927)
AUTHORS NIH-MGC Http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbe@email.nih.gov
Tissue Procurement: DCTD/BTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2771 row: c column: 09
High quality sequence stop: 643.
Location/Qualifiers
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        Site_2: EcoRI; cDNA made by oligo-dT priming.
        Directionally cloned into EcoRI/XhoI sites using the
        following 5' adaptor: GGCAGAG(G). Library constructed by
        Ling Hong in the laboratory of Gerald M. Rubin (University
        of California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies).
        Note: this is a NIH_MGC Library."
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ORIGIN	Query Match Best Local Similarity 15.0%; Score 536; DB 5; Length 927; Matches 686; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1892 ATCTCTTGGATATAAATGAATGAGGTGTGTGGCTTGTCAACACAGAAATTCAGGCCTC 1951
Db	712 ATCTCTTGGATATAAATGAATGAGGTGTGTGGCTTGTCAACACAGAAATTCAGGCCTC 653
Qy	1952 ATTGCTATCCAGCATCTTAAACCTTTGATGCTTTGGATTCATGACGAGGCAAT 2011
Db	652 ATTGCTATCCAGCATCTTAAACCTTTGATGCTTTGGAATTCATGACGAGGCAAT 593
Qy	2012 GACTCCTGCTTAACCTTATGAAGAAAGTTAAACATGAATCTTGGAGTCTACATTTCTT 2071
Db	592 GACTCCTGCTTAACCTTATGAAGAAAGTTAAACATGAATCTTGGAGTCTACATTTCTT 533
Qy	2072 ATCCAGGAGCTGGACTGCCATCTCTTATAAATGCCCTTAACACAGGCGGGTCTGGTGG 2131
Db	532 ATCCAGGAGCTGGACTGCCATCTCTTATAAATGCCCTTAACACAGGCGGGTCTGGTGG 473
Qy	2132 CTCATGCTGTAATCCAGCATCTTGAGAGGCTGAGGTGCGGAGCTGCTGAGGTGAG 2191
Db	472 CTCATGCTGTAATCCAGCATCTTGAGAGGCTGAGGTGCGGAGCTGCTGAGGTGAG 413
Qy	2192 GAATTCAGACAGCAGCTGCGCAACATGCAAAACCCCATCTCTACTTAAATAAATAAATAA 2251
Db	412 GAATTCAGACAGCAGCTGCGCAACATGCAAAACCCCATCTCTACTTAAATAAATAAATAA 353
Qy	2252 TATTAGCTGGGATGCTGTGTGCTGTATCCAGCTACTCAGGAGGATGAGGCAAG 2311
Db	352 TATTAGCTGGGATGCTGTGTGCTGTATCCAGCTACTCAGGAGGATGAGGCAAG 293
Qy	2312 AGACCTGCTGAACCTGAGGTGAGGTGCGAGCGGAGGTGCGACCACTGCACTCC 2371
Db	292 AGACCTGCTGAACCTGAGGTGAGGTGCGAGCGGAGGTGCGACCACTGCACTCC 233
Qy	2372 AGTCTGGGTAAACAGAGCAGACTTTCTAGAAAAGCCTTAACAAACAGATAAGGTAGGACT 2431
Db	232 AGTCTGGGTAAACAGAGCAGACTTTCTAGAAAAGCCTTAACAAACAGATAAGGTAGGACT 173
Qy	2432 CAACCAACTGAACTGACTTTTCCCTGTACCTTTAGCCCTGTCAGGCTAGTAACCTC 2491
Db	172 CAACCAACTGAACTGACTTTTCCCTGTACCTTTAGCCCTGTCAGGCTAGTAACCTC 113
Qy	2492 TTGAGACCTCTCCCTGACAGGAGCAAGCAGGAGCAATTTAGAGCTTTTATAGATAAAC 2551
Db	112 TTGAGACCTCTCCCTGACAGGAGCAAGCAGGAGCAATTTAGAGCTTTTATAGATAAAC 53
Qy	2552 TGGTTTCTTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2580
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RESULT 8  
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LOCUS AWB15410 527 bp mRNA linear EST 17-MAY-2000  
DEFINITION QV0-ST0215-140200-100-c05 ST0215 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AWB15410  
VERSION AWB15410.1 GI:7908404  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 527)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,  
Goldman,G.H., Carvalho,A.F., Matukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
PUBMED	10737800
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the PAPESP/LiCR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l=st2-QV0-ST0215-140 200-100-c05&t3=2000-02-14&t4=1) Seq primer: puc 18 forward High quality sequence stop: 527. Location/Qualifiers 1..527 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_lib="ST0215" /note="Organ: stomach; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
FEATURES	source
ORIGIN	Query Match 14.7%; Score 527; DB 2; Length 527; Best Local Similarity 100.0%; Pred. No. 2.1e-182; Matches 527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1496 CCCAGTGCCAGGCGACTTTGCTCAAGAAATAGCAACACTGCTAACTCTGTTTCTAGCCG 1555
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Qy	1676 CTGACACCCCGCTCAGCAGGAGGCCCAAGTGGCCCAATGCAGACCTCCTGTTGGGGT 1735
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DEFINITION      na224805.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3435945 3',
mRNA sequence.
ACCESSION      BF940697
VERSION      BF940697.1
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 527)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 505.
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Location/Qualifiers
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/clone="IMAGE:3435945"
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strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTCGAGCGCGCGACATTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
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Qy      3242 TCCTGCGACGTTGGCTCGGGCAGCGTCATGGAATGGCCCATGCTCCCTTCGCTGCGTGGACG 3301
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Qy      3422 GCGCCCGCCCGCCCGCCACACCGTCCAGGGGCGCGGTAGACAAAGTGGAGTTCGCGCTTTGG 3481
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Qy      3482 GCTGCTGCGCAGCAGAGGTAGCCCTTGATGTCAGTGGCGGAGCGCGTCTCCGCGACCTGGA 3541
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Db      47 AGCAGCGCGCGTCCACACAGCAGCAACCGCGTGGCGCT 9
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LOCUS      BM459709
DEFINITION      AGENCOURT 6417932 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5534341
5', mRNA sequence.
ACCESSION      BM459709
VERSION      BM459709.1
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 908)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1220 row: k column: 14
High quality sequence stop: 698.
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Location/Qualifiers
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."
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Best Local Similarity 100.0%; Pred. No. 4.6e-178;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1637 GCTGAGAGTGGCGCTCGCTTGGGCATTCACAGAACCCCTGGACCCCGCTCAGAGG 1696
Db      1 GCTGAGAGTGGCGCTCGCTTGGGCATTCACAGAACCCCTGGACCCCGCTCAGAGG 60
Qy      1697 AGGCCCCAAGTCCCAATGCAGACCCCTCACTGTTGGGGTGTAGCTGGGTCTACAGTCAGA 1756
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